

Report

Assay info

Project name	F1
Assessment type	Multiple choice assessment
Multiple zones	Yes
Include arena as zone	No

Number of trials	3
Number of genotypes	3
Number of experiments	112

Track files

Total: 112 track files

[illegible]

Trial	Arena	Genotype Zone 1	Plant Zone 1	Leaf Zone 1	Genotype Zone 2	Plant Zone 2	Leaf Zone 2	Genotype Zone 3	Data file
Trial 2	29	Cur3	11	3	RMX180	16	3	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 2-30-Subject 1.txt
Trial 2	30	Cur3	13	4	RMX180	14	4	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 2-31-Subject 1.txt
Trial 2	31	Cur3	14	4	RMX180	20	4	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 2-32-Subject 1.txt
Trial 2	32	Cur3	11	4	RMX180	17	4	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 2-33-Subject 1.txt
Trial 2	33	Cur3	19	4	RMX180	11	4	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 2-34-Subject 1.txt
Trial 2	34	Cur3	17	4	RMX180	13	4	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 2-35-Subject 1.txt
Trial 2	35	Cur3	16	4	RMX180	16	4	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 2-36-Subject 1.txt
Trial 2	36	Cur3	12	4	RMX180	19	4	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 2-37-Subject 1.txt
Trial 2	37	Cur3	20	4	RMX180	15	4	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 2-38-Subject 1.txt
Trial 2	38	Cur3	18	4	RMX180	18	4	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 2-39-Subject 1.txt
Trial 2	39	Cur3	15	4	RMX180	12	4	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 2-40-Subject 1.txt
Trial 3	0	Cur3	22	1	RMX180	24	1	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-1-Subject 1.txt
Trial 3	1	Cur3	26	1	RMX180	25	1	Neutral	..\Track-Frankliniella-Arabidopsis-Trial 3-2-Subject 1.txt
Trial 3	2	Cur3	27	1	RMX180	30	1	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-3-Subject 1.txt
Trial 3	3	Cur3	21	1	RMX180	28	1	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-4-Subject 1.txt
Trial 3	4	Cur3	23	1	RMX180	22	1	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-5-Subject 1.txt
Trial 3	5	Cur3	25	1	RMX180	27	1	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-6-Subject 1.txt
Trial 3	6	Cur3	24	1	RMX180	23	1	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-7-Subject 1.txt
Trial 3	7	Cur3	28	1	RMX180	26	1	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-8-Subject 1.txt
Trial 3	8	Cur3	29	1	RMX180	21	1	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-9-Subject 1.txt
Trial 3	9	Cur3	30	2	RMX180	29	2	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-10-Subject 1.txt
Trial 3	10	Cur3	27	2	RMX180	26	2	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-11-Subject 1.txt
Trial 3	11	Cur3	29	2	RMX180	25	2	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-12-Subject 1.txt
Trial 3	12	Cur3	26	2	RMX180	21	2	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-13-Subject 1.txt
Trial 3	13	Cur3	22	2	RMX180	24	2	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-14-Subject 1.txt
Trial 3	14	Cur3	25	2	RMX180	29	2	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-15-Subject 1.txt
Trial 3	15	Cur3	23	2	RMX180	23	2	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-16-Subject 1.txt
Trial 3	16	Cur3	30	2	RMX180	27	2	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-17-Subject 1.txt
Trial 3	17	Cur3	24	2	RMX180	22	2	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-18-Subject 1.txt
Trial 3	18	Cur3	28	2	RMX180	28	2	Neutral	..\Track-Frankliniella-Arabidopsis-Trial 3-19-Subject 1.txt
Trial 3	19	Cur3	21	2	RMX180	30	2	Neutral	..\Track-Frankliniella-Arabidopsis-Trial 3-20-Subject 1.txt
Trial 3	20	Cur3	29	3	RMX180	26	3	Neutral	..\Track-Frankliniella-Arabidopsis-Trial 3-21-Subject 1.txt
Trial 3	21	Cur3	27	3	RMX180	30	3	Neutral	..\Track-Frankliniella-Arabidopsis-Trial 3-22-Subject 1.txt
Trial 3	22	Cur3	21	3	RMX180	22	3	Neutral	..\Track-Frankliniella-Arabidopsis-Trial 3-23-Subject 1.txt
Trial 3	23	Cur3	22	3	RMX180	29	3	Neutral	..\Track-Frankliniella-Arabidopsis-Trial 3-24-Subject 1.txt
Trial 3	24	Cur3	25	3	RMX180	23	3	Neutral	..\Track-Frankliniella-Arabidopsis-Trial 3-25-Subject 1.txt
Trial 3	25	Cur3	23	3	RMX180	28	3	Neutral	..\Track-Frankliniella-Arabidopsis-Trial 3-26-Subject 1.txt
Trial 3	26	Cur3	28	3	RMX180	24	3	Neutral	..\Track-Frankliniella-Arabidopsis-Trial 3-27-Subject 1.txt
Trial 3	27	Cur3	24	3	RMX180	27	3	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-28-Subject 1.txt
Trial 3	28	Cur3	30	3	RMX180	21	3	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-29-Subject 1.txt
Trial 3	29	Cur3	26	3	RMX180	25	3	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-30-Subject 1.txt
Trial 3	30	Cur3	22	4	RMX180	24	4	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-31-Subject 1.txt
Trial 3	31	Cur3	25	4	RMX180	30	4	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-32-Subject 1.txt
Trial 3	32	Cur3	27	4	RMX180	23	4	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-33-Subject 1.txt
Trial 3	33	Cur3	30	4	RMX180	29	4	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-34-Subject 1.txt
Trial 3	34	Cur3	26	4	RMX180	25	4	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-35-Subject 1.txt
Trial 3	35	Cur3	21	4	RMX180	28	4	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-36-Subject 1.txt
Trial 3	36	Cur3	24	4	RMX180	26	4	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-37-Subject 1.txt
Trial 3	37	Cur3	29	4	RMX180	27	4	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-38-Subject 1.txt
Trial 3	38	Cur3	28	4	RMX180	22	4	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-39-Subject 1.txt
Trial 3	39	Cur3	23	4	RMX180	21	4	Neutral	..\Frankliniella-Arabidopsis\Track-Frankliniella-Arabidopsis-Trial 3-40-Subject 1.txt

Event extraction

Event extraction	
Setting	Value
Look-ahead window size	4
Is-moving velocity threshold	0.025
Halting from non-detect events recovery	True

Event filters	
Filter	Settings
Filter extreme velocity events	Velocity threshold = 8

Data selection

Record filters	
Filter	Settings
Filter by inactivity	Halt duration threshold = 3600
Filter by detection percentage	Minimal detection percentage = 50
Filter by event count	Number of events = 1000

Selected trials		
Trial	Total experiments	Selected experiments
Trial 3	40	39

Selected analysis levels				
Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Total experiments	Selected experiments
Cur3	RMX180	Neutral	112	39

Behaviour statistics

Behaviour statistic	Setting	Value
Average halting duration per zone		
	Selected zones	Zone 1, Zone 2

Behaviour statistic	Setting	Value
Average halting duration per zone per hour	Data transformation	Natural logarithm
	Include in analysis	yes
	Selected hours	0, 1, 2, 3, 4, 5, 6, 7
	Selected zones	Zone 1, Zone 2
Average halting duration per zone per short/medium/long	Data transformation	Natural logarithm
	Include in analysis	yes
	Selected zones	Zone 1, Zone 2
	Event duration categories	duration < 2, 2 <= duration < 10, duration >= 10
Average movement distance per zone	Data transformation	Natural logarithm
	Include in analysis	yes
	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
Average movement distance per zone per hour	Include in analysis	yes
	Selected hours	0, 1, 2, 3, 4, 5, 6, 7
	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
Average movement duration per zone	Include in analysis	yes
	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
	Include in analysis	yes
Average movement duration per zone per hour	Selected hours	0, 1, 2, 3, 4, 5, 6, 7
	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
	Include in analysis	yes
Average movement duration per zone per short/medium/long	Selected zones	Zone 1, Zone 2
	Event duration categories	duration < 2, 2 <= duration < 5, duration >= 5
	Data transformation	Natural logarithm
	Include in analysis	yes
Average velocity per zone	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
	Include in analysis	yes
	Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Average velocity per zone per hour	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
	Include in analysis	yes
	Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Estimated distance moved per zone	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
	Include in analysis	yes
	Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Estimated distance moved per zone per hour	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
	Include in analysis	yes
	Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Estimated duration halting per zone	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
	Include in analysis	yes
	Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Estimated duration halting per zone per hour	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
	Include in analysis	yes
	Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Estimated duration halting per zone per short/medium/long	Selected zones	Zone 1, Zone 2
	Event duration categories	duration < 2, 2 <= duration < 10, duration >= 10
	Data transformation	Natural logarithm
	Include in analysis	yes
Estimated duration moving per zone	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
	Include in analysis	yes
	Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Estimated duration moving per zone per hour	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
	Include in analysis	yes
	Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Estimated duration moving per zone per short/medium/long	Selected zones	Zone 1, Zone 2
	Event duration categories	duration < 2, 2 <= duration < 5, duration >= 5
	Data transformation	Natural logarithm
	Include in analysis	yes
Estimated duration moving per zone per slow/medium/fast	Selected zones	Zone 1, Zone 2
	Velocity categories	velocity < 0.025, 0.025 <= velocity < 0.075, velocity >= 0.075
	Data transformation	Natural logarithm
	Include in analysis	yes
Halt frequency per zone	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
	Include in analysis	yes
	Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Halt frequency per zone per hour	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
	Include in analysis	yes
	Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Halt frequency per zone per short/medium/long	Selected zones	Zone 1, Zone 2
	Event duration categories	duration < 2, 2 <= duration < 10, duration >= 10
	Data transformation	Natural logarithm
	Include in analysis	yes
Movement frequency per zone	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
	Include in analysis	yes
	Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Movement frequency per zone per hour	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
	Include in analysis	yes
	Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Movement frequency per zone per short/medium/long	Selected zones	Zone 1, Zone 2
	Event duration categories	duration < 2, 2 <= duration < 5, duration >= 5
	Data transformation	Natural logarithm
	Include in analysis	yes
Movement frequency per zone per slow/medium/fast	Selected zones	Zone 1, Zone 2
	Velocity categories	velocity < 0.025, 0.025 <= velocity < 0.075, velocity >= 0.075
	Data transformation	Natural logarithm
	Include in analysis	yes
Ratio detection to total trial duration per zone	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
	Include in analysis	yes
	Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Ratio detection to total trial duration per zone per hour	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
	Include in analysis	yes
	Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Ratio halting to detection duration per zone	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
	Include in analysis	yes
	Selected hours	0, 1, 2, 3, 4, 5, 6, 7

Behaviour statistic	Setting	Value
	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
	Include in analysis	yes
Ratio halting to total trial duration per zone		
	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
	Include in analysis	yes
Ratio halting to total trial duration per zone per hour		
	Selected hours	0, 1, 2, 3, 4, 5, 6, 7
	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
	Include in analysis	yes
Ratio movement to detection duration per zone		
	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
	Include in analysis	yes
Ratio movement to detection duration per zone per hour		
	Selected hours	0, 1, 2, 3, 4, 5, 6, 7
	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
	Include in analysis	yes
Ratio movement to halting duration per zone		
	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
	Include in analysis	yes
Ratio movement to halting duration per zone per hour		
	Selected hours	0, 1, 2, 3, 4, 5, 6, 7
	Selected zones	Zone 1, Zone 2
	Data transformation	Natural logarithm
	Include in analysis	yes

Experimental design

Replicates Trial 3							
Genotype Zone 1	Plant Zone 1	Leaf Zone 1	Genotype Zone 2	Plant Zone 2	Leaf Zone 2	Genotype Zone 3	Replicates
Cur3	21	3	RMX180	22	3	Neutral	1
Cur3	21	1	RMX180	28	1	Neutral	1
Cur3	21	4	RMX180	28	4	Neutral	1
Cur3	21	2	RMX180	30	2	Neutral	1
Cur3	22	1	RMX180	24	1	Neutral	1
Cur3	22	2	RMX180	24	2	Neutral	1
Cur3	22	4	RMX180	24	4	Neutral	1
Cur3	22	3	RMX180	29	3	Neutral	1
Cur3	23	1	RMX180	22	1	Neutral	1
Cur3	23	2	RMX180	23	2	Neutral	1
Cur3	24	2	RMX180	22	2	Neutral	1
Cur3	24	1	RMX180	23	1	Neutral	1
Cur3	24	4	RMX180	26	4	Neutral	1
Cur3	24	3	RMX180	27	3	Neutral	1
Cur3	25	3	RMX180	23	3	Neutral	1
Cur3	25	1	RMX180	27	1	Neutral	1
Cur3	25	2	RMX180	29	2	Neutral	1
Cur3	25	4	RMX180	30	4	Neutral	1
Cur3	26	2	RMX180	21	2	Neutral	1
Cur3	26	1	RMX180	25	1	Neutral	1
Cur3	26	3	RMX180	25	3	Neutral	1
Cur3	26	4	RMX180	25	4	Neutral	1
Cur3	27	4	RMX180	23	4	Neutral	1
Cur3	27	2	RMX180	26	2	Neutral	1
Cur3	27	1	RMX180	30	1	Neutral	1
Cur3	27	3	RMX180	30	3	Neutral	1
Cur3	28	4	RMX180	22	4	Neutral	1
Cur3	28	3	RMX180	24	3	Neutral	1
Cur3	28	1	RMX180	26	1	Neutral	1
Cur3	28	2	RMX180	28	2	Neutral	1
Cur3	29	1	RMX180	21	1	Neutral	1
Cur3	29	2	RMX180	25	2	Neutral	1
Cur3	29	3	RMX180	26	3	Neutral	1
Cur3	29	4	RMX180	27	4	Neutral	1
Cur3	30	3	RMX180	21	3	Neutral	1
Cur3	30	2	RMX180	27	2	Neutral	1
Cur3	30	2	RMX180	29	2	Neutral	1
Cur3	30	4	RMX180	29	4	Neutral	1
Cur3	23	3	RMX180	28	3	Neutral	1

Replicates Trial 1			
Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Replicates
Replicates Trial 2			
Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Replicates

Analysis results

Date/time analysis	01-17-2019 9:57
Duration analysis run	00:03:36
EthoAnalysis version	1.3.0.6

Summary analysis zone differences

Summary of zone difference tests: p values and 95% confidence intervals of the ratio between Zone 1 (Cur3) and Zone 2 (RMX180).

Behaviour statistic	Transformation	sig	p	95% CI	Remark
Average halting duration (diff. Zone 1 - Zone 2)	Logit	**	0.00501	[1.09, 1.55]	
Average halting duration H0 (diff. Zone 1 - Zone 2)	Logit		0.375	[0.299, 1.62]	
Average halting duration H1 (diff. Zone 1 - Zone 2)	Logit		0.152	[0.895, 1.87]	CR
Average halting duration H2 (diff. Zone 1 - Zone 2)	Logit		0.126	[0.893, 2.18]	CR
Average halting duration H3 (diff. Zone 1 - Zone 2)	Logit	*	0.0145	[1.09, 1.85]	
Average halting duration H4 (diff. Zone 1 - Zone 2)	Logit		0.23	[0.883, 1.56]	
Average halting duration H5 (diff. Zone 1 - Zone 2)	Logit		0.284	[0.788, 2.06]	
Average halting duration H6 (diff. Zone 1 - Zone 2)	Logit		0.269	[0.531, 1.23]	
Average halting duration H7 (diff. Zone 1 - Zone 2)	Logit		0.955	[0.525, 1.97]	
Average halting duration duration < 2 (diff. Zone 1 - Zone 2)	Logit		0.894	[0.967, 1.03]	CR
Average halting duration duration 2 <= duration < 10 (diff. Zone 1 - Zone 2)	Logit		0.9	[0.957, 1.05]	CR
Average halting duration duration >= 10 (diff. Zone 1 - Zone 2)	Logit	***	0.000809	[1.08, 1.3]	
Average movement distance (diff. Zone 1 - Zone 2)	Logit	****	3.54E-05	[2.04, 3.83]	
Average movement distance H0 (diff. Zone 1 - Zone 2)	Logit	**	0.00403	[1.54, 5.96]	CR
Average movement distance H1 (diff. Zone 1 - Zone 2)	Logit	*	0.0122	[1.24, 3.87]	CR
Average movement distance H2 (diff. Zone 1 - Zone 2)	Logit	****	2.8E-08	[2.24, 4.21]	CR
Average movement distance H3 (diff. Zone 1 - Zone 2)	Logit	*	0.0494	[1, 3.93]	
Average movement distance H4 (diff. Zone 1 - Zone 2)	Logit	**	0.006	[1.47, 5.61]	
Average movement distance H5 (diff. Zone 1 - Zone 2)	Logit	*	0.0165	[1.22, 4.36]	
Average movement distance H6 (diff. Zone 1 - Zone 2)	Logit	***	0.000116	[1.87, 3.81]	
Average movement distance H7 (diff. Zone 1 - Zone 2)	Logit	**	0.00788	[1.31, 3.28]	
Average movement duration (diff. Zone 1 - Zone 2)	Logit	****	2.58E-11	[1.52, 1.92]	
Average movement duration H0 (diff. Zone 1 - Zone 2)	Logit	***	0.000892	[1.52, 2.73]	
Average movement duration H1 (diff. Zone 1 - Zone 2)	Logit	***	0.000126	[1.42, 2.2]	
Average movement duration H2 (diff. Zone 1 - Zone 2)	Logit	*	0.0177	[1.11, 2.3]	
Average movement duration H3 (diff. Zone 1 - Zone 2)	Logit		0.082	[0.959, 1.75]	CR
Average movement duration H4 (diff. Zone 1 - Zone 2)	Logit	**	0.00331	[1.26, 2.17]	
Average movement duration H5 (diff. Zone 1 - Zone 2)	Logit	*	0.0488	[1, 2.18]	
Average movement duration H6 (diff. Zone 1 - Zone 2)	Logit	****	3.56E-06	[1.49, 2.29]	
Average movement duration H7 (diff. Zone 1 - Zone 2)	Logit	*	0.0149	[1.1, 1.94]	
Average movement duration duration < 2 (diff. Zone 1 - Zone 2)	Logit		0.07	[0.941, 1]	CR
Average movement duration duration 2 <= duration < 5 (diff. Zone 1 - Zone 2)	Logit		0.497	[0.971, 1.01]	CR
Average movement duration duration >= 5 (diff. Zone 1 - Zone 2)	Logit	****	4.86E-11	[1.33, 1.56]	CR
Average velocity (diff. Zone 1 - Zone 2)	Logit	***	0.000461	[1.37, 2.17]	
Average velocity H0 (diff. Zone 1 - Zone 2)	Logit	*	0.0213	[1.09, 2.35]	
Average velocity H1 (diff. Zone 1 - Zone 2)	Logit		0.102	[0.909, 2.45]	
Average velocity H2 (diff. Zone 1 - Zone 2)	Logit	****	2.46E-06	[1.46, 2.23]	
Average velocity H3 (diff. Zone 1 - Zone 2)	Logit	*	0.0362	[1.04, 2.22]	
Average velocity H4 (diff. Zone 1 - Zone 2)	Logit	*	0.0193	[1.12, 2.77]	
Average velocity H5 (diff. Zone 1 - Zone 2)	Logit	*	0.0151	[1.13, 2.35]	
Average velocity H6 (diff. Zone 1 - Zone 2)	Logit	*	0.0243	[1.05, 1.82]	
Average velocity H7 (diff. Zone 1 - Zone 2)	Logit		0.12	[0.845, 3.29]	
Estimated distance moved (diff. Zone 1 - Zone 2)	Logit		0.118	[0.769, 1.04]	
Estimated distance moved H0 (diff. Zone 1 - Zone 2)	Logit		0.771	[0.681, 1.34]	

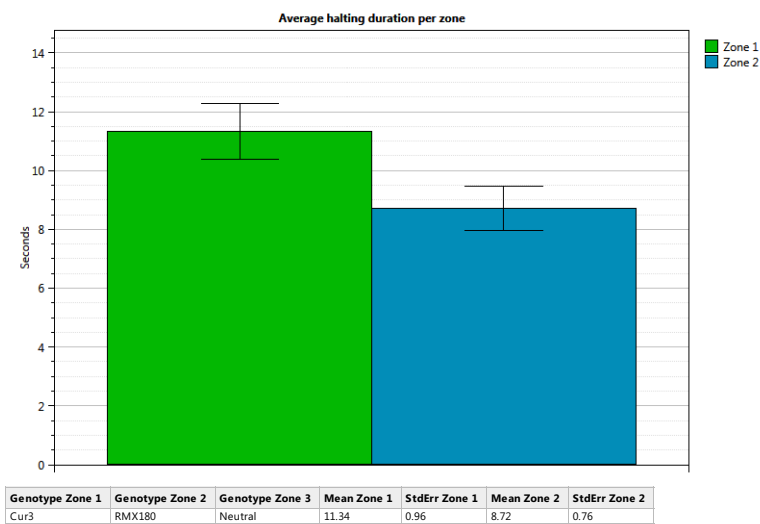
Behaviour statistic	Transformation	sig	p	95% CI	Remark
Estimated distance moved H1 (diff. Zone 1 - Zone 2)	Logit		0.309	[0.915, 1.31]	
Estimated distance moved H2 (diff. Zone 1 - Zone 2)	Logit		0.422	[0.679, 1.2]	
Estimated distance moved H3 (diff. Zone 1 - Zone 2)	Logit		0.226	[0.744, 1.07]	
Estimated distance moved H4 (diff. Zone 1 - Zone 2)	Logit		0.076	[0.565, 1.04]	
Estimated distance moved H5 (diff. Zone 1 - Zone 2)	Logit		0.0637	[0.524, 1.02]	
Estimated distance moved H6 (diff. Zone 1 - Zone 2)	Logit		0.615	[0.734, 1.2]	
Estimated distance moved H7 (diff. Zone 1 - Zone 2)	Logit		0.121	[0.492, 1.11]	
Estimated duration halting (diff. Zone 1 - Zone 2)	Logit	**	0.00476	[0.177, 0.564]	
Estimated duration halting H0 (diff. Zone 1 - Zone 2)	Logit	****	8.57E-06	[0.133, 0.416]	CR
Estimated duration halting H1 (diff. Zone 1 - Zone 2)	Logit	*	0.0355	[0.295, 0.948]	CR
Estimated duration halting H2 (diff. Zone 1 - Zone 2)	Logit		0.0822	[0.12, 1.18]	
Estimated duration halting H3 (diff. Zone 1 - Zone 2)	Logit	*	0.0362	[0.174, 0.929]	CR
Estimated duration halting H4 (diff. Zone 1 - Zone 2)	Logit	*	0.0377	[0.17, 0.926]	CR
Estimated duration halting H5 (diff. Zone 1 - Zone 2)	Logit	**	0.00532	[0.143, 0.602]	CR
Estimated duration halting H6 (diff. Zone 1 - Zone 2)	Logit	**	0.00431	[0.0696, 0.504]	CR
Estimated duration halting H7 (diff. Zone 1 - Zone 2)	Logit	**	0.00316	[0.081, 0.487]	CR
Estimated duration halting duration < 2 (diff. Zone 1 - Zone 2)	Logit	****	1.25E-05	[0.151, 0.34]	
Estimated duration halting 2 <= duration < 10 (diff. Zone 1 - Zone 2)	Logit	****	2.7E-05	[0.152, 0.35]	
Estimated duration halting duration >= 10 (diff. Zone 1 - Zone 2)	Logit	*	0.0129	[0.181, 0.727]	
Estimated duration moving (diff. Zone 1 - Zone 2)	Logit	***	0.000403	[0.375, 0.665]	CR
Estimated duration moving H0 (diff. Zone 1 - Zone 2)	Logit	*	0.0451	[0.385, 0.987]	
Estimated duration moving H1 (diff. Zone 1 - Zone 2)	Logit	*	0.0157	[0.519, 0.93]	
Estimated duration moving H2 (diff. Zone 1 - Zone 2)	Logit	**	0.00426	[0.336, 0.736]	CR
Estimated duration moving H3 (diff. Zone 1 - Zone 2)	Logit	**	0.00289	[0.362, 0.756]	
Estimated duration moving H4 (diff. Zone 1 - Zone 2)	Logit	*	0.0127	[0.19, 0.768]	CR
Estimated duration moving H5 (diff. Zone 1 - Zone 2)	Logit	**	0.00138	[0.213, 0.602]	CR
Estimated duration moving H6 (diff. Zone 1 - Zone 2)	Logit	**	0.00339	[0.302, 0.737]	
Estimated duration moving H7 (diff. Zone 1 - Zone 2)	Logit	**	0.00891	[0.242, 0.756]	CR
Estimated duration moving duration < 2 (diff. Zone 1 - Zone 2)	Logit	***	0.000274	[0.151, 0.391]	
Estimated duration moving 2 <= duration < 5 (diff. Zone 1 - Zone 2)	Logit	****	2.58E-05	[0.134, 0.33]	CR
Estimated duration moving duration >= 5 (diff. Zone 1 - Zone 2)	Logit	**	0.00275	[0.454, 0.797]	
Estimated duration moving velocity < 0.025 (diff. Zone 1 - Zone 2)	Logit	***	0.000244	[0.123, 0.349]	
Estimated duration moving 0.025 <= velocity < 0.075 (diff. Zone 1 - Zone 2)	Logit	****	5.86E-05	[0.104, 0.333]	
Estimated duration moving velocity >= 0.075 (diff. Zone 1 - Zone 2)	Logit	*	0.0102	[0.62, 0.915]	
Halt frequency (diff. Zone 1 - Zone 2)	Logit	****	7.73E-05	[0.159, 0.38]	
Halt frequency H0 (diff. Zone 1 - Zone 2)	Logit	***	0.000622	[0.142, 0.463]	CR
Halt frequency H1 (diff. Zone 1 - Zone 2)	Logit	***	0.000185	[0.156, 0.467]	
Halt frequency H2 (diff. Zone 1 - Zone 2)	Logit	**	0.00314	[0.128, 0.56]	CR
Halt frequency H3 (diff. Zone 1 - Zone 2)	Logit	**	0.00358	[0.164, 0.617]	CR
Halt frequency H4 (diff. Zone 1 - Zone 2)	Logit	**	0.00279	[0.113, 0.497]	CR
Halt frequency H5 (diff. Zone 1 - Zone 2)	Logit	***	0.000343	[0.1, 0.379]	CR
Halt frequency H6 (diff. Zone 1 - Zone 2)	Logit	***	0.000276	[0.108, 0.398]	CR
Halt frequency H7 (diff. Zone 1 - Zone 2)	Logit	**	0.00422	[0.0984, 0.501]	CR
Halt frequency duration < 2 (diff. Zone 1 - Zone 2)	Logit	****	8.17E-06	[0.152, 0.345]	CR
Halt frequency 2 <= duration < 10 (diff. Zone 1 - Zone 2)	Logit	****	2.39E-05	[0.148, 0.348]	
Halt frequency duration >= 10 (diff. Zone 1 - Zone 2)	Logit	**	0.00413	[0.167, 0.58]	
Movement frequency (diff. Zone 1 - Zone 2)	Logit	****	6E-05	[0.198, 0.426]	
Movement frequency H0 (diff. Zone 1 - Zone 2)	Logit	**	0.00131	[0.166, 0.53]	
Movement frequency H1 (diff. Zone 1 - Zone 2)	Logit	****	7.34E-06	[0.276, 0.566]	
Movement frequency H2 (diff. Zone 1 - Zone 2)	Logit	**	0.00204	[0.177, 0.572]	CR
Movement frequency H3 (diff. Zone 1 - Zone 2)	Logit	**	0.00195	[0.221, 0.626]	
Movement frequency H4 (diff. Zone 1 - Zone 2)	Logit	**	0.00322	[0.134, 0.548]	CR
Movement frequency H5 (diff. Zone 1 - Zone 2)	Logit	***	0.000302	[0.128, 0.418]	CR
Movement frequency H6 (diff. Zone 1 - Zone 2)	Logit	****	2.16E-06	[0.151, 0.413]	CR
Movement frequency H7 (diff. Zone 1 - Zone 2)	Logit	**	0.00281	[0.119, 0.533]	CR
Movement frequency duration < 2 (diff. Zone 1 - Zone 2)	Logit	***	0.000342	[0.155, 0.403]	
Movement frequency 2 <= duration < 5 (diff. Zone 1 - Zone 2)	Logit	****	2.7E-05	[0.133, 0.33]	CR
Movement frequency duration >= 5 (diff. Zone 1 - Zone 2)	Logit	***	0.000128	[0.307, 0.583]	
Movement frequency velocity < 0.025 (diff. Zone 1 - Zone 2)	Logit	****	5.69E-05	[0.152, 0.384]	CR
Movement frequency 0.025 <= velocity < 0.075 (diff. Zone 1 - Zone 2)	Logit	****	7.51E-05	[0.122, 0.333]	
Movement frequency velocity >= 0.075 (diff. Zone 1 - Zone 2)	Logit	****	3.56E-05	[0.408, 0.626]	
Ratio detection to total trial duration (diff. Zone 1 - Zone 2)	Logit	**	0.00172	[0.27, 0.582]	
Ratio detection to total trial duration H0 (diff. Zone 1 - Zone 2)	Logit	***	0.000125	[0.278, 0.633]	CR
Ratio detection to total trial duration H1 (diff. Zone 1 - Zone 2)	Logit	*	0.0181	[0.422, 0.918]	
Ratio detection to total trial duration H2 (diff. Zone 1 - Zone 2)	Logit	*	0.0191	[0.267, 0.859]	CR
Ratio detection to total trial duration H3 (diff. Zone 1 - Zone 2)	Logit	*	0.013	[0.269, 0.817]	CR
Ratio detection to total trial duration H4 (diff. Zone 1 - Zone 2)	Logit	*	0.02	[0.199, 0.819]	CR
Ratio detection to total trial duration H5 (diff. Zone 1 - Zone 2)	Logit	****	3.09E-05	[0.198, 0.523]	CR
Ratio detection to total trial duration H6 (diff. Zone 1 - Zone 2)	Logit	****	3.4E-05	[0.19, 0.516]	CR
Ratio detection to total trial duration H7 (diff. Zone 1 - Zone 2)	Logit	**	0.00444	[0.156, 0.587]	CR
Ratio halting to detection duration (diff. Zone 1 - Zone 2)	Logit	*	0.0291	[0.711, 0.976]	
Ratio halting to detection duration H0 (diff. Zone 1 - Zone 2)	Logit	*	0.0322	[0.482, 0.961]	
Ratio halting to detection duration H1 (diff. Zone 1 - Zone 2)	Logit	*	0.0484	[0.573, 0.998]	
Ratio halting to detection duration H2 (diff. Zone 1 - Zone 2)	Logit		0.244	[0.52, 1.22]	
Ratio halting to detection duration H3 (diff. Zone 1 - Zone 2)	Logit		0.432	[0.586, 1.3]	
Ratio halting to detection duration H4 (diff. Zone 1 - Zone 2)	Logit		0.197	[0.601, 1.12]	
Ratio halting to detection duration H5 (diff. Zone 1 - Zone 2)	Logit		0.198	[0.558, 1.15]	
Ratio halting to detection duration H6 (diff. Zone 1 - Zone 2)	Logit	**	0.00164	[0.403, 0.789]	
Ratio halting to detection duration H7 (diff. Zone 1 - Zone 2)	Logit	*	0.0326	[0.349, 0.944]	
Ratio halting to total trial duration (diff. Zone 1 - Zone 2)	Logit	***	0.000283	[0.234, 0.532]	
Ratio halting to total trial duration H0 (diff. Zone 1 - Zone 2)	Logit	****	5.49E-05	[0.188, 0.527]	CR
Ratio halting to total trial duration H1 (diff. Zone 1 - Zone 2)	Logit	**	0.00827	[0.325, 0.837]	CR
Ratio halting to total trial duration H2 (diff. Zone 1 - Zone 2)	Logit	*	0.0124	[0.213, 0.778]	CR
Ratio halting to total trial duration H3 (diff. Zone 1 - Zone 2)	Logit	*	0.0315	[0.273, 0.926]	CR
Ratio halting to total trial duration H4 (diff. Zone 1 - Zone 2)	Logit	**	0.00968	[0.199, 0.742]	CR
Ratio halting to total trial duration H5 (diff. Zone 1 - Zone 2)	Logit	**	0.006	[0.179, 0.68]	CR
Ratio halting to total trial duration H6 (diff. Zone 1 - Zone 2)	Logit	***	0.000819	[0.121, 0.467]	CR
Ratio halting to total trial duration H7 (diff. Zone 1 - Zone 2)	Logit	**	0.00404	[0.156, 0.622]	CR
Ratio movement to detection duration (diff. Zone 1 - Zone 2)	Logit	**	0.00335	[1.07, 1.36]	
Ratio movement to detection duration H0 (diff. Zone 1 - Zone 2)	Logit	**	0.0076	[1.06, 1.45]	CR
Ratio movement to detection duration H1 (diff. Zone 1 - Zone 2)	Logit	*	0.0233	[1.03, 1.39]	
Ratio movement to detection duration H2 (diff. Zone 1 - Zone 2)	Logit	**	0.00569	[1.08, 1.54]	
Ratio movement to detection duration H3 (diff. Zone 1 - Zone 2)	Logit		0.844	[0.803, 1.2]	
Ratio movement to detection duration H4 (diff. Zone 1 - Zone 2)	Logit		0.166	[0.917, 1.54]	
Ratio movement to detection duration H5 (diff. Zone 1 - Zone 2)	Logit		0.367	[0.827, 1.59]	
Ratio movement to detection duration H6 (diff. Zone 1 - Zone 2)	Logit	*	0.0353	[1.02, 1.78]	
Ratio movement to detection duration H7 (diff. Zone 1 - Zone 2)	Logit		0.441	[0.778, 1.66]	
Ratio movement to halting duration (diff. Zone 1 - Zone 2)	Logit	**	0.00183	[1.31, 2.33]	
Ratio movement to halting duration H0 (diff. Zone 1 - Zone 2)	Logit	*	0.0143	[1.29, 6.37]	
Ratio movement to halting duration H1 (diff. Zone 1 - Zone 2)	Logit		0.142	[0.732, 6.21]	
Ratio movement to halting duration H2 (diff. Zone 1 - Zone 2)	Logit		0.0535	[0.984, 5.34]	
Ratio movement to halting duration H3 (diff. Zone 1 - Zone 2)	Logit		0.196	[0.678, 5.51]	
Ratio movement to halting duration H4 (diff. Zone 1 - Zone 2)	Logit		0.204	[0.672, 5.05]	
Ratio movement to halting duration H5 (diff. Zone 1 - Zone 2)	Logit		0.0525	[0.985, 6.87]	
Ratio movement to halting duration H6 (diff. Zone 1 - Zone 2)	Logit	****	1.31E-05	[2.37, 6.83]	
Ratio movement to halting duration H7 (diff. Zone 1 - Zone 2)	Logit		0.087	[0.84, 7.22]	

(p ≤ 0.05)*, (p ≤ 0.01)**, (p ≤ 0.001)***, (p ≤ 0.0001)****
CR = Check residuals

Behaviour statistic correlation analysis

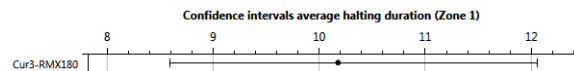
Spearman rank correlation matrix

Data summary



Analysis average halting duration (Zone 1)

Analysis model	Linear mixed model fit by REML: Average_halting_duration_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	10.18	8.589	12.06	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_halting_duration_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 51.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.2956	-0.6483	-0.1858	0.4395	2.3936

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000000	0.00000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.003947	0.06282
Residual		0.202193	0.44966

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

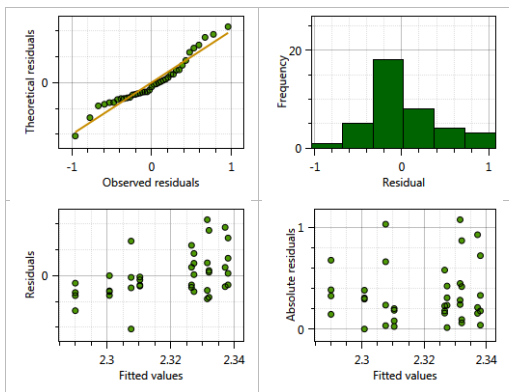
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	2.32015	0.07471	8.78456	31.06	2.75e-10 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

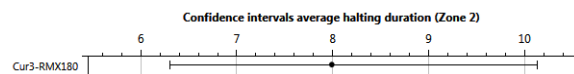
Model residuals

Statistic	Value
Sample skewness	0.5706
Sample excess kurtosis	0.5048
Passed Shapiro Wilk normality test	Yes (p-value = 0.07023 > 0.05)



Analysis average halting duration (Zone 2)

Analysis model	Linear mixed model fit by REML: Average_halting_duration_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	7.991	6.299	10.14	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_halting_duration_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 40.5

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.4660	-0.6630	-0.1507	0.4058	3.2737

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.013011	0.11407
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.007342	0.08568
Residual		0.137537	0.37086

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

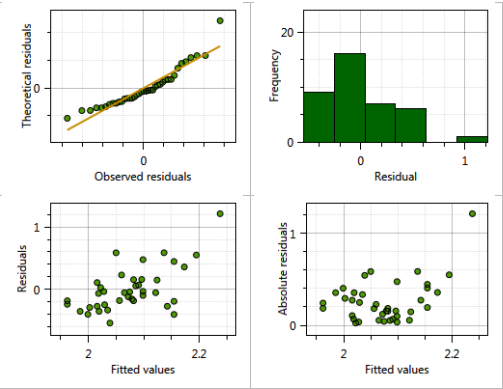
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	2.07828	0.07464	2.99431	27.84	0.000103 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

Statistic	Value
Sample skewness	1.319
Sample excess kurtosis	2.428
Passed Shapiro Wilk normality test	No (p-value = 0.003259 < 0.05)

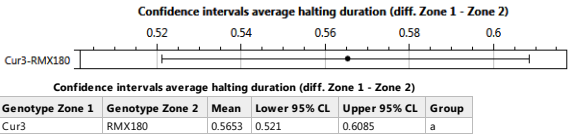


Data points with high residuals

Trial	Arena
Trial 3	12

Analysis average halting duration (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_halting_duration_Zone_1,Average_halting_duration_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 68.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.14144	-0.46288	-0.04596	0.53432	2.16217

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000	0.000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000	0.000
Residual		1.494	1.222

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

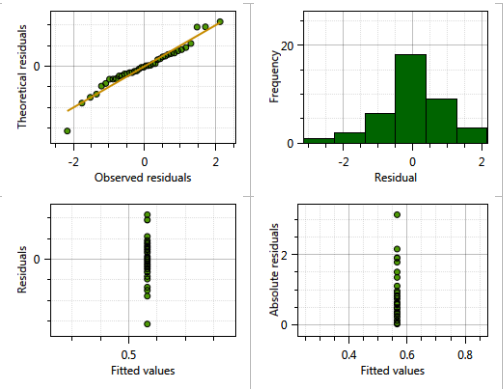
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.26270	0.08816	38.00000	2.98	0.00501 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 1.222

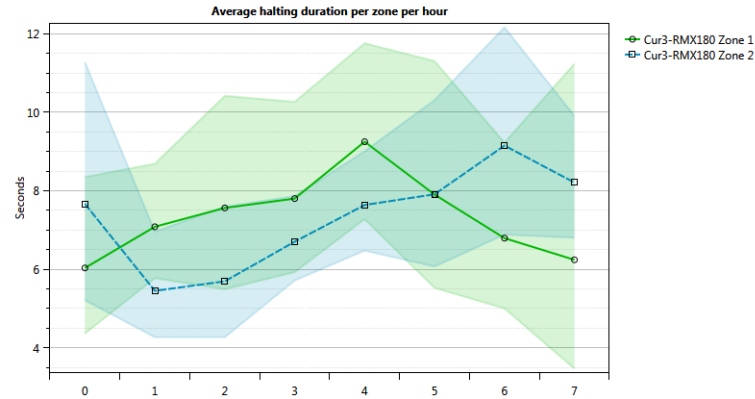
Model residuals

Statistic	Value
Sample skewness	-0.3915
Sample excess kurtosis	1.938
Passed Shapiro Wilk normality test	Yes (p-value = 0.1407 > 0.05)



Average halting duration per zone per hour

Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



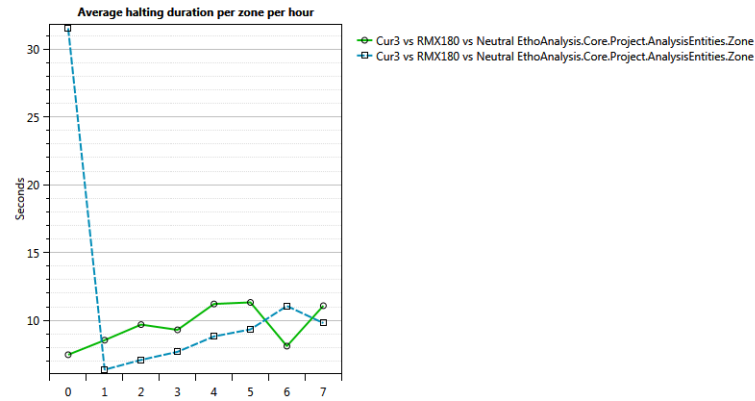
Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.		
Behaviour statistic	Cur3-RMX180	Remark
Average halting duration H0 (diff. Zone 1 - Zone 2)	p=0.375 [-1.21, 0.483]	
Average halting duration H1 (diff. Zone 1 - Zone 2)	p=0.152 [-0.111, 0.629]	CR
Average halting duration H2 (diff. Zone 1 - Zone 2)	p=0.126 [-0.113, 0.779]	CR
Average halting duration H3 (diff. Zone 1 - Zone 2)	p=0.0145* [0.0848, 0.614]	
Average halting duration H4 (diff. Zone 1 - Zone 2)	p=0.23 [-0.125, 0.448]	
Average halting duration H5 (diff. Zone 1 - Zone 2)	p=0.284 [-0.238, 0.722]	
Average halting duration H6 (diff. Zone 1 - Zone 2)	p=0.269 [-0.634, 0.204]	
Average halting duration H7 (diff. Zone 1 - Zone 2)	p=0.955 [-0.644, 0.678]	

CR = Check residuals

The model predictions and 95% confidence intervals for each statistic.		
Statistic	Cur3-RMX180	Remark
Average halting duration (H0 - Zone 1)	6.03 [4.36, 8.35]	
Average halting duration (H0 - Zone 2)	7.67 [5.21, 11.3]	CR
Average halting duration (H1 - Zone 1)	7.08 [5.77, 8.69]	
Average halting duration (H1 - Zone 2)	5.45 [4.27, 6.96]	CR
Average halting duration (H2 - Zone 1)	7.56 [5.49, 10.4]	
Average halting duration (H2 - Zone 2)	5.69 [4.27, 7.6]	CR
Average halting duration (H3 - Zone 1)	7.8 [5.93, 10.3]	CR
Average halting duration (H3 - Zone 2)	6.7 [5.71, 7.87]	CR
Average halting duration (H4 - Zone 1)	9.25 [7.28, 11.8]	
Average halting duration (H4 - Zone 2)	7.64 [6.48, 9.01]	CR
Average halting duration (H5 - Zone 1)	7.9 [5.53, 11.3]	CR
Average halting duration (H5 - Zone 2)	7.91 [6.07, 10.3]	
Average halting duration (H6 - Zone 1)	6.79 [5, 9.23]	
Average halting duration (H6 - Zone 2)	9.15 [6.88, 12.2]	
Average halting duration (H7 - Zone 1)	6.24 [3.47, 11.2]	
Average halting duration (H7 - Zone 2)	8.21 [6.8, 9.91]	

CR = Check residuals

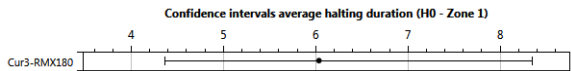
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean H0 - Zone 1	StdErr H0 - Zone 1	Mean H0 - Zone 2	StdErr H0 - Zone 2	Mean H1 - Zone 1	StdErr H1 - Zone 1	Mean H1 - Zone 2	StdErr H1 - Zone 2	Mean H2 - Zone 1	StdErr H2 - Zone 1	Mean H2 - Zone 2	StdErr H2 - Zone 2	Mean H3 - Zone 1	StdErr H3 - Zone 1	Mean H3 - Zone 2	StdErr H3 - Zone 2	Mean H4 - Zone 1	StdErr H4 - Zone 1	Mean H4 - Zone 2	StdErr H4 - Zone 2	Mean H5 - Zone 1	StdErr H5 - Zone 1	Mean H5 - Zone 2	StdErr H5 - Zone 2	Mean H6 - Zone 1	StdErr H6 - Zone 1	Mean H6 - Zone 2	StdErr H6 - Zone 2
Cur3	RMX180	Neutral	7.47	0.99	31.53	23.15	8.54	1.01	6.36	0.65	9.69	1.27	7.09	0.76	9.3	0.83	7.68	0.78	11.21	1.41	8.82	0.98	11.33	1.72	9.33	0.98	8.1	1.03	11.06	1.39

Analysis average halting duration (H0 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_halting_duration_H0_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals average halting duration (H0 - Zone 1)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	6.035	4.362	8.35	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_halting_duration_H0_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 71.1

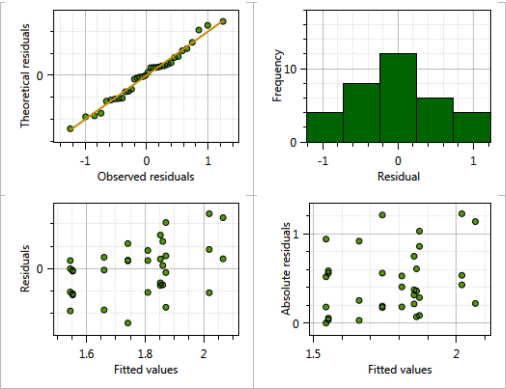
Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.92583 -0.76676  0.05571  0.44182  1.94882

Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.0782   0.2796
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.0000   0.0000
Residual                                0.3950   0.6285
Number of obs: 34, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    1.7976     0.1401  7.7753   12.83 1.65e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

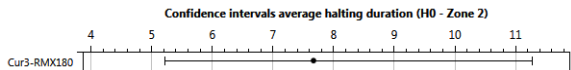
Model residuals

Statistic	Value
Sample skewness	0.07507
Sample excess kurtosis	-0.2603
Passed Shapiro Wilk normality test	Yes (p-value = 0.743 > 0.05)



Analysis average halting duration (H0 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_halting_duration_H0_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals average halting duration (H0 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	7.668	5.212	11.28	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_halting_duration_H0_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 105.8

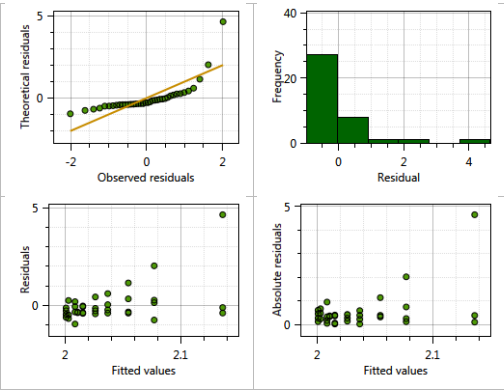
Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.0101 -0.4218 -0.2981  0.1139  4.8864

Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  2.175e-02  1.475e-01
Genotype_Zone_2:Plant_Zone_2 (Intercept)  3.881e-15  6.230e-08
Residual                                9.057e-01  9.517e-01
Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    2.0370     0.1613  6.6202   12.62 7.08e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model residuals

Statistic	Value
Sample skewness	3.682
Sample excess kurtosis	16.46
Passed Shapiro Wilk normality test	No (p-value = 6.594E-09 < 0.05)

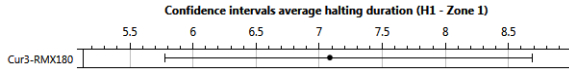


Data points with high residuals

Trial	Arena
Trial 3	25

Analysis average halting duration (H1 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_halting_duration_H1_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	7.084	5.775	8.69	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_halting_duration_H1_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + Genotype_Zone_2:Plant_Zone_2 (1 |
Data: data

REML criterion at convergence: 67.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.41261	-0.76989	-0.00741	0.49657	2.54776

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		0.3647	0.6039

Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

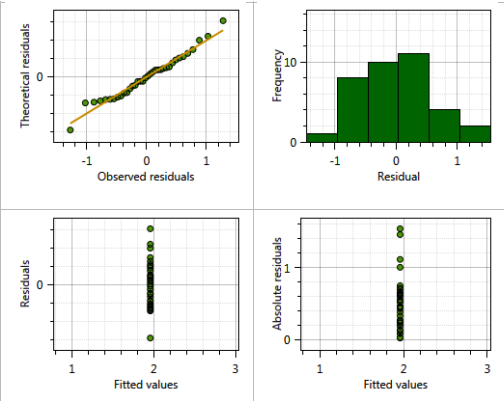
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	1.9578	0.1007	35.0000	19.45	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

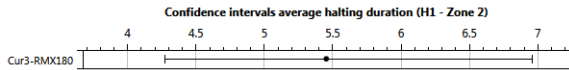
Model residuals

Statistic	Value
Sample skewness	0.2652
Sample excess kurtosis	0.4891
Passed Shapiro Wilk normality test	Yes (p-value = 0.7121 > 0.05)



Analysis average halting duration (H1 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_halting_duration_H1_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	5.452	4.27	6.961	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_halting_duration_H1_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + Genotype_Zone_2:Plant_Zone_2 (1 |
Data: data

REML criterion at convergence: 75.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-----	----	--------	----	-----

-4.4738 -0.1726 0.0960 0.4564 2.4451

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0140	0.1183
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		0.3952	0.6287

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

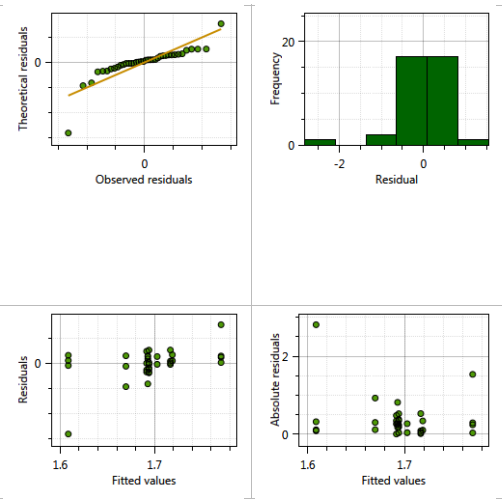
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	1.6960	0.1087	9.3867	15.6	4.99e-08 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

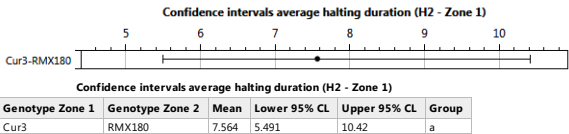
Model residuals

Statistic	Value
Sample skewness	-2.325
Sample excess kurtosis	11.79
Passed Shapiro Wilk normality test	No (p-value = 1.133E-06 < 0.05)



Analysis average halting duration (H2 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_halting_duration_H2_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_halting_duration_H2_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 77.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.4858	-0.7845	-0.1022	0.6327	1.8255

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.066548	0.25797
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.001158	0.03404
Residual		0.435447	0.65988

Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

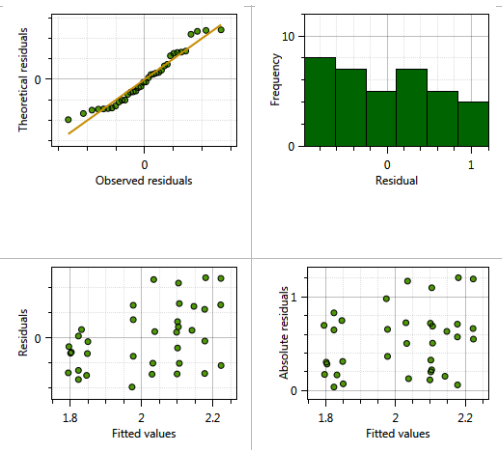
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	2.023	0.138	7.705	14.67	6.63e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

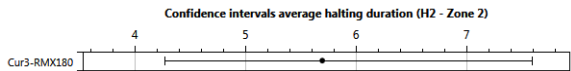
Model residuals

Statistic	Value
Sample skewness	0.4355
Sample excess kurtosis	-0.7754
Passed Shapiro Wilk normality test	Yes (p-value = 0.07148 > 0.05)



Analysis average halting duration (H2 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_halting_duration_H2_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals average halting duration (H2 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	5.694	4.269	7.596	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_halting_duration_H2_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 89.8

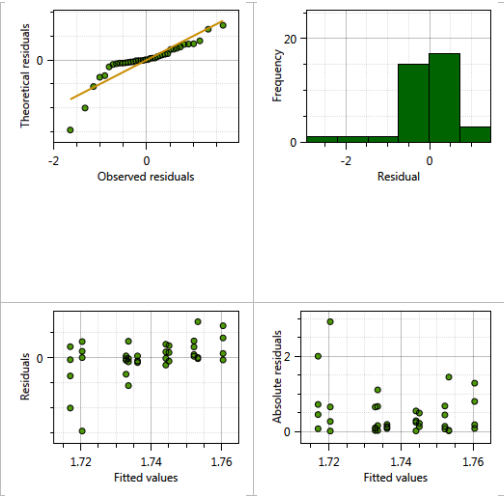
Scaled residuals:
    Min       1Q   Median       3Q      Max
-3.7883 -0.1618  0.0192  0.5143  1.8772

Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.000000 0.00000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.005714 0.07559
Residual                                0.595878 0.77193
Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   1.7395     0.1275 9.0543   13.64 2.41e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

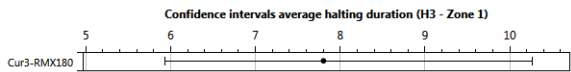
Model residuals

Statistic	Value
Sample skewness	-1.761
Sample excess kurtosis	5.815
Passed Shapiro Wilk normality test	No (p-value = 3.917E-05 < 0.05)



Analysis average halting duration (H3 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_halting_duration_H3_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals average halting duration (H3 - Zone 1)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	7.802	5.928	10.27	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_halting_duration_H3_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 69.9

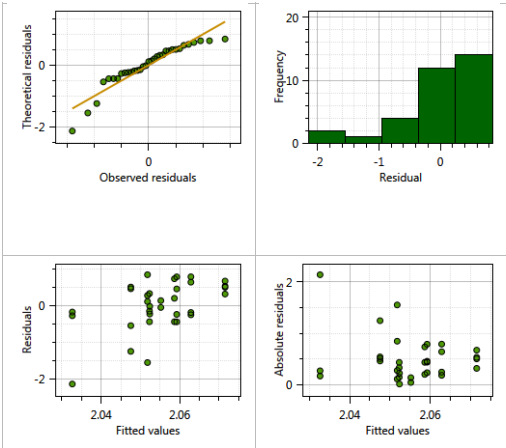
Scaled residuals:
    Min       1Q   Median       3Q      Max
-3.1427 -0.3646  0.1673  0.7421  1.2457

Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.000000 0.00000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.003903 0.06247
Residual                                0.462812 0.68030
Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   2.0544     0.1202 8.4241   17.1 7.78e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

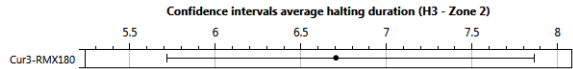
Model residuals

Statistic	Value
Sample skewness	-1.351
Sample excess kurtosis	2.345
Passed Shapiro Wilk normality test	No (p-value = 0.002548 < 0.05)



Analysis average halting duration (H3 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_halting_duration_H3_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	6.704	5.715	7.865	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_halting_duration_H3_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 57.7

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.7503	-0.5595	-0.3436	0.6613	2.6563

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000e+00	0.000e+00
Genotype_Zone_2:Plant_Zone_2	(Intercept)	3.843e-15	6.199e-08
Residual		2.428e-01	4.928e-01

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

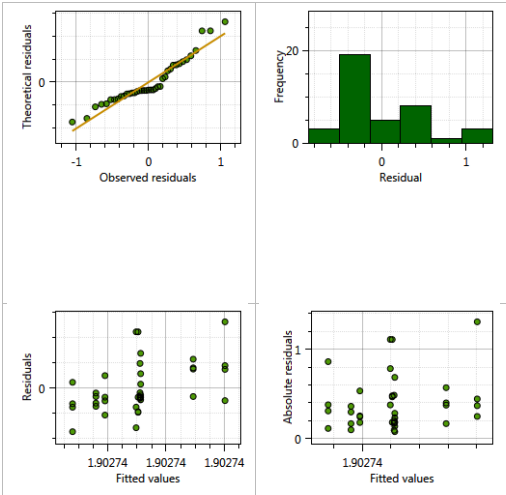
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	1.9027	0.0789	38.0000	24.11	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

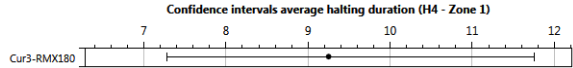
Model residuals

Statistic	Value
Sample skewness	0.9489
Sample excess kurtosis	0.7666
Passed Shapiro Wilk normality test	No (p-value = 0.005579 < 0.05)



Analysis average halting duration (H4 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_halting_duration_H4_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	9.25	7.276	11.76	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_halting_duration_H4_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

```
REML criterion at convergence: 57

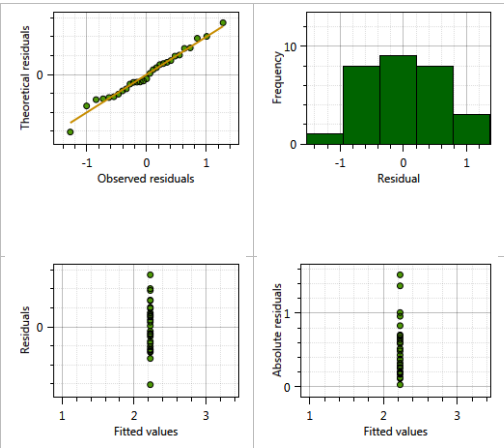
Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.4115 -0.6861 -0.1794  0.5850  2.1743

Random effects:
Groups:                               Name      Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0000   0.000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.0000   0.000
Residual                                0.3981   0.631
Number of obs: 29, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   2.2246     0.1172 28.0000   18.99  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

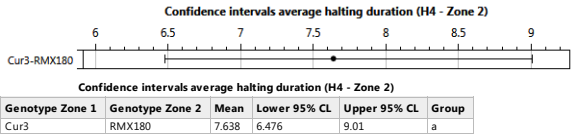
Model residuals

Statistic	Value
Sample skewness	0.02392
Sample excess kurtosis	0.1875
Passed Shapiro Wilk normality test	Yes (p-value = 0.9624 > 0.05)



Analysis average halting duration (H4 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_halting_duration_H4_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_halting_duration_H4_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 55.2

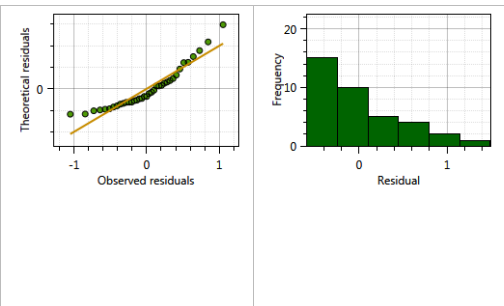
Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.1936 -0.6855 -0.3604  0.3866  3.0120

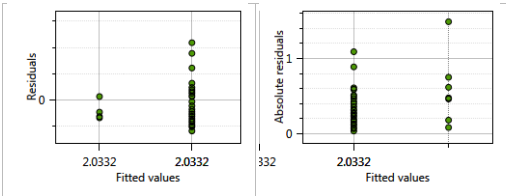
Random effects:
Groups:                               Name      Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 7.258e-17 8.520e-09
Genotype_Zone_2:Plant_Zone_2 (Intercept) 1.758e-19 4.192e-10
Residual                                2.452e-01 4.952e-01
Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   2.0332     0.0814 36.0000   24.98  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model residuals

Statistic	Value
Sample skewness	1.233
Sample excess kurtosis	1.235
Passed Shapiro Wilk normality test	No (p-value = 0.00169 < 0.05)



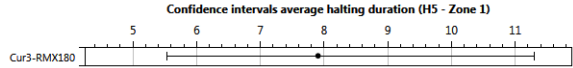


Data points with high residuals

Trial	Arena
Trial 3	12

Analysis average halting duration (H5 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_halting_duration_H5_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	7.904	5.527	11.3	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_halting_duration_H5_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 87.1

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.3539	-0.3992	0.0251	0.5901	1.6529

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		0.9514	0.9754

Number of obs: 31, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

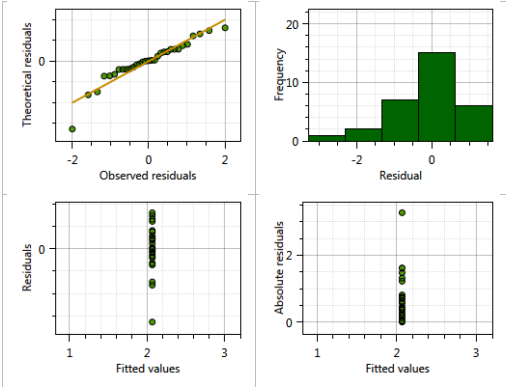
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	2.0674	0.1752	30.0000	11.8	8.46e-13 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

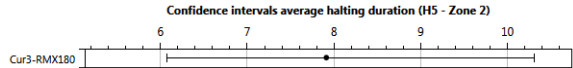
Model residuals

Statistic	Value
Sample skewness	-1.168
Sample excess kurtosis	3.199
Passed Shapiro Wilk normality test	No (p-value = 0.02326 < 0.05)



Analysis average halting duration (H5 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_halting_duration_H5_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	7.912	6.07	10.31	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_halting_duration_H5_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 67.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.5492	-0.7561	-0.2024	0.6358	2.3580

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.02478	0.1574
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.02724	0.1651
Residual		0.27123	0.5208

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

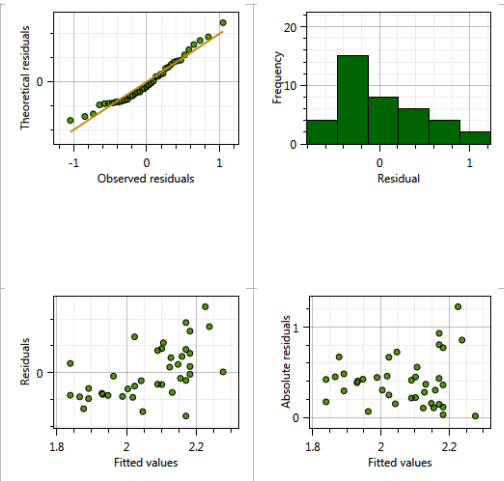
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	2.0683	0.1104	6.5128	18.74	6.55e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

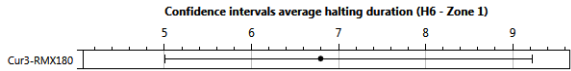
Model residuals

Statistic	Value
Sample skewness	0.6097
Sample excess kurtosis	-0.2208
Passed Shapiro Wilk normality test	Yes (p-value = 0.162 > 0.05)



Analysis average halting duration (H6 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_halting_duration_H6_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	6.794	5.002	9.228	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_halting_duration_H6_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 47.7

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.5281	-0.5942	-0.2682	0.7055	1.9203

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.07038	0.2653
Residual		0.27041	0.5200

Number of obs: 27, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

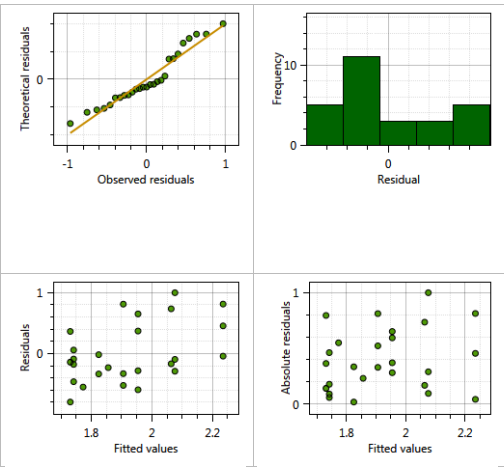
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	1.9160	0.1336	8.2849	14.34	3.87e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

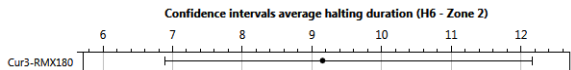
Model residuals

Statistic	Value
Sample skewness	0.6113
Sample excess kurtosis	-0.5554
Passed Shapiro Wilk normality test	Yes (p-value = 0.06944 > 0.05)



Analysis average halting duration (H6 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_halting_duration_H6_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals average halting duration (H6 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	9.151	6.884	12.16	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_halting_duration_H6_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 69.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.7740	-0.6720	-0.1559	0.6015	2.7034

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.002518	0.05018
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.043334	0.20817
Residual		0.314569	0.56086

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

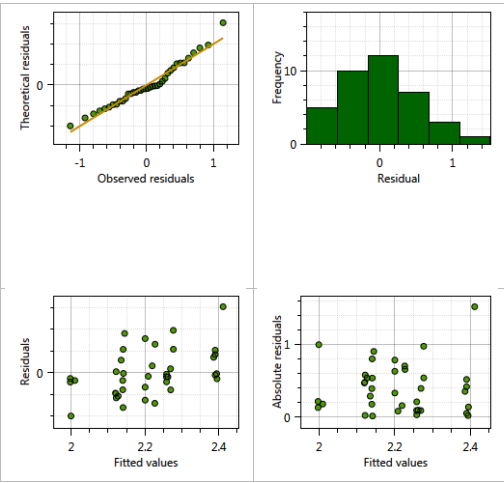
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	2.2139	0.1136	5.4627	19.49	2.93e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

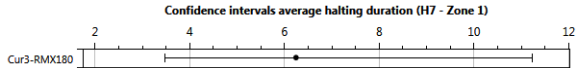
Model residuals

Statistic	Value
Sample skewness	0.6789
Sample excess kurtosis	0.5566
Passed Shapiro Wilk normality test	Yes (p-value = 0.2945 > 0.05)



Analysis average halting duration (H7 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_halting_duration_H7_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals average halting duration (H7 - Zone 1)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	6.243	3.468	11.24	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_halting_duration_H7_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 75.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.55025	-0.37595	0.06307	0.41382	1.96696

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.2337	0.4834
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.1517	0.3895
Residual		0.6678	0.8172

Number of obs: 27, groups: Genotype_Zone_2:Plant_Zone_2, 10; Genotype_Zone_1:Plant_Zone_1, 9

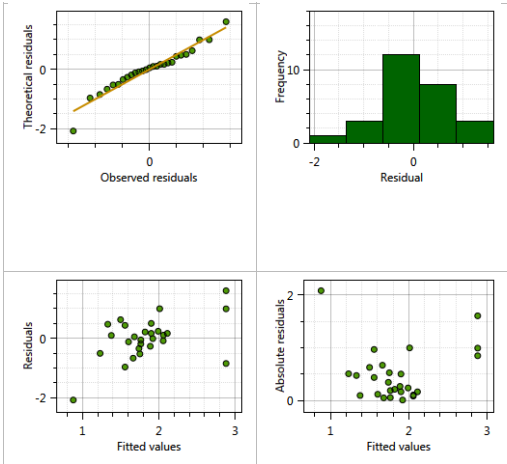
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	1.8314	0.2622	9.5852	6.984	4.69e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

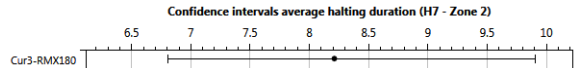
Model residuals

Statistic	Value
Sample skewness	-0.5238
Sample excess kurtosis	2.302
Passed Shapiro Wilk normality test	Yes (p-value = 0.2957 > 0.05)



Analysis average halting duration (H7 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_halting_duration_H7_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals average halting duration (H7 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	8.21	6.803	9.908	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_halting_duration_H7_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 70.1

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.58238	-0.79765	-0.02972	0.65364	2.66451

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000e+00	0.000e+00
Genotype_Zone_2:Plant_Zone_2	(Intercept)	5.189e-17	7.204e-09
Residual		3.362e-01	5.798e-01

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

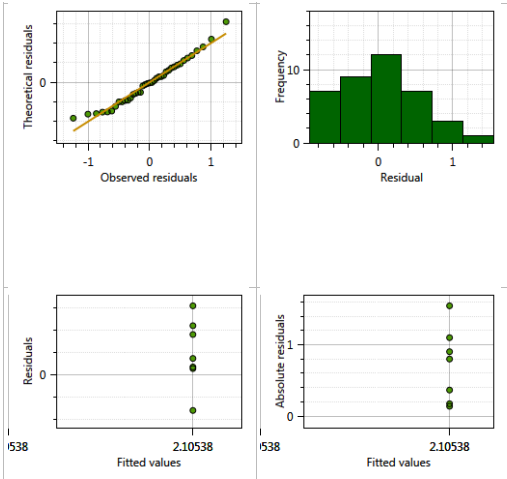
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	2.10538	0.09285	38.00000	22.68	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

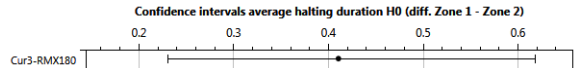
Model residuals

Statistic	Value
Sample skewness	0.4867
Sample excess kurtosis	-0.04724
Passed Shapiro Wilk normality test	Yes (p-value = 0.411 > 0.05)



Analysis average halting duration H0 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_halting_duration_H0_Zone_1,Average_halting_duration_H0_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals average halting duration H0 (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4104	0.2301	0.6184	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziformula
Data: data

Weights: wi

REML criterion at convergence: 117

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.6038	-0.4878	0.1438	0.6131	1.6180

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.5205	0.7214
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.7290	0.8538
Residual		3.6078	1.8994

Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

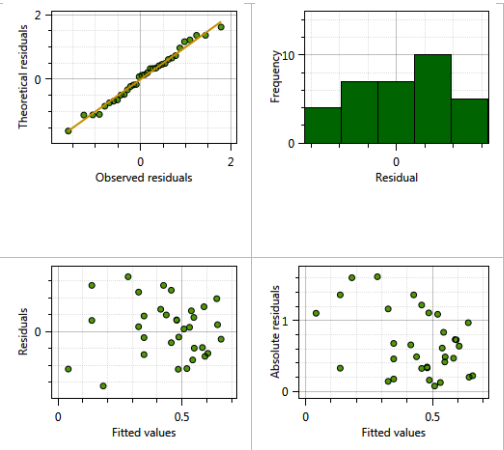
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.3623	0.3966	15.0184	-0.913	0.375

Dispersion: 1.899

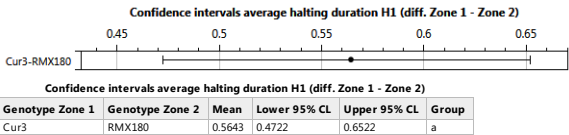
Model residuals

Statistic	Value
Sample skewness	-0.05106
Sample excess kurtosis	-0.6438
Passed Shapiro Wilk normality test	Yes (p-value = 0.8327 > 0.05)



Analysis average halting duration H1 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_halting_duration_H1_Zone_1,Average_halting_duration_H1_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: ziFormula

Data: data

Weights: wi

REML criterion at convergence: 90.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.3289	-0.5574	-0.1687	0.2065	2.8032

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.09854	0.3139
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.00000	0.0000
Residual		2.28479	1.5116

Number of obs: 35, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

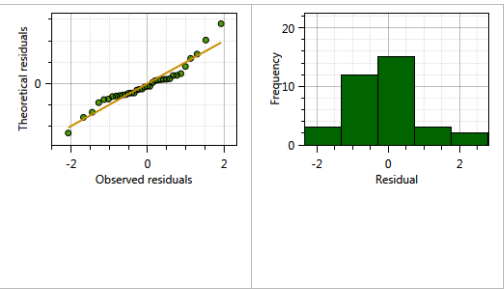
Fixed effects:

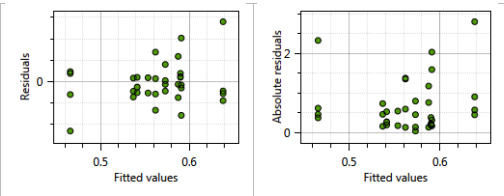
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.2586	0.1680	10.9647	1.539	0.152

Dispersion: 1.512

Model residuals

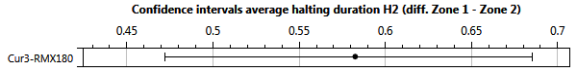
Statistic	Value
Sample skewness	0.7441
Sample excess kurtosis	2.376
Passed Shapiro Wilk normality test	No (p-value = 0.03246 < 0.05)





Analysis average halting duration H2 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_halting_duration_H2_Zone_1,Average_halting_duration_H2_Zone_2) ~ 1 + (1 Genotype_Zone_1 Plant_Zone_1) + (1 Genotype_Zone_2 Plant_Zone_2)
Transformation	Logit



Confidence intervals average halting duration H2 (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5825	0.4719	0.6854	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 92.3

Scaled residuals:
Min 1Q Median 3Q Max
-1.3563 -0.6502 -0.2767 0.1186 2.4838

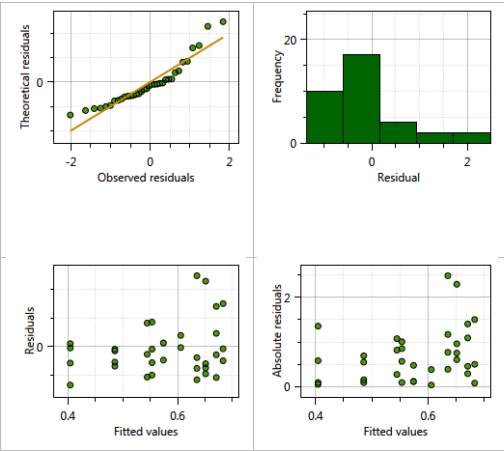
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.2282 0.4777
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.0000 0.0000
Residual 2.1641 1.4711
Number of obs: 35, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 0.3330 0.1987 9.5356 1.676 0.126

Dispersion: 1.471

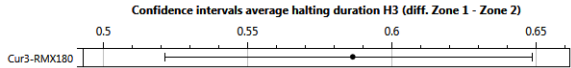
Model residuals

Statistic	Value
Sample skewness	1.284
Sample excess kurtosis	1.56
Passed Shapiro Wilk normality test	No (p-value = 0.002221 < 0.05)



Analysis average halting duration H3 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_halting_duration_H3_Zone_1,Average_halting_duration_H3_Zone_2) ~ 1 + (1 Genotype_Zone_1 Plant_Zone_1) + (1 Genotype_Zone_2 Plant_Zone_2)
Transformation	Logit



Confidence intervals average halting duration H3 (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5864	0.5212	0.6488	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 71.3

Scaled residuals:
Min 1Q Median 3Q Max
-2.17619 -0.60581 -0.00441 0.64222 1.40181

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.006669 0.08167
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.000000 0.00000
Residual 1.721786 1.31217
Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

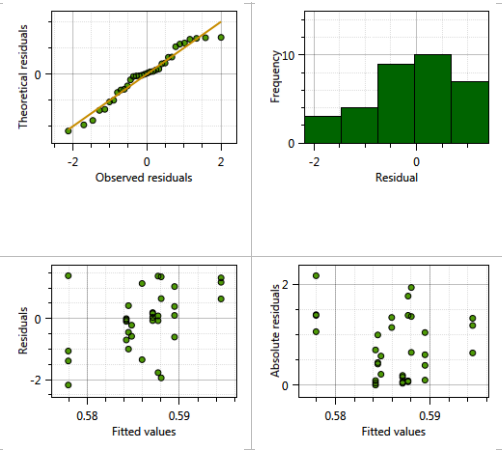
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 0.3492 0.1195 10.5588 2.922 0.0145 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 1.312

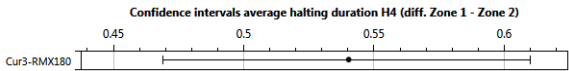
Model residuals

Statistic	Value
Sample skewness	-0.3546
Sample excess kurtosis	-0.4697
Passed Shapiro Wilk normality test	Yes (p-value = 0.194 > 0.05)



Analysis average halting duration H4 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_halting_duration_H4_Zone_1,Average_halting_duration_H4_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



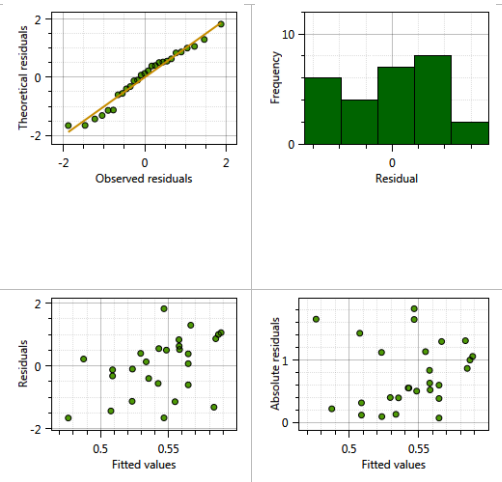
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5403	0.4688	0.6101	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi
REML criterion at convergence: 48.8
Scaled residuals:
Min 1Q Median 3Q Max
-1.6572 -0.5782 0.1341 0.5940 1.8245
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.004435 0.06659
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.045816 0.21405
Residual 1.173738 1.08339
Number of obs: 27, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 0.1615 0.1244 8.0931 1.298 0.23
Dispersion: 1.083

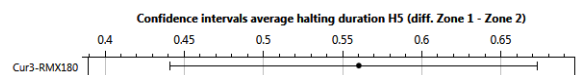
Model residuals

Statistic	Value
Sample skewness	-0.2447
Sample excess kurtosis	-0.6918
Passed Shapiro Wilk normality test	Yes (p-value = 0.4638 > 0.05)



Analysis average halting duration H5 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_halting_duration_H5_Zone_1,Average_halting_duration_H5_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals average halting duration H5 (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5602	0.4407	0.6731	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 85.2

Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.0323 -0.7033 -0.2510  0.4618  1.7943

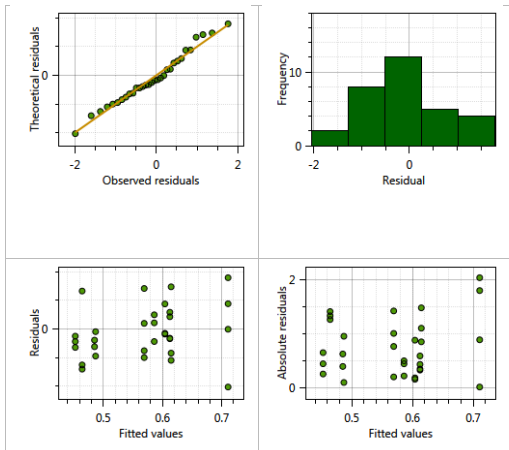
Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.2335   0.4832
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.0000   0.0000
Residual                2.9094   1.7057
Number of obs: 31, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    0.2421     0.2124  9.0069    1.14   0.284

Dispersion: 1.706
```

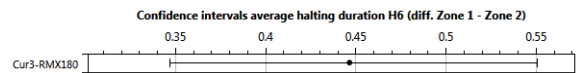
Model residuals

Statistic	Value
Sample skewness	0.2972
Sample excess kurtosis	-0.2266
Passed Shapiro Wilk normality test	Yes (p-value = 0.7477 > 0.05)



Analysis average halting duration H6 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_halting_duration_H6_Zone_1,Average_halting_duration_H6_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals average halting duration H6 (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4465	0.3467	0.5507	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 65.4

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.8190 -0.5598 -0.2856  0.4750  2.1531

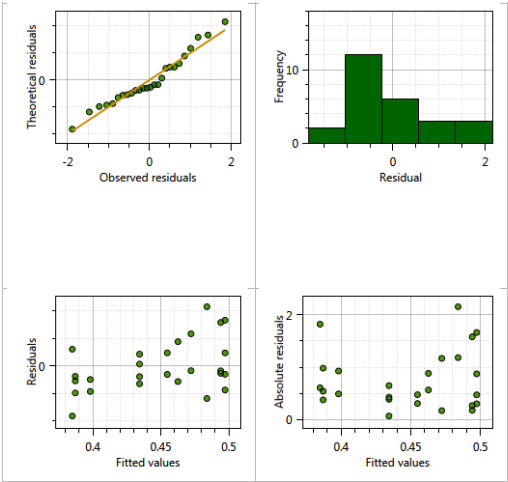
Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.1018   0.3191
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.0000   0.0000
Residual                2.4347   1.5603
Number of obs: 26, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   -0.215     0.181   7.874   -1.188   0.269

Dispersion: 1.56
```

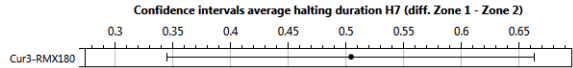
Model residuals

Statistic	Value
Sample skewness	0.6024
Sample excess kurtosis	0.1224
Passed Shapiro Wilk normality test	Yes (p-value = 0.3142 > 0.05)



Analysis average halting duration H7 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_halting_duration_H7_Zone_1,Average_halting_duration_H7_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



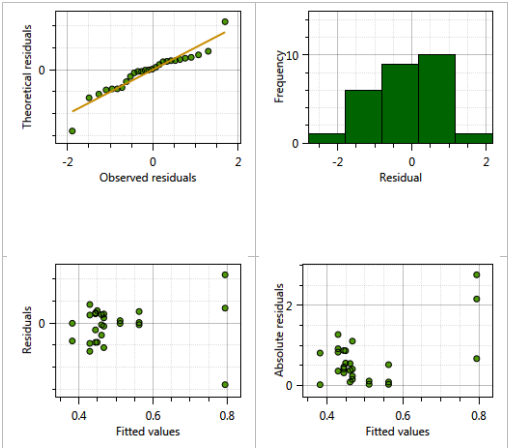
Confidence intervals average halting duration H7 (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5043	0.3444	0.6633	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi
REML criterion at convergence: 83.5
Scaled residuals:
Min 1Q Median 3Q Max
-2.76783 -0.67564 -0.01331 0.40722 2.16157
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_2:Plant_Zone_2 (Intercept) 1.085e-15 3.293e-08
Genotype_Zone_1:Plant_Zone_1 (Intercept) 4.827e-01 6.947e-01
Residual 3.497e+00 1.870e+00
Number of obs: 27, groups: Genotype_Zone_2:Plant_Zone_2, 10; Genotype_Zone_1:Plant_Zone_1, 9
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 0.01709 0.29732 10.19447 0.057 0.955
Dispersion: 1.87

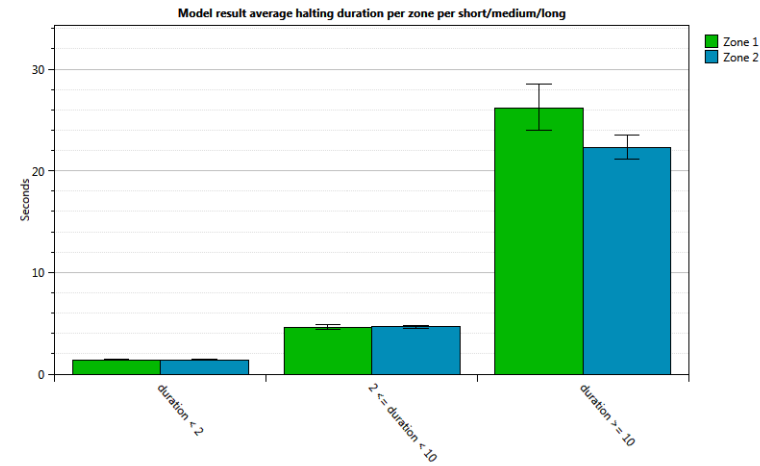
Model residuals

Statistic	Value
Sample skewness	-0.5453
Sample excess kurtosis	2.84
Passed Shapiro Wilk normality test	Yes (p-value = 0.05562 > 0.05)



Average halting duration per zone per short/medium/long

Selected zones	Zone 1, Zone 2
Event duration categories	duration < 2, 2 <= duration < 10, duration >= 10
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

Behaviour statistic	Cur3-RMX180	Remark
Average halting duration duration < 2 (diff. Zone 1 - Zone 2)	p=0.894 [-0.034, 0.0298]	CR
Average halting duration 2 <= duration < 10 (diff. Zone 1 - Zone 2)	p=0.9 [-0.0435, 0.0488]	CR
Average halting duration duration >= 10 (diff. Zone 1 - Zone 2)	p=0.000809*** [0.0753, 0.264]	

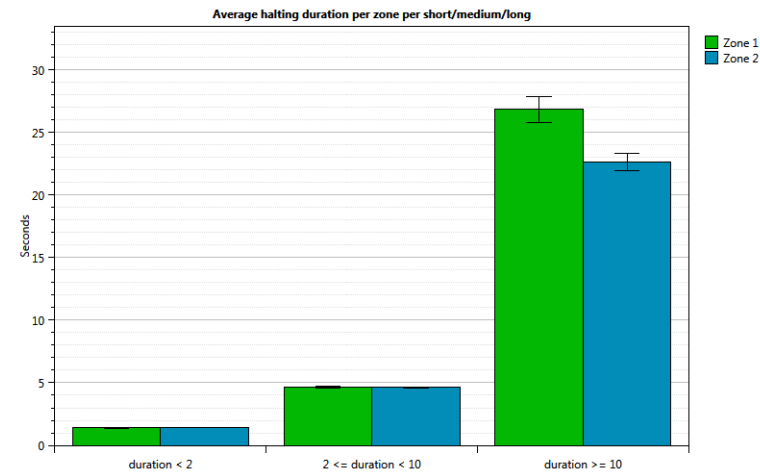
CR = Check residuals

The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Average halting duration (duration < 2 - Zone 1)	1.4 [1.36, 1.44]	CR
Average halting duration (2 <= duration < 10 - Zone 1)	4.63 [4.41, 4.85]	CR
Average halting duration (duration >= 10 - Zone 1)	26.2 [24, 28.6]	
Average halting duration (duration < 2 - Zone 2)	1.41 [1.37, 1.45]	
Average halting duration (2 <= duration < 10 - Zone 2)	4.64 [4.54, 4.74]	CR
Average halting duration (duration >= 10 - Zone 2)	22.3 [21.2, 23.6]	CR

CR = Check residuals

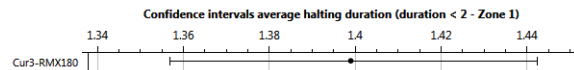
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean duration < 2 - Zone 1	StdErr duration < 2 - Zone 1	Mean 2 <= duration < 10 - Zone 1	StdErr 2 <= duration < 10 - Zone 1	Mean duration >= 10 - Zone 1	StdErr duration >= 10 - Zone 1	Mean duration < 2 - Zone 2	StdErr duration < 2 - Zone 2	Mean 2 <= duration < 10 - Zone 2	StdErr 2 <= duration < 10 - Zone 2	Mean duration >= 10 - Zone 2	StdErr duration >= 10 - Zone 2
Cur3	RMX180	Neutral	1.4	0.02	4.64	0.07	26.84	1.03	1.41	0.01	4.65	0.04	22.65	0.67

Analysis average halting duration (duration < 2 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_halting_duration_duration_2_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	1.399	1.357	1.442	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_halting_duration_duration_2_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: -66.2

Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.3252 -0.3880  0.2390  0.6133  1.6646

Random effects:
              Name                Variance Std.Dev.
Groups
Genotype_Zone_1:Plant_Zone_1 (Intercept) 1.738e-17 4.169e-09
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.000e+00 0.000e+00
Residual                                8.432e-03 9.182e-02
Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
```

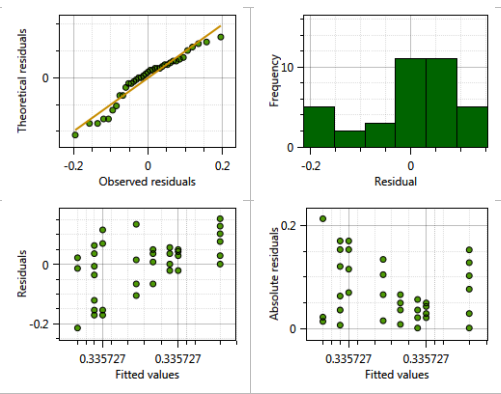
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.3357	0.0151	36.0000	22.24	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

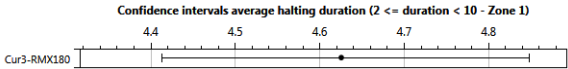
Model residuals

Statistic	Value
Sample skewness	-0.6699
Sample excess kurtosis	-0.1355
Passed Shapiro Wilk normality test	No (p-value = 0.04946 < 0.05)



Analysis average halting duration (2 <= duration < 10 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_halting_duration_2_duration_10_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	4.625	4.413	4.848	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method [`lmerModLmerTest`]
Formula: Average_halting_duration_2_duration_10_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: -65

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.0009	-0.2823	0.1156	0.3411	1.9189

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0015244	0.03904
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0007447	0.02729
Residual		0.0074323	0.08621

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

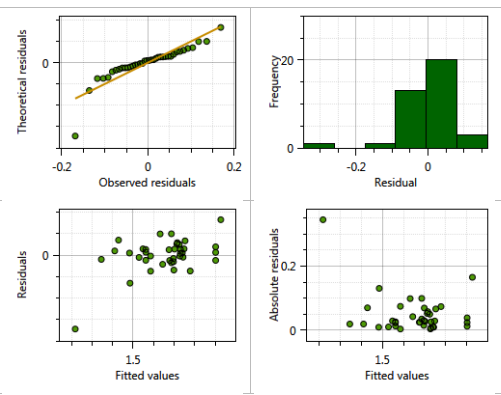
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	1.53155	0.02064	8.52040	74.21	2.81e-13 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

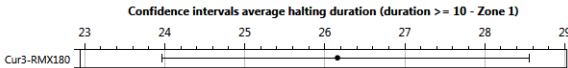
Model residuals

Statistic	Value
Sample skewness	-2.13
Sample excess kurtosis	9.427
Passed Shapiro Wilk normality test	No (p-value = 2.572E-05 < 0.05)



Analysis average halting duration (duration >= 10 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_halting_duration_duration_10_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	26.16	23.96	28.56	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_halting_duration_duration_10_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: -2.3

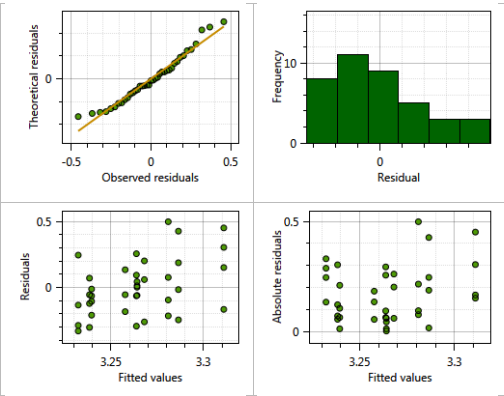
Scaled residuals:
  Min       1Q   Median       3Q      Max
-1.5163 -0.6875 -0.0740  0.5234  2.2895

Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.002997 0.05474
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.000000 0.00000
Residual                        0.047445 0.21782
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  3.26419    0.03896 9.24035  83.79 1.25e-14 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

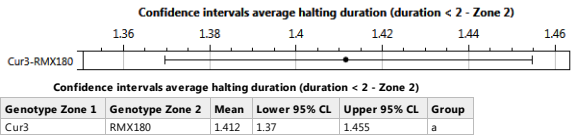
Model residuals

Statistic	Value
Sample skewness	0.5589
Sample excess kurtosis	-0.1396
Passed Shapiro Wilk normality test	Yes (p-value = 0.2061 > 0.05)



Analysis average halting duration (duration < 2 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_halting_duration_duration_2_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_halting_duration_duration_2_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: -95.5

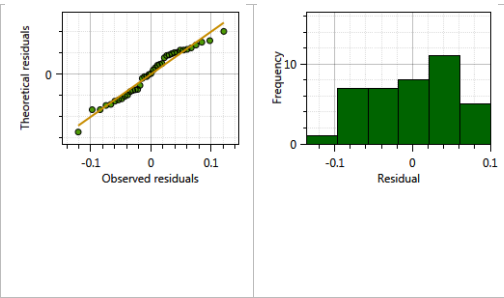
Scaled residuals:
  Min       1Q   Median       3Q      Max
-2.24566 -0.74076  0.02459  0.81630  1.66152

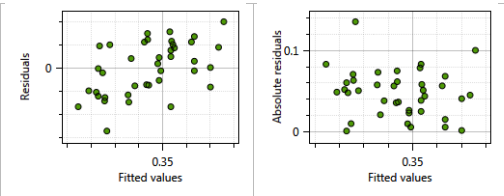
Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0004311 0.02076
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.0003798 0.01949
Residual                        0.0036621 0.06051
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  0.34467    0.01324 8.53269  26.03 1.98e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model residuals

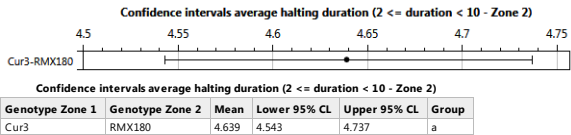
Statistic	Value
Sample skewness	-0.2925
Sample excess kurtosis	-0.7283
Passed Shapiro Wilk normality test	Yes (p-value = 0.2521 > 0.05)





Analysis average halting duration (2 <= duration < 10 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_halting_duration_2_duration_10_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_halting_duration_2_duration_10_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: -109.1

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-1.65901	-0.75232	-0.01197	0.40155	2.34031

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000000	0.00000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0001094	0.01046
Residual		0.0029124	0.05397

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

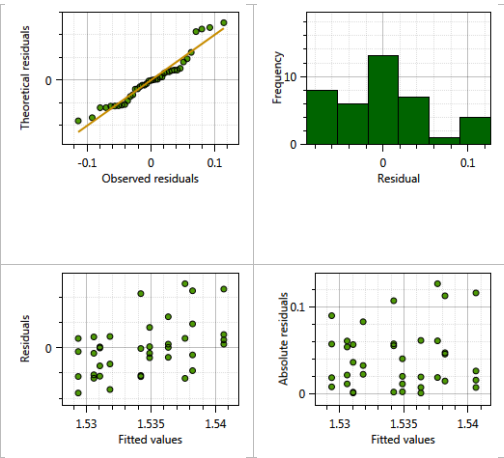
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	1.534469	0.009256	8.952201	165.8	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

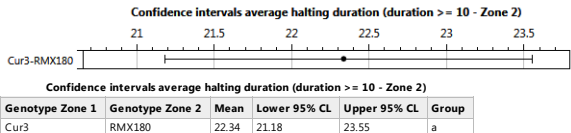
Model residuals

Statistic	Value
Sample skewness	0.7158
Sample excess kurtosis	0.3747
Passed Shapiro Wilk normality test	No (p-value = 0.02918 < 0.05)



Analysis average halting duration (duration >= 10 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_halting_duration_duration_10_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_halting_duration_duration_10_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: -25.9

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-1.5504	-0.5691	-0.0756	0.3998	3.5633

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	5.461e-19	7.39e-10
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000e+00	0.00e+00
Residual		2.690e-02	1.64e-01

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

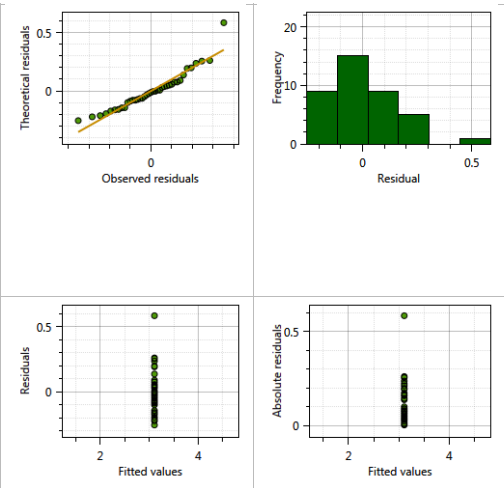
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	3.10616	0.02626	38.00000	118.3	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

Statistic	Value
Sample skewness	1.254
Sample excess kurtosis	2.946
Passed Shapiro Wilk normality test	No (p-value = 0.009713 < 0.05)

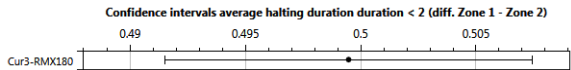


Data points with high residuals

Trial	Arena
Trial 3	12

Analysis average halting duration duration < 2 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_halting_duration_duration_2_Zone_1,Average_halting_duration_duration_2_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4995	0.4915	0.5075	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: -63.1

Scaled residuals:
Min 1Q Median 3Q Max
-2.48503 -0.51011 -0.05089 0.87496 1.29443

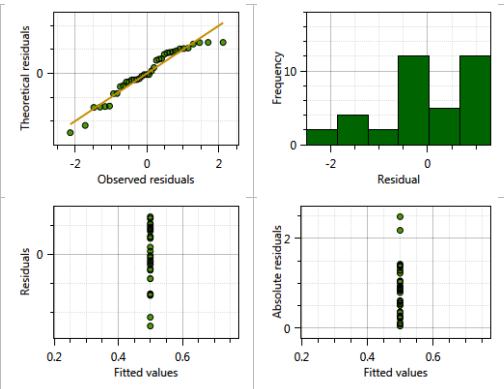
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.000000 0.00000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.000000 0.00000
Residual 0.006443 0.08027
Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -0.002114 0.015738 36.000000 -0.134 0.894

Dispersion: 0.08027

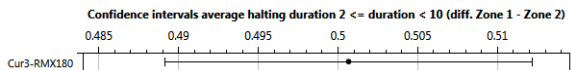
Model residuals

Statistic	Value
Sample skewness	-0.6361
Sample excess kurtosis	-0.1831
Passed Shapiro Wilk normality test	No (p-value = 0.03379 < 0.05)



Analysis average halting duration 2 <= duration < 10 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_halting_duration_2_duration_10_Zone_1,Average_halting_duration_2_duration_10_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals average halting duration 2 <= duration < 10 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5007	0.4891	0.5122	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: -52.2

Scaled residuals:
Min 1Q Median 3Q Max
-4.2372 -0.4083 -0.0444 0.6203 1.2931

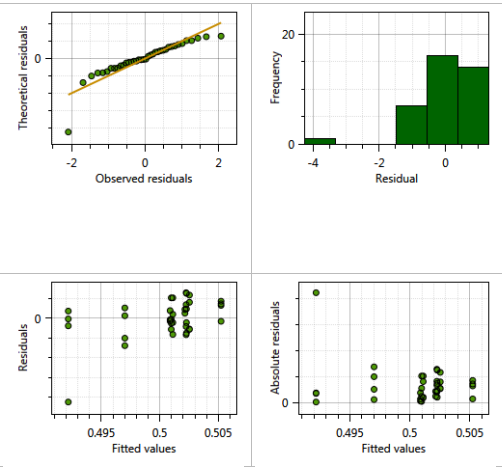
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 9.325e-04 3.054e-02
Genotype_Zone_2:Plant_Zone_2 (Intercept) 4.501e-17 6.709e-09
Residual 2.820e-02 1.679e-01
Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 0.002636 0.020382 8.926491 0.129 0.9

Dispersion: 0.1679

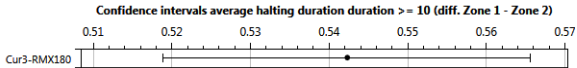
Model residuals

Statistic	Value
Sample skewness	-2.18
Sample excess kurtosis	8.725
Passed Shapiro Wilk normality test	No (p-value = 4.291E-05 < 0.05)



Analysis average halting duration duration >= 10 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_halting_duration_duration_10_Zone_1,Average_halting_duration_duration_10_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals average halting duration duration >= 10 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5423	0.5188	0.5656	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 18.1

Scaled residuals:
Min 1Q Median 3Q Max
-2.3386 -0.6071 -0.1946 0.5297 2.3232

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.00 0.00
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.00 0.00
Residual 1.04 1.02
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

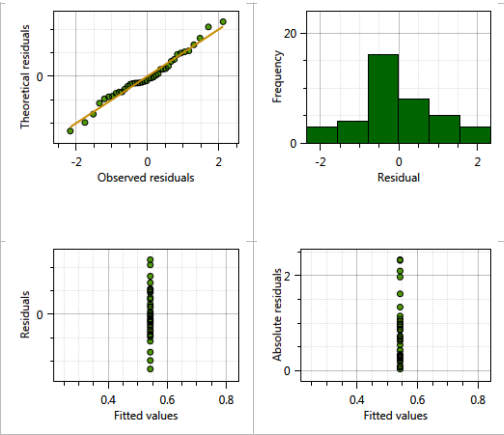
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 0.1696 0.0466 38.0000 3.64 0.000809 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 1.02

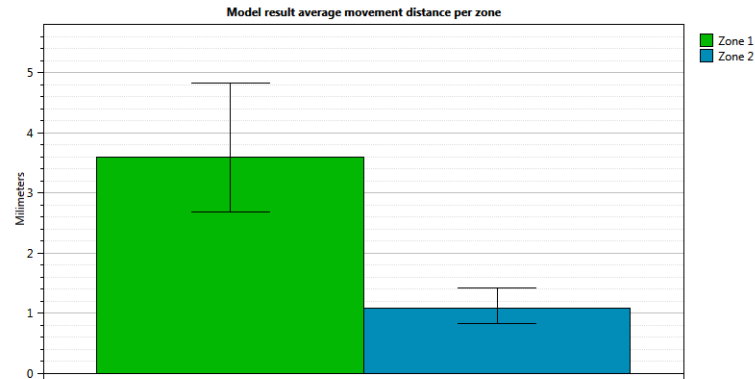
Model residuals

Statistic	Value
Sample skewness	0.1779
Sample excess kurtosis	0.4665
Passed Shapiro Wilk normality test	Yes (p-value = 0.6761 > 0.05)



Average movement distance per zone

Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

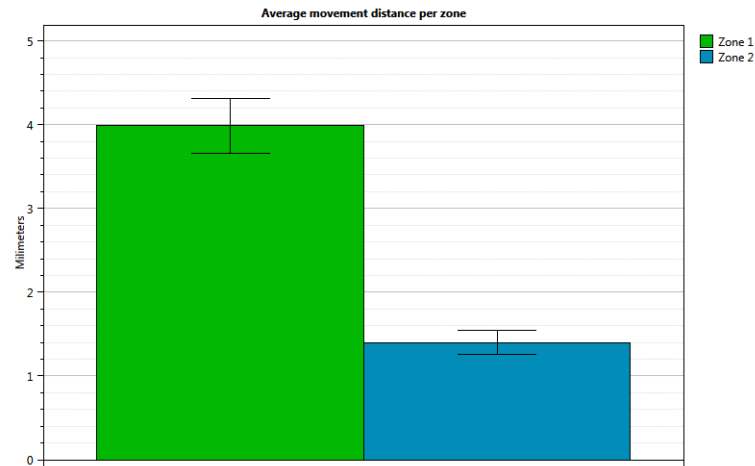
Behaviour statistic	Cur3-RMX180
Average movement distance (diff. Zone 1 - Zone 2)	p=3.54E-05**** [0.711, 1.34]

The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Average movement distance (Zone 1)	3.6 [2.68, 4.83]	CR
Average movement distance (Zone 2)	1.08 [0.821, 1.42]	CR

CR = Check residuals

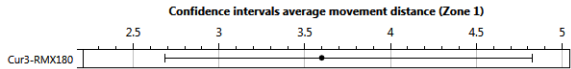
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean Zone 1	StdErr Zone 1	Mean Zone 2	StdErr Zone 2
Cur3	RMX180	Neutral	3.99	0.33	1.4	0.14

Analysis average movement distance (Zone 1)

Analysis model	Linear mixed model fit by REML: Average_movement_distance_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	3.598	2.682	4.827	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_distance_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 54.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.6652	-0.2116	0.1607	0.4877	1.2779

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.05131	0.2265
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.08149	0.2855
Residual		0.15018	0.3875

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

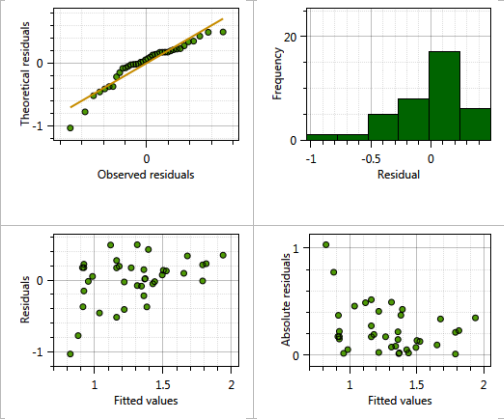
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	1.2805	0.1316	9.8337	9.732	2.31e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

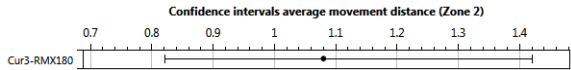
Model residuals

Statistic	Value
Sample skewness	-1.186
Sample excess kurtosis	1.759
Passed Shapiro Wilk normality test	No (p-value = 0.006385 < 0.05)



Analysis average movement distance (Zone 2)

Analysis model	Linear mixed model fit by REML: Average_movement_distance_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	1.08	0.8207	1.421	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_distance_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 98.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.0737	-0.3693	0.2280	0.5901	1.6095

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000	0.0000
Residual		0.717	0.8468

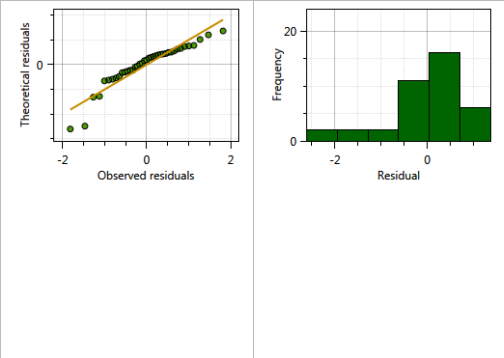
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

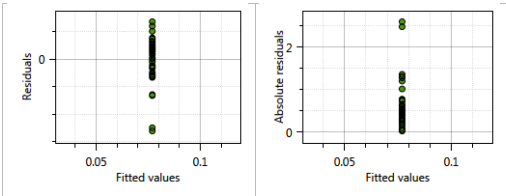
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.07693	0.13559	38.00000	0.567	0.574

Model residuals

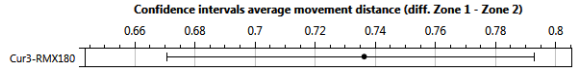
Statistic	Value
Sample skewness	-1.39
Sample excess kurtosis	2.662
Passed Shapiro Wilk normality test	No (p-value = 0.00129 < 0.05)





Analysis average movement distance (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_movement_distance_Zone_1,Average_movement_distance_Zone_2) ~ 1 + (1 Genotype_Zone_1 Plant_Zone_1) + (1 Genotype_Zone_2 Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.7363	0.6706	0.7929	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: zFormula
Data: data
Weights: w1

REML criterion at convergence: 87

Scaled residuals:
Min 1Q Median 3Q Max
-2.51640 -0.62178 0.03957 0.69447 1.72543

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.00000 0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.09832 0.3136
Residual 0.38573 0.6211
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

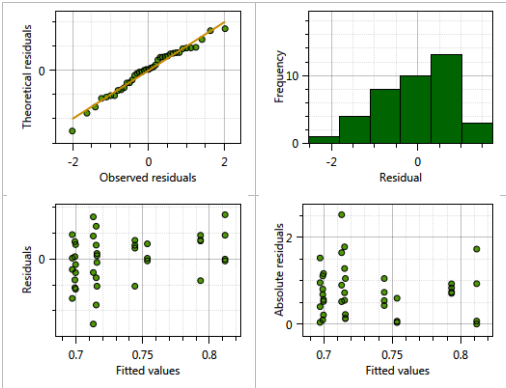
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 1.0267 0.1407 9.4449 7.298 3.54e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.6211

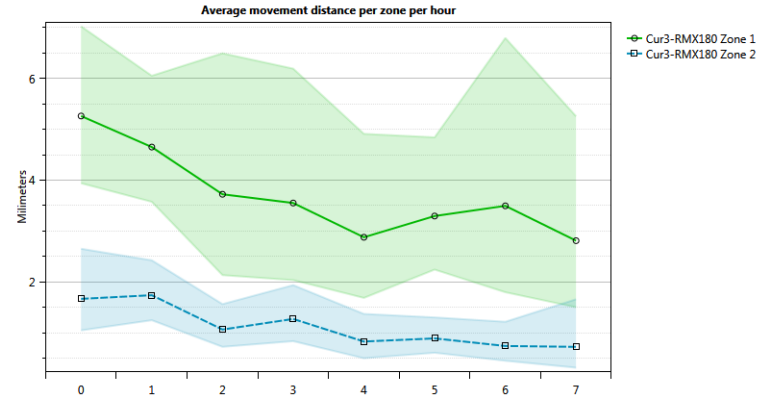
Model residuals

Statistic	Value
Sample skewness	-0.4995
Sample excess kurtosis	0.1404
Passed Shapiro Wilk normality test	Yes (p-value = 0.5277 > 0.05)



Average movement distance per zone per hour

Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

Behaviour statistic	Cur3-RMX180	Remark
Average movement distance H0 (diff. Zone 1 - Zone 2)	p=0.00403** (0.434, 1.78)	CR

Behaviour statistic	Cur3-RMX180	Remark
Average movement distance H1 (diff. Zone 1 - Zone 2)	p=0.0122* [0.215, 1.35]	CR
Average movement distance H2 (diff. Zone 1 - Zone 2)	p=2.8E-08**** [0.805, 1.44]	CR
Average movement distance H3 (diff. Zone 1 - Zone 2)	p=0.0494* [0.00253, 1.37]	
Average movement distance H4 (diff. Zone 1 - Zone 2)	p=0.006** [0.388, 1.72]	
Average movement distance H5 (diff. Zone 1 - Zone 2)	p=0.0165* [0.195, 1.47]	
Average movement distance H6 (diff. Zone 1 - Zone 2)	p=0.000116*** [0.625, 1.34]	
Average movement distance H7 (diff. Zone 1 - Zone 2)	p=0.00788** [0.273, 1.19]	

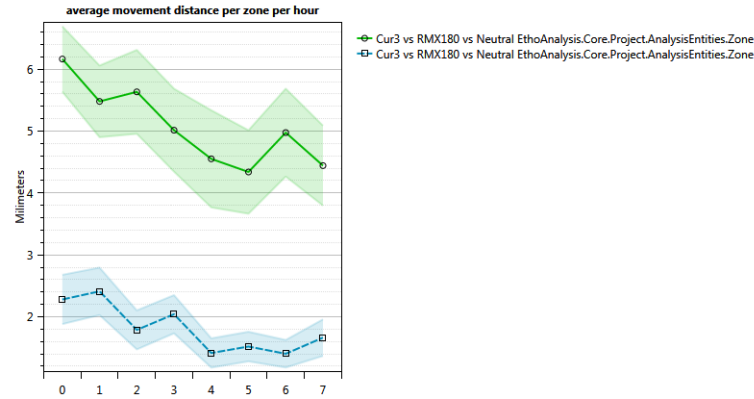
CR = Check residuals

The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Average movement distance (H0 - Zone 1)	5.26 [3.94, 7.02]	
Average movement distance (H0 - Zone 2)	1.67 [1.05, 2.65]	
Average movement distance (H1 - Zone 1)	4.65 [3.58, 6.05]	
Average movement distance (H1 - Zone 2)	1.74 [1.25, 2.43]	
Average movement distance (H2 - Zone 1)	3.72 [2.14, 6.49]	
Average movement distance (H2 - Zone 2)	1.07 [0.727, 1.57]	CR
Average movement distance (H3 - Zone 1)	3.55 [2.04, 6.19]	CR
Average movement distance (H3 - Zone 2)	1.28 [0.838, 1.94]	
Average movement distance (H4 - Zone 1)	2.88 [1.69, 4.91]	
Average movement distance (H4 - Zone 2)	0.832 [0.503, 1.37]	
Average movement distance (H5 - Zone 1)	3.3 [2.24, 4.84]	
Average movement distance (H5 - Zone 2)	0.893 [0.611, 1.31]	
Average movement distance (H6 - Zone 1)	3.5 [1.8, 6.79]	
Average movement distance (H6 - Zone 2)	0.744 [0.454, 1.22]	
Average movement distance (H7 - Zone 1)	2.81 [1.5, 5.26]	CR
Average movement distance (H7 - Zone 2)	0.727 [0.318, 1.66]	

CR = Check residuals

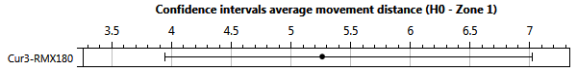
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean H0 - Zone 1	StdErr H0 - Zone 1	Mean H0 - Zone 2	StdErr H0 - Zone 2	Mean H1 - Zone 1	StdErr H1 - Zone 1	Mean H1 - Zone 2	StdErr H1 - Zone 2	Mean H2 - Zone 1	StdErr H2 - Zone 1	Mean H2 - Zone 2	StdErr H2 - Zone 2	Mean H3 - Zone 1	StdErr H3 - Zone 1	Mean H3 - Zone 2	StdErr H3 - Zone 2	Mean H4 - Zone 1	StdErr H4 - Zone 1	Mean H4 - Zone 2	StdErr H4 - Zone 2	Mean H5 - Zone 1	StdErr H5 - Zone 1	Mean H5 - Zone 2	StdErr H5 - Zone 2	Mean H6 - Zone 1	StdErr H6 - Zone 1	Mean H6 - Zone 2	StdErr H6 - Zone 2
Cur3	RMX180	Neutral	6.17	0.53	2.28	0.4	5.48	0.58	2.41	0.38	5.64	0.68	1.79	0.32	5.02	0.67	2.04	0.31	4.55	0.79	1.42	0.24	4.34	0.67	1.52	0.24	4.98	0.71	1.4	0.22

Analysis average movement distance (H0 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_movement_distance_H0_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	5.26	3.941	7.022	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_distance_H0_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 59.1

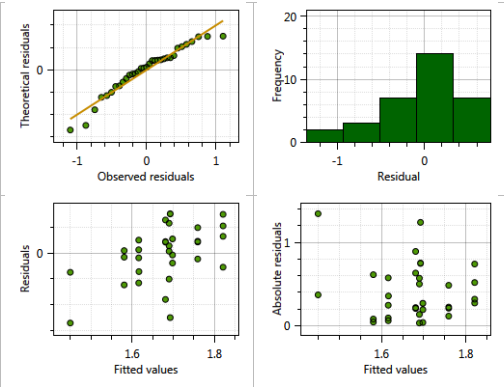
Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.4422 -0.4958  0.1113  0.4914  1.3682

Random effects:
Groups              Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.03725  0.1930
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.00000  0.0000
Residual              0.30338  0.5508
Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   1.6602     0.1149  5.4020  14.45  1.6e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

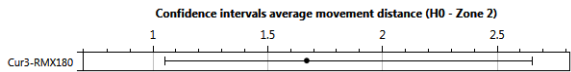
Model residuals

Statistic	Value
Sample skewness	-0.8225
Sample excess kurtosis	0.5607
Passed Shapiro Wilk normality test	Yes (p-value = 0.07464 > 0.05)



Analysis average movement distance (H0 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_movement_distance_H0_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	1.67	1.051	2.654	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_distance_H0_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 82.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.75795	-0.42394	0.00947	0.43522	2.28622

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.05512	0.2348
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.22184	0.4710
Residual		0.38967	0.6242

Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

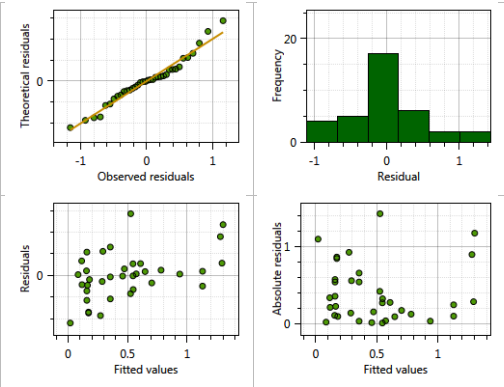
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.5127	0.1976	7.3037	2.595	0.0344 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

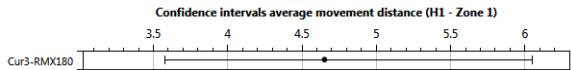
Model residuals

Statistic	Value
Sample skewness	0.3837
Sample excess kurtosis	0.7731
Passed Shapiro Wilk normality test	Yes (p-value = 0.4072 > 0.05)



Analysis average movement distance (H1 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_movement_distance_H1_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	4.651	3.575	6.051	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_distance_H1_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 57.1

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.7053	-0.7978	0.1293	0.5695	2.1609

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.07535	0.2745
Residual		0.21988	0.4689

Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

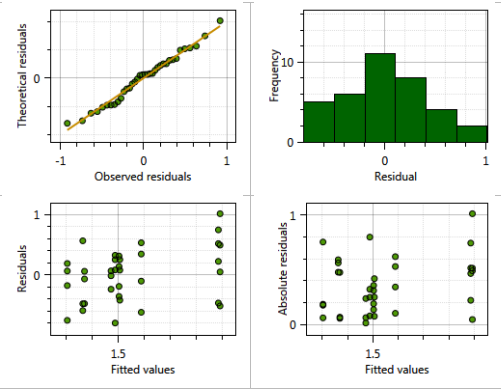
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	1.5371	0.1171	9.4032	13.13	2.32e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

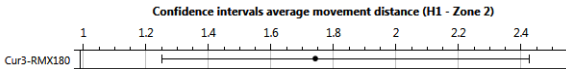
Model residuals

Statistic	Value
Sample skewness	0.07504
Sample excess kurtosis	-0.4166
Passed Shapiro Wilk normality test	Yes (p-value = 0.7779 > 0.05)



Analysis average movement distance (H1 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_movement_distance_H1_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	1.742	1.25	2.427	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_distance_H1_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 88.7

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.5653	-0.6755	-0.1552	0.5843	2.2784

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.04864	0.2206
Residual		0.58238	0.7631

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

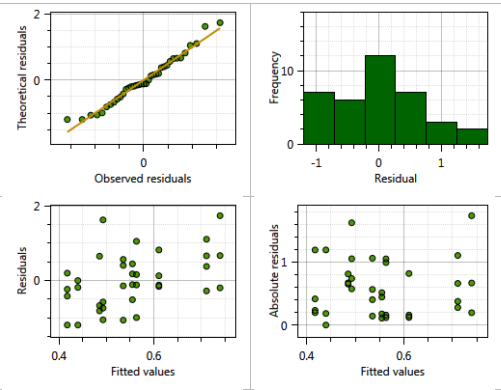
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.5549	0.1437	7.9443	3.86	0.00487 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

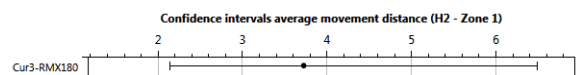
Model residuals

Statistic	Value
Sample skewness	0.3934
Sample excess kurtosis	-0.1209
Passed Shapiro Wilk normality test	Yes (p-value = 0.4396 > 0.05)



Analysis average movement distance (H2 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_movement_distance_H2_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	3.724	2.136	6.492	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_distance_H2_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 104

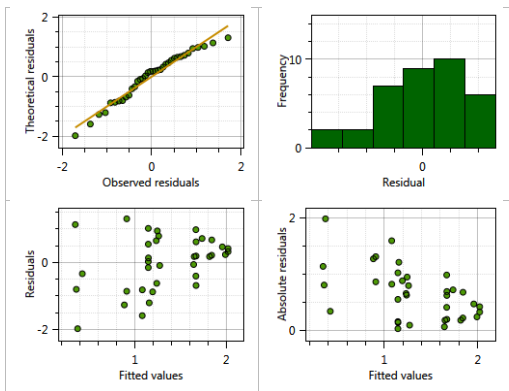
Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.2279 -0.7191  0.1991  0.7050  1.4704

Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.01867  0.1366
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.36568  0.6047
Residual                        0.79004  0.8888
Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   1.3147     0.2464  9.1682   5.336 0.000442 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

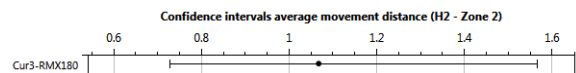
Model residuals

Statistic	Value
Sample skewness	-0.5742
Sample excess kurtosis	-0.2727
Passed Shapiro Wilk normality test	Yes (p-value = 0.2587 > 0.05)



Analysis average movement distance (H2 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_movement_distance_H2_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	1.067	0.7272	1.567	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_distance_H2_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 115.9

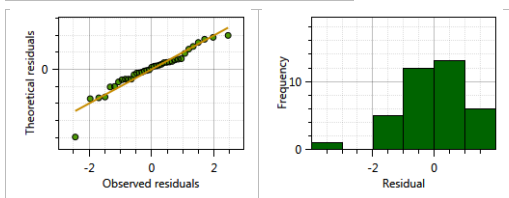
Scaled residuals:
    Min       1Q   Median       3Q      Max
-3.4552 -0.5005  0.1089  0.4824  1.7322

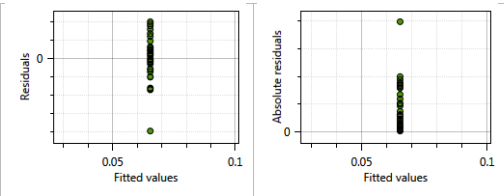
Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 2.364e-20 1.537e-10
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.000e+00 0.000e+00
Residual                        1.325e+00 1.151e+00
Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   0.06529     0.18924 36.00000   0.345   0.732
```

Model residuals

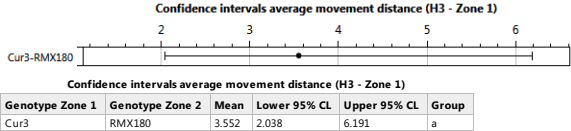
Statistic	Value
Sample skewness	-0.9723
Sample excess kurtosis	2.858
Passed Shapiro Wilk normality test	No (p-value = 0.03027 < 0.05)





Analysis average movement distance (H3 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_movement_distance_H3_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_distance_H3_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 91.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.8539	-0.5646	0.1962	0.7301	1.2822

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.01863	0.1365
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.37739	0.6143
Residual		0.68299	0.8264

Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

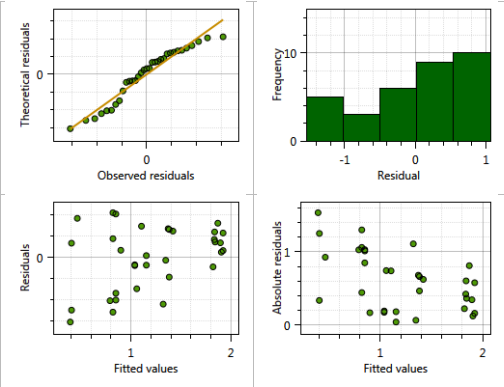
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	1.268	0.247	9.335	5.133	0.00055 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

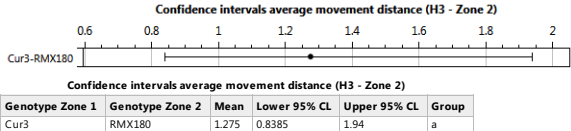
Model residuals

Statistic	Value
Sample skewness	-0.5541
Sample excess kurtosis	-0.7968
Passed Shapiro Wilk normality test	No (p-value = 0.04515 < 0.05)



Analysis average movement distance (H3 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_movement_distance_H3_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_distance_H3_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 119.1

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.5484	-0.3246	0.1167	0.7216	1.5708

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	6.652e-17	8.156e-09
Genotype_Zone_2:Plant_Zone_2	(Intercept)	3.913e-02	1.978e-01
Residual		1.187e+00	1.090e+00

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

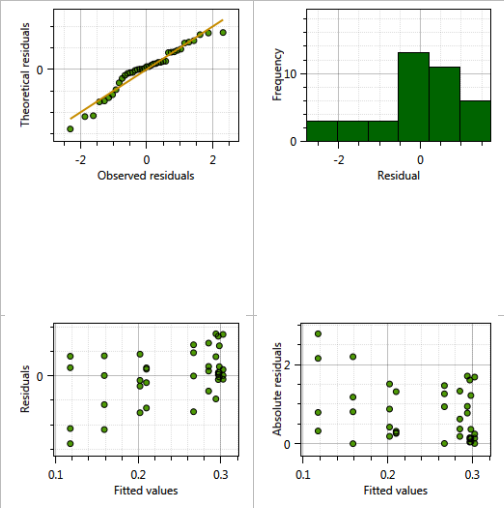
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.2431	0.1854	9.0136	1.311	0.222

Model residuals

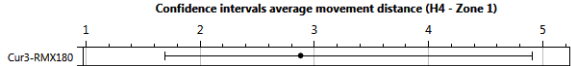
Statistic	Value
Sample skewness	-0.6799

Statistic	Value
Sample excess kurtosis	0.3124
Passed Shapiro Wilk normality test	Yes (p-value = 0.07678 > 0.05)



Analysis average movement distance (H4 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_movement_distance_H4_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	2.879	1.688	4.911	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_distance_H4_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 92.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.8078	-0.4285	0.1923	0.5910	1.4764

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.09144	0.3024
Residual		1.17559	1.0842

Number of obs: 30, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

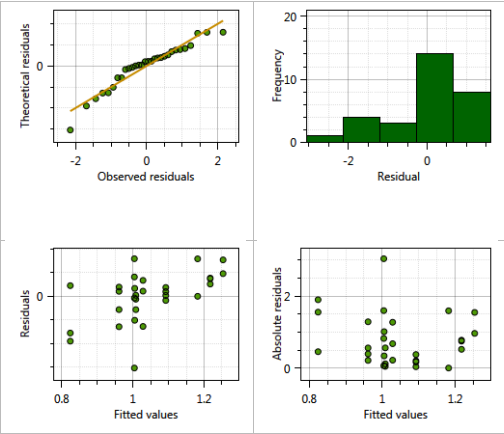
Fixed effects:

	Estimate	Std. Error	df t	value	Pr(> t)
(Intercept)	1.058	0.221	6.336	4.786	0.00263 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

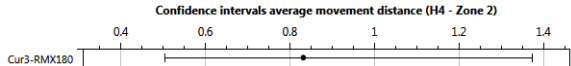
Model residuals

Statistic	Value
Sample skewness	-0.9359
Sample excess kurtosis	1.256
Passed Shapiro Wilk normality test	Yes (p-value = 0.06194 > 0.05)



Analysis average movement distance (H4 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_movement_distance_H4_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.8317	0.5033	1.374	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_distance_H4_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 115.2

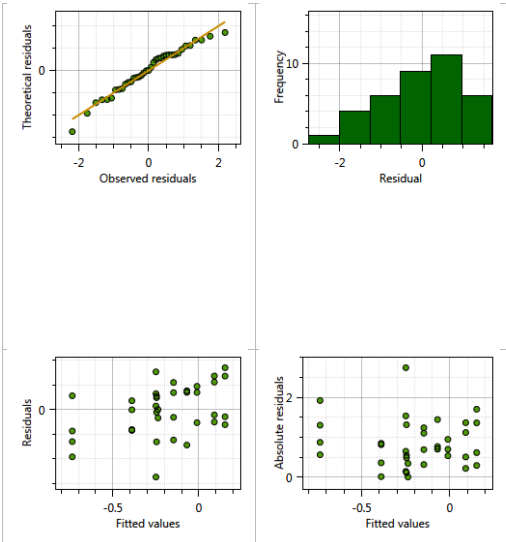
Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.54788 -0.57031  0.00163  0.65023  1.58060

Random effects:
Groups:                               Name      Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0000   0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.1813   0.4258
Residual                                1.1617   1.0778
Number of obs: 37, groups:  Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -0.1843    0.2234   9.3944  -0.825   0.43
```

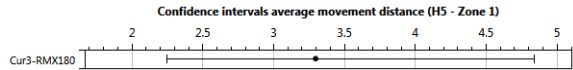
Model residuals

Statistic	Value
Sample skewness	-0.5362
Sample excess kurtosis	0.0118
Passed Shapiro Wilk normality test	Yes (p-value = 0.4125 > 0.05)



Analysis average movement distance (H5 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_movement_distance_H5_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	3.296	2.244	4.842	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_distance_H5_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 75.2

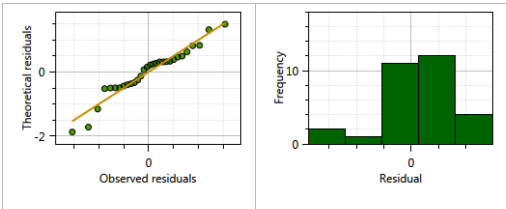
Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.3694 -0.5425  0.2346  0.4707  1.8836

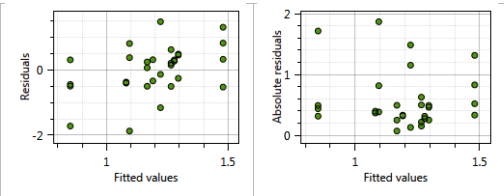
Random effects:
Groups:                               Name      Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.09135   0.3022
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.00000   0.0000
Residual                                0.62376   0.7898
Number of obs: 30, groups:  Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   1.1928    0.1742  10.7759   6.845 3.09e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model residuals

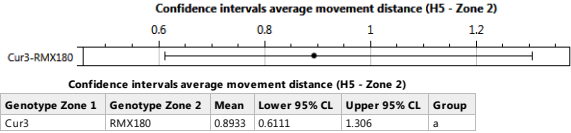
Statistic	Value
Sample skewness	-0.5661
Sample excess kurtosis	0.9411
Passed Shapiro Wilk normality test	Yes (p-value = 0.1503 > 0.05)





Analysis average movement distance (H5 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_movement_distance_H5_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_distance_H5_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + Genotype_Zone_2:Plant_Zone_2
Data: data

REML criterion at convergence: 123.5

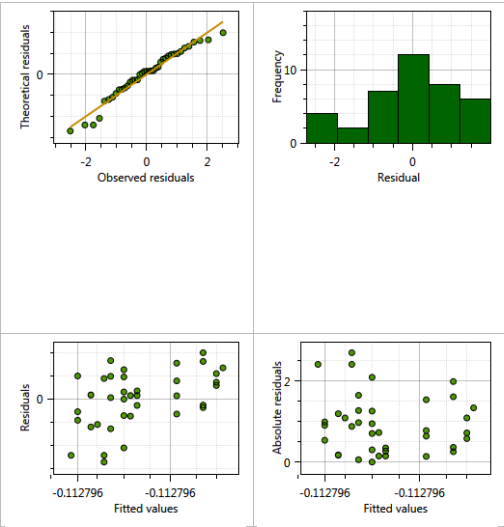
Scaled residuals:
Min 1Q Median 3Q Max
-2.3052 -0.5763 0.1298 0.7823 1.6979

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 3.056e-18 1.748e-09
Genotype_Zone_2:Plant_Zone_2 (Intercept) 6.282e-17 7.926e-09
Residual 1.373e+00 1.172e+00
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -0.1128 0.1876 38.0000 -0.601 0.551

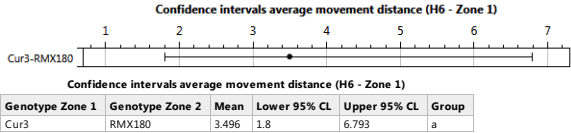
Model residuals

Statistic	Value
Sample skewness	-0.5789
Sample excess kurtosis	-0.06877
Passed Shapiro Wilk normality test	Yes (p-value = 0.1784 > 0.05)



Analysis average movement distance (H6 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_movement_distance_H6_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_distance_H6_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + Genotype_Zone_2:Plant_Zone_2
Data: data

REML criterion at convergence: 79

Scaled residuals:
Min 1Q Median 3Q Max
-2.0123 -0.4240 0.1497 0.6202 1.4500

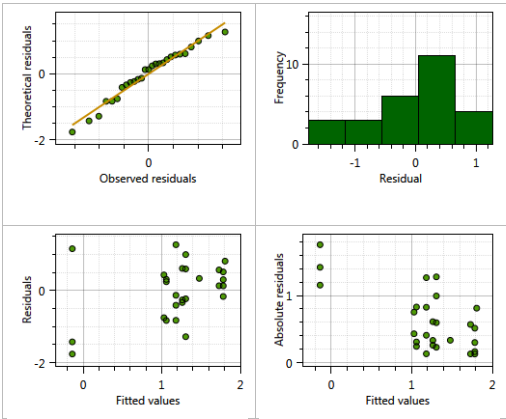
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0000 0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.5246 0.7243
Residual 0.7625 0.8732
Number of obs: 27, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 1.252 0.291 8.505 4.301 0.00227 **

Signif. codes: 0 '****' 0.001 '***' 0.01 '**' 0.05 '.' 0.1 ' ' 1

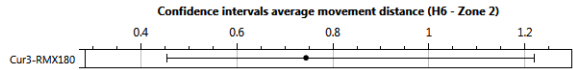
Model residuals

Statistic	Value
Sample skewness	-0.5406
Sample excess kurtosis	-0.1658
Passed Shapiro Wilk normality test	Yes (p-value = 0.4935 > 0.05)



Analysis average movement distance (H6 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_movement_distance_H6_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype_Zone_1	Genotype_Zone_2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.7439	0.4537	1.22	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method [`lmerModLmerTest`]
Formula: Average_movement_distance_H6_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 129.5

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.1996	-0.8562	0.2745	0.7633	1.5573

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000000	0.00000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.005831	0.07636
Residual		1.750447	1.32304

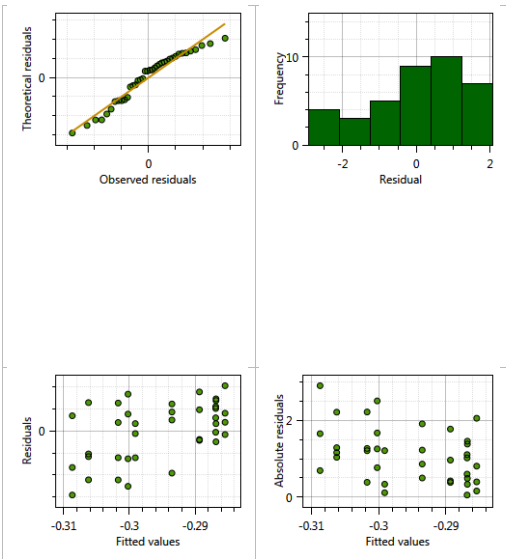
Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.2958	0.2160	8.3361	-1.369	0.207

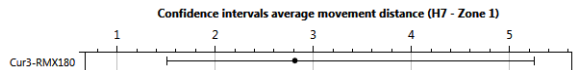
Model residuals

Statistic	Value
Sample skewness	-0.5662
Sample excess kurtosis	-0.6657
Passed Shapiro Wilk normality test	Yes (p-value = 0.0605 > 0.05)



Analysis average movement distance (H7 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_movement_distance_H7_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals average movement distance (H7 - Zone 1)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	2.812	1.505	5.256	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_distance_H7_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 93.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.7819	-0.1907	0.1337	0.3710	1.2744

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_2:Plant_Zone_2	(Intercept)	1.578e-01	3.973e-01
Genotype_Zone_1:Plant_Zone_1	(Intercept)	1.176e-14	1.084e-07
Residual		1.504e+00	1.226e+00

Number of obs: 28, groups: Genotype_Zone_2:Plant_Zone_2, 10; Genotype_Zone_1:Plant_Zone_1, 9

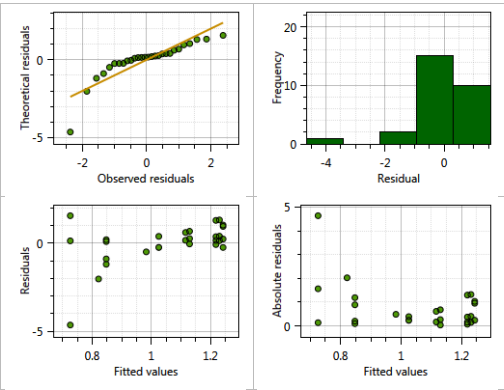
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	1.0340	0.2673	7.3945	3.868	0.00553 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

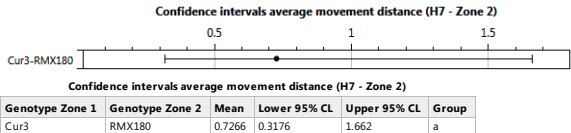
Model residuals

Statistic	Value
Sample skewness	-2.411
Sample excess kurtosis	8.447
Passed Shapiro Wilk normality test	No (p-value = 4.246E-05 < 0.05)



Analysis average movement distance (H7 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_movement_distance_H7_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_distance_H7_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 134.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.5881	-0.5940	-0.1449	0.6564	1.3616

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.6414	0.8009
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.4355	0.6599
Residual		1.1736	1.0833

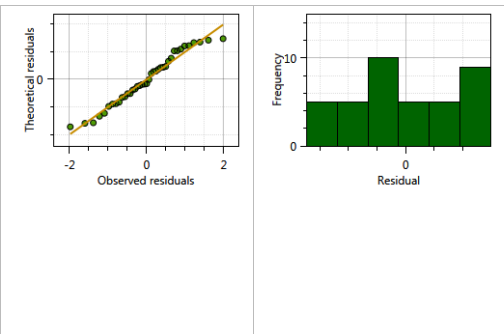
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

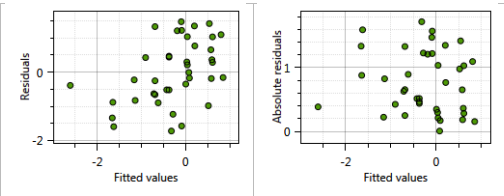
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.3194	0.3716	10.0430	-0.86	0.41

Model residuals

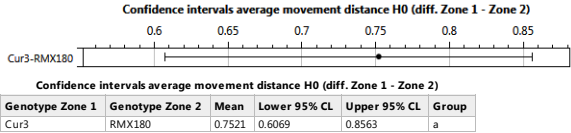
Statistic	Value
Sample skewness	-0.0709
Sample excess kurtosis	-0.9584
Passed Shapiro Wilk normality test	Yes (p-value = 0.203 > 0.05)





Analysis average movement distance H0 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_movement_distance_H0_Zone_1,Average_movement_distance_H0_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



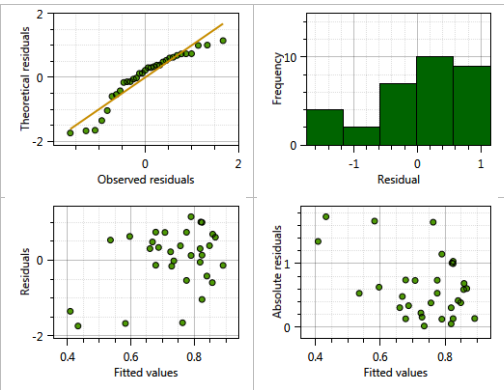
Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1
REML criterion at convergence: 88.7
Scaled residuals:
Min 1Q Median 3Q Max
-1.7369 -0.2223 0.2639 0.6123 1.1484
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.3365 0.5801
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.4183 0.6468
Residual 0.6353 0.7971
Number of obs: 32, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 1.1096 0.3072 11.0967 3.612 0.00403 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Dispersion: 0.7971

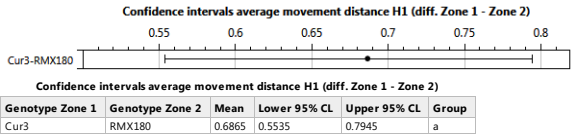
Model residuals

Statistic	Value
Sample skewness	-0.9714
Sample excess kurtosis	0.1997
Passed Shapiro Wilk normality test	No (p-value = 0.006346 < 0.05)



Analysis average movement distance H1 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_movement_distance_H1_Zone_1,Average_movement_distance_H1_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Model summary

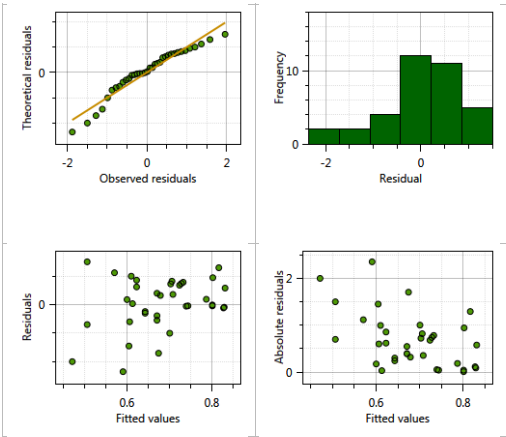
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1
REML criterion at convergence: 107.9
Scaled residuals:
Min 1Q Median 3Q Max
-2.3508 -0.3239 0.1047 0.7275 1.4998
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0306 0.1749
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.3658 0.6048
Residual 1.3170 1.1476
Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 0.7837 0.2526 9.2656 3.103 0.0122 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 1.148

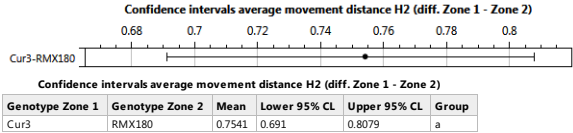
Model residuals

Statistic	Value
Sample skewness	-0.9039
Sample excess kurtosis	0.6421
Passed Shapiro Wilk normality test	No (p-value = 0.04698 < 0.05)



Analysis average movement distance H2 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_movement_distance_H2_Zone_1,Average_movement_distance_H2_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 99.2

Scaled residuals:
   Min       1Q   Median       3Q      Max
-3.2976 -0.4876  0.0476  0.6308  1.5389

Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.000    0.000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.000    0.000
Residual              1.195    1.093

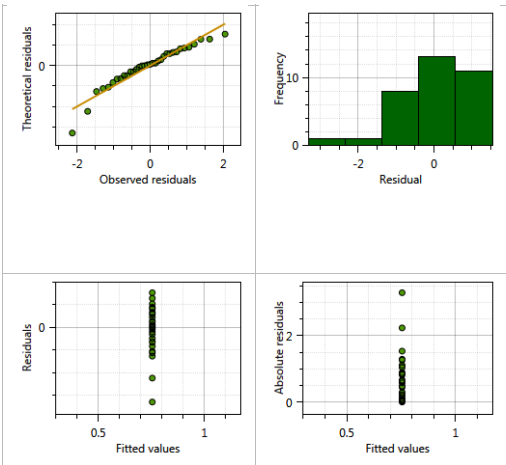
Number of obs: 34, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   1.1208    0.1552 33.0000   7.221 2.8e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 1.093
```

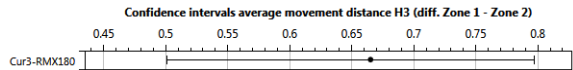
Model residuals

Statistic	Value
Sample skewness	-1.189
Sample excess kurtosis	2.462
Passed Shapiro Wilk normality test	No (p-value = 0.02781 < 0.05)



Analysis average movement distance H3 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_movement_distance_H3_Zone_1,Average_movement_distance_H3_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals average movement distance H3 (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.6651	0.5006	0.7973	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 97.9

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.9148 -0.4261 -0.0397  0.6086  1.3697

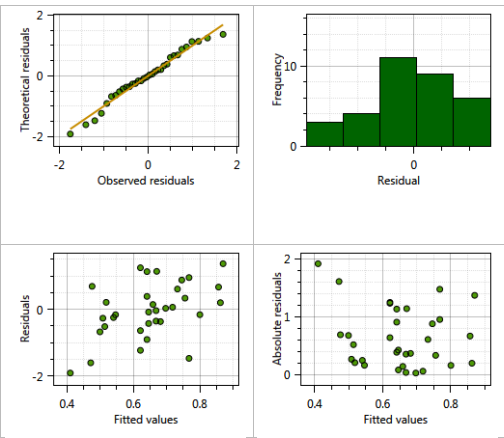
Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.2710   0.5206
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.3886   0.6234
Residual                                0.7889   0.8882
Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    0.6861     0.2905  7.1679   2.362   0.0494 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.8882
```

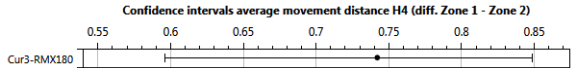
Model residuals

Statistic	Value
Sample skewness	-0.3484
Sample excess kurtosis	-0.172
Passed Shapiro Wilk normality test	Yes (p-value = 0.5998 > 0.05)



Analysis average movement distance H4 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_movement_distance_H4_Zone_1,Average_movement_distance_H4_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals average movement distance H4 (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.742	0.5958	0.8488	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 80.9

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.76460 -0.78153  0.00054  0.68940  1.38088

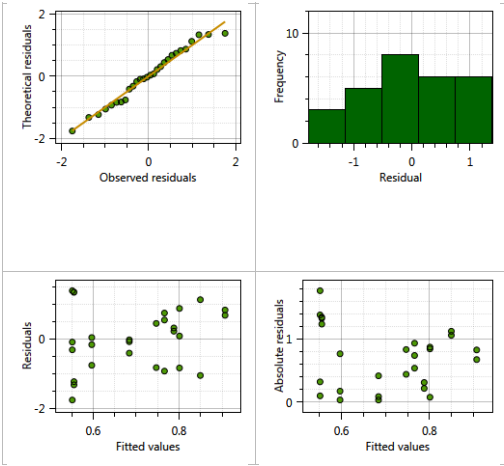
Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0000   0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.6296   0.7935
Residual                                0.6461   0.8038
Number of obs: 28, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    1.0565     0.2952  8.9504   3.578   0.006 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.8038
```

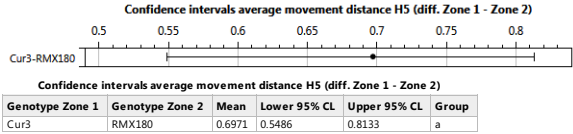
Model residuals

Statistic	Value
Sample skewness	-0.1464
Sample excess kurtosis	-0.8148
Passed Shapiro Wilk normality test	Yes (p-value = 0.5972 > 0.05)



Analysis average movement distance H5 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_movement_distance_H5_Zone_1Average_movement_distance_H5_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 99.9

Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.14457 -0.41393  0.03687  0.39553  1.45128

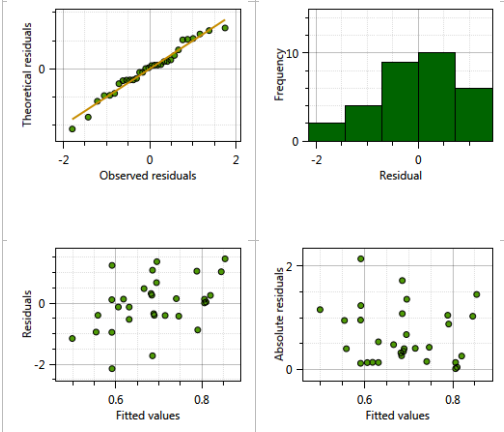
Random effects:
Groups              Name      Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.2253  0.4747
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.2672  0.5169
Residual              0.9214  0.9599
Number of obs: 31, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   0.8333      0.2793  8.4511   2.983   0.0165 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.9599
```

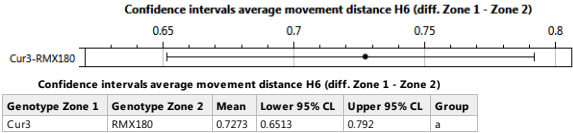
Model residuals

Statistic	Value
Sample skewness	-0.3439
Sample excess kurtosis	0.1728
Passed Shapiro Wilk normality test	Yes (p-value = 0.5249 > 0.05)



Analysis average movement distance H6 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_movement_distance_H6_Zone_1Average_movement_distance_H6_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
```

```
Weights: wi

REML criterion at convergence: 64.1

Scaled residuals:
  Min       1Q   Median       3Q      Max
-1.8268 -0.5901 -0.1812  0.4946  1.8278

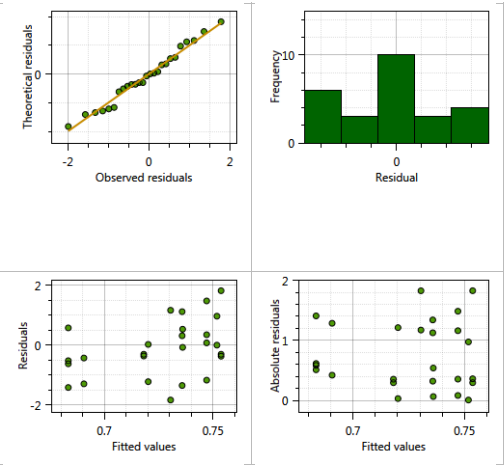
Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.06083  0.2466
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.00000  0.0000
Residual                                  0.67211  0.8198
Number of obs: 26, groups:  Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    0.9808      0.1594  9.8218   6.153 0.000116 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.8198
```

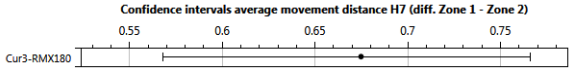
Model residuals

Statistic	Value
Sample skewness	0.1692
Sample excess kurtosis	-0.5367
Passed Shapiro Wilk normality test	Yes (p-value = 0.7738 > 0.05)



Analysis average movement distance H7 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_movement_distance_H7_Zone_1,Average_movement_distance_H7_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.6748	0.5678	0.7662	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 81.7

Scaled residuals:
  Min       1Q   Median       3Q      Max
-1.89826 -0.70426  0.07844  0.81380  1.25545

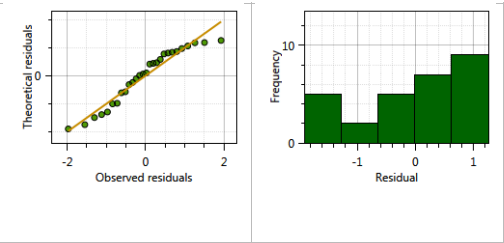
Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.0664  0.2577
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.0000  0.0000
Residual                                  1.0392  1.0194
Number of obs: 28, groups:  Genotype_Zone_2:Plant_Zone_2, 10; Genotype_Zone_1:Plant_Zone_1, 9

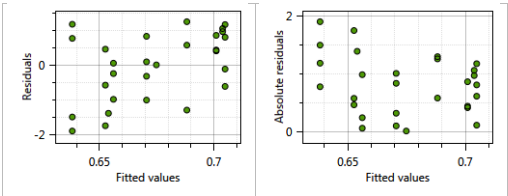
Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    0.7299      0.1869  6.0237   3.905 0.00788 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 1.019
```

Model residuals

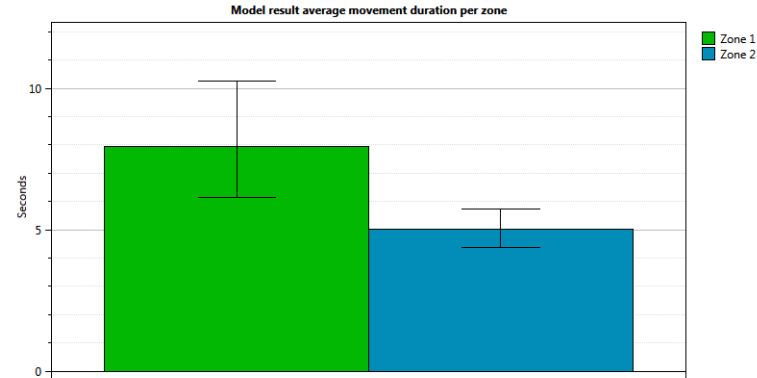
Statistic	Value
Sample skewness	-0.4784
Sample excess kurtosis	-0.9836
Passed Shapiro Wilk normality test	Yes (p-value = 0.06193 > 0.05)





Average movement duration per zone

Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

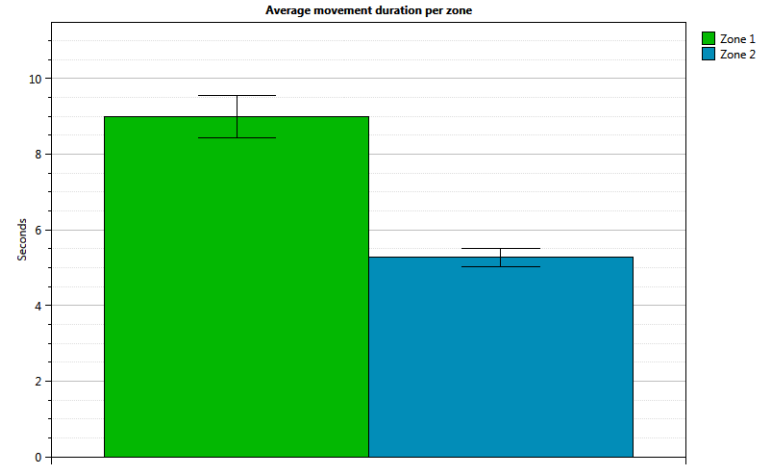
Behaviour statistic	Cur3-RMX180
Average movement duration (diff. Zone 1 - Zone 2)	p=2.58E-11**** [0.419, 0.653]

The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Average movement duration (Zone 1)	7.95 [6.15, 10.3]	CR
Average movement duration (Zone 2)	5 [4.37, 5.73]	CR

CR = Check residuals

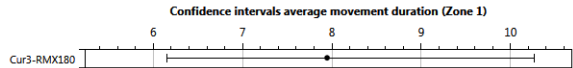
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean Zone 1	StdErr Zone 1	Mean Zone 2	StdErr Zone 2
Cur3	RMX180	Neutral	9	0.56	5.26	0.23

Analysis average movement duration (Zone 1)

Analysis model	Linear mixed model fit by REML: Average_movement_duration_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	7.946	6.149	10.27	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_duration_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 73.3

Scaled residuals:
Min 1Q Median 3Q Max
-4.0541 -0.2324 0.3074 0.4970 1.2577

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.04313 0.2077

Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.00000 0.0000
Residual 0.33214 0.5763
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

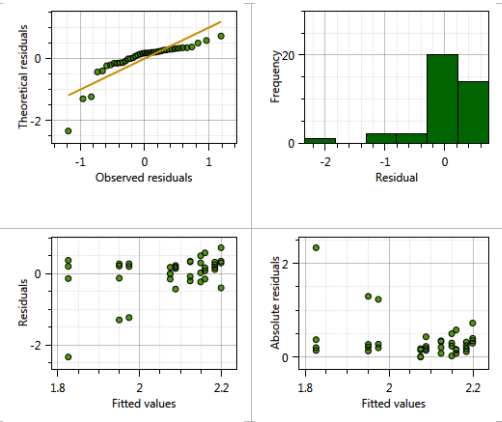
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	2.0727	0.1133	8.9994	18.29	2e-08 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

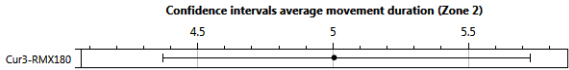
Model residuals

Statistic	Value
Sample skewness	-2.611
Sample excess kurtosis	8.476
Passed Shapiro Wilk normality test	No (p-value = 3.747E-07 < 0.05)



Analysis average movement duration (Zone 2)

Analysis model	Linear mixed model fit by REML: Average_movement_duration_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	5.004	4.37	5.73	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_duration_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 31.4

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-2.91276	-0.29127	0.09983	0.49370	1.47134

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.004816	0.0694
Residual		0.117320	0.3425

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

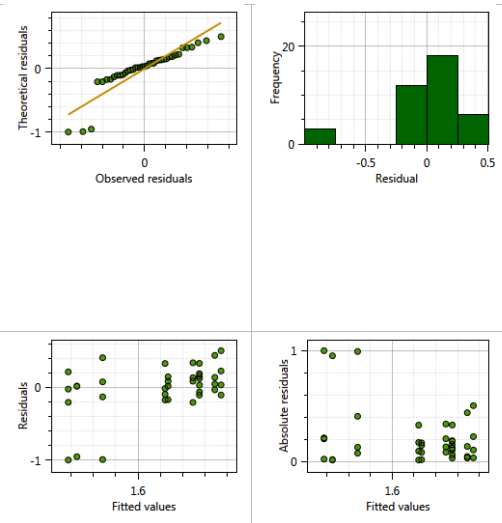
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	1.6102	0.0591	8.2808	27.25	2.12e-09 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

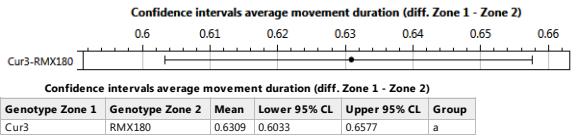
Model residuals

Statistic	Value
Sample skewness	-1.756
Sample excess kurtosis	3.823
Passed Shapiro Wilk normality test	No (p-value = 1.314E-05 < 0.05)



Analysis average movement duration (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_movement_duration_Zone_1,Average_movement_duration_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 36.8

Scaled residuals:
  Min       1Q   Median       3Q      Max
-2.5921 -0.6428 -0.2202  0.6305  2.7771

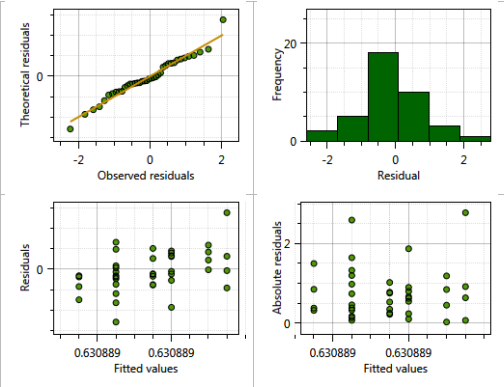
Random effects:
Groups              Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.000e+00 0.00e+00
Genotype_Zone_2:Plant_Zone_2 (Intercept) 2.191e-16 1.48e-08
Residual                                4.316e-01 6.57e-01
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  0.53603    0.05773 38.00000   9.285 2.58e-11 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.657
```

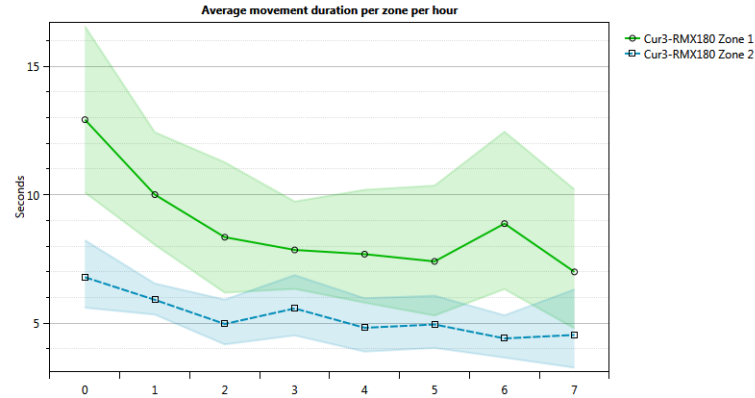
Model residuals

Statistic	Value
Sample skewness	0.1189
Sample excess kurtosis	1.223
Passed Shapiro Wilk normality test	Yes (p-value = 0.5398 > 0.05)



Average movement duration per zone per hour

Selected hours	0 1 2 3 4 5 6 7
Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

Behaviour statistic	Cur3-RMX180	Remark
Average movement duration H0 (diff. Zone 1 - Zone 2)	p=0.000892*** [0.416, 1.01]	
Average movement duration H1 (diff. Zone 1 - Zone 2)	p=0.000126*** [0.354, 0.787]	
Average movement duration H2 (diff. Zone 1 - Zone 2)	p=0.0177* [0.104, 0.835]	
Average movement duration H3 (diff. Zone 1 - Zone 2)	p=0.082 [-0.0421, 0.561]	CR
Average movement duration H4 (diff. Zone 1 - Zone 2)	p=0.00331** [0.231, 0.777]	
Average movement duration H5 (diff. Zone 1 - Zone 2)	p=0.0488* [0.00278, 0.779]	
Average movement duration H6 (diff. Zone 1 - Zone 2)	p=3.56E-06*** [0.4, 0.828]	
Average movement duration H7 (diff. Zone 1 - Zone 2)	p=0.0149* [0.0976, 0.665]	

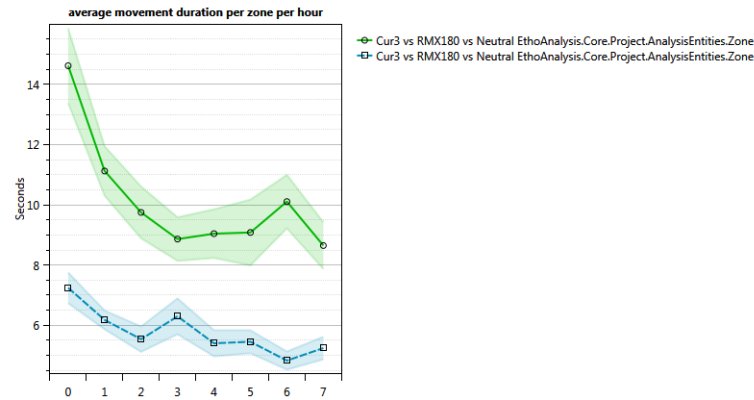
CR = Check residuals

The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Average movement duration (H0 - Zone 1)	12.9	CR
	[10.1, 16.6]	
Average movement duration (H0 - Zone 2)	6.79	
	[5.6, 8.23]	
Average movement duration (H1 - Zone 1)	10	CR
	[8.05, 12.4]	
Average movement duration (H1 - Zone 2)	5.91	CR
	[5.34, 6.55]	
Average movement duration (H2 - Zone 1)	8.35	
	[6.19, 11.3]	
Average movement duration (H2 - Zone 2)	4.97	CR
	[4.17, 5.92]	
Average movement duration (H3 - Zone 1)	7.85	
	[6.33, 9.74]	
Average movement duration (H3 - Zone 2)	5.58	
	[4.52, 6.87]	
Average movement duration (H4 - Zone 1)	7.69	CR
	[5.8, 10.2]	
Average movement duration (H4 - Zone 2)	4.82	
	[3.89, 5.97]	
Average movement duration (H5 - Zone 1)	7.41	CR
	[5.3, 10.4]	
Average movement duration (H5 - Zone 2)	4.95	CR
	[4.04, 6.07]	
Average movement duration (H6 - Zone 1)	8.88	CR
	[6.33, 12.5]	
Average movement duration (H6 - Zone 2)	4.41	CR
	[3.66, 5.31]	
Average movement duration (H7 - Zone 1)	7	CR
	[4.8, 10.2]	
Average movement duration (H7 - Zone 2)	4.54	
	[3.27, 6.32]	

CR = Check residuals

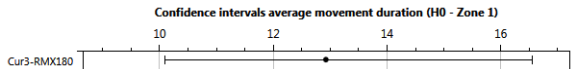
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean H0 - Zone 1	StdErr H0 - Zone 1	Mean H0 - Zone 2	StdErr H0 - Zone 2	Mean H1 - Zone 1	StdErr H1 - Zone 1	Mean H1 - Zone 2	StdErr H1 - Zone 2	Mean H2 - Zone 1	StdErr H2 - Zone 1	Mean H2 - Zone 2	StdErr H2 - Zone 2	Mean H3 - Zone 1	StdErr H3 - Zone 1	Mean H3 - Zone 2	StdErr H3 - Zone 2	Mean H4 - Zone 1	StdErr H4 - Zone 1	Mean H4 - Zone 2	StdErr H4 - Zone 2	Mean H5 - Zone 1	StdErr H5 - Zone 1	Mean H5 - Zone 2	StdErr H5 - Zone 2	Mean H6 - Zone 1	StdErr H6 - Zone 1	Mean H6 - Zone 2	StdErr H6 - Zone 2
Cur3	RMX180	Neutral	14.62	1.24	7.25	0.51	11.12	0.82	6.18	0.31	9.75	0.86	5.54	0.42	8.86	0.72	6.3	0.6	9.04	0.81	5.4	0.44	9.08	1.09	5.45	0.38	10.11	0.89	4.83	0.3

Analysis average movement duration (H0 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_movement_duration_H0_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	12.92	10.09	16.56	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_duration_H0_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 54

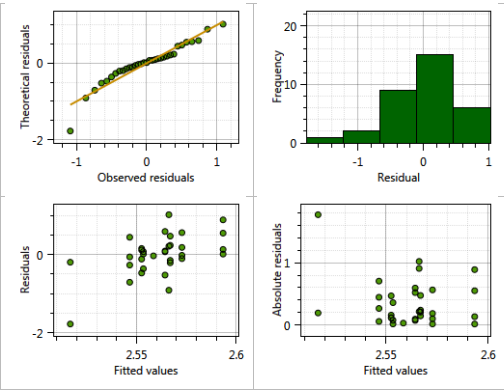
Scaled residuals:
    Min       1Q   Median       3Q      Max
-3.3621 -0.3663  0.0321  0.4087  1.9378

Random effects:
Groups              Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.005997 0.07744
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.000000 0.00000
Residual                                0.278653 0.52788
Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  2.55908    0.09538  4.82653   26.83 1.93e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

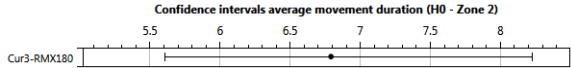
Model residuals

Statistic	Value
Sample skewness	-1.037
Sample excess kurtosis	3.32
Passed Shapiro Wilk normality test	No (p-value = 0.02896 < 0.05)



Analysis average movement duration (H0 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_movement_duration_H0_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	6.791	5.604	8.229	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_duration_H0_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 32

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.66493	-0.62514	0.00281	0.48572	2.24009

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.003904	0.06248
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.022952	0.15150
Residual		0.111452	0.33384

Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

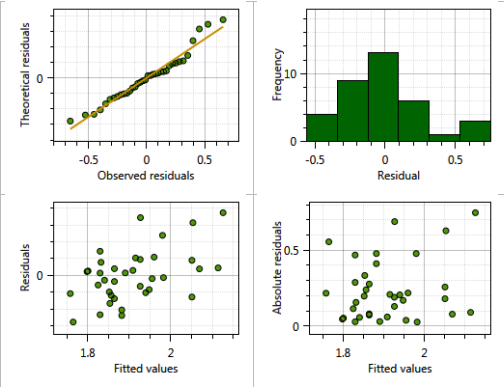
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	1.91556	0.07647	5.41478	25.05	8.29e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

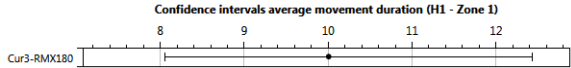
Model residuals

Statistic	Value
Sample skewness	0.5883
Sample excess kurtosis	0.4034
Passed Shapiro Wilk normality test	Yes (p-value = 0.2081 > 0.05)



Analysis average movement duration (H1 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_movement_duration_H1_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	10.01	8.051	12.43	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_duration_H1_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 55

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.0344	-0.4744	0.2194	0.4840	2.0994

Random effects:

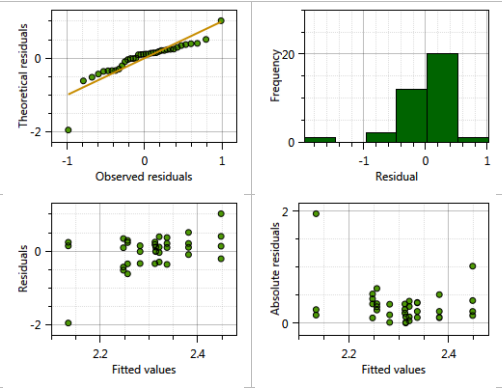
Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.02519	0.1587

Residual 0.23407 0.4838
Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 2.30315 0.09516 8.47230 24.2 4.05e-09 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

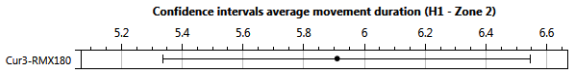
Model residuals

Statistic	Value
Sample skewness	-1.97
Sample excess kurtosis	8.263
Passed Shapiro Wilk normality test	No (p-value = 5.626E-05 < 0.05)



Analysis average movement duration (H1 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_movement_duration_H1_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	5.91	5.335	6.547	a

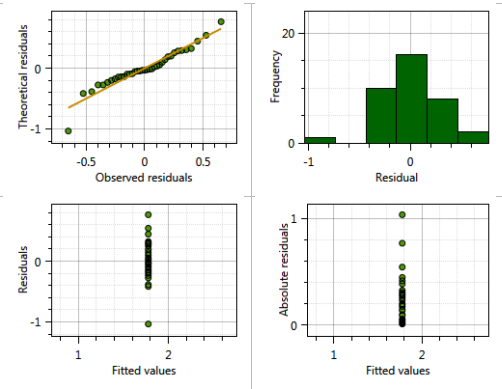
Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_duration_H1_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data
REML criterion at convergence: 20.7
Scaled residuals:
Min 1Q Median 3Q Max
-3.3717 -0.4548 -0.1064 0.6207 2.5004
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.00000 0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.00000 0.0000
Residual 0.09418 0.3069
Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 1.77663 0.05045 36.00000 35.22 <2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

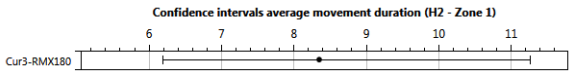
Model residuals

Statistic	Value
Sample skewness	-0.475
Sample excess kurtosis	3.141
Passed Shapiro Wilk normality test	No (p-value = 0.03997 < 0.05)



Analysis average movement duration (H2 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_movement_duration_H2_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	8.348	6.186	11.27	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_duration_H2_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 64.9

Scaled residuals:
Min 1Q Median 3Q Max
-2.37695 -0.43917 0.04724 0.61878 1.75294

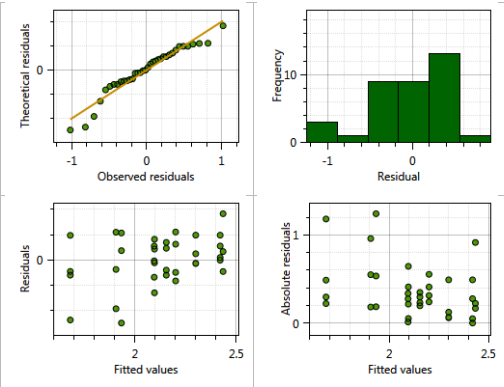
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.00000 0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.09905 0.3147
Residual 0.27221 0.5217
Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 2.1220 0.1325 8.9941 16.02 6.42e-08 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

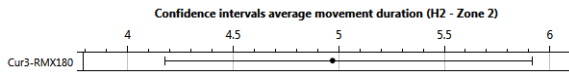
Model residuals

Statistic	Value
Sample skewness	-0.8304
Sample excess kurtosis	0.8605
Passed Shapiro Wilk normality test	Yes (p-value = 0.05553 > 0.05)



Analysis average movement duration (H2 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_movement_duration_H2_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	4.97	4.174	5.918	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_duration_H2_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 59.2

Scaled residuals:
Min 1Q Median 3Q Max
-4.0394 -0.1730 0.0900 0.4223 2.3222

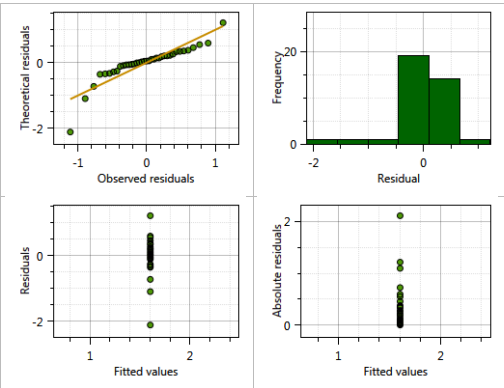
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.000 0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.000 0.0000
Residual 0.274 0.5234
Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 1.60349 0.08605 36.00000 18.63 <2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

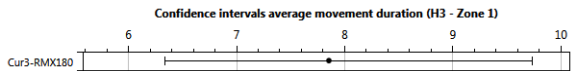
Model residuals

Statistic	Value
Sample skewness	-1.805
Sample excess kurtosis	7.346
Passed Shapiro Wilk normality test	No (p-value = 5.105E-05 < 0.05)



Analysis average movement duration (H3 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_movement_duration_H3_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals average movement duration (H3 - Zone 1)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	7.853	6.334	9.737	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_duration_H3_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 53.8

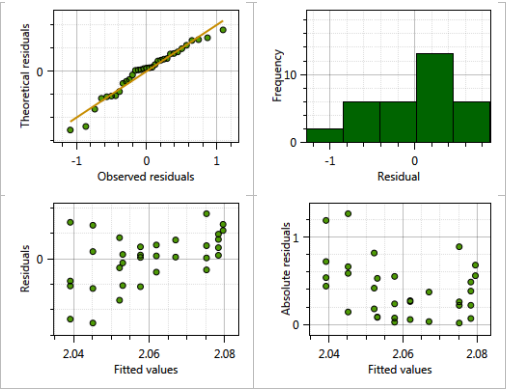
Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.4075 -0.4994  0.1303  0.7047  1.6897

Random effects:
Groups              Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.004185  0.06469
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.000000  0.00000
Residual                                0.278459  0.52769
Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  2.06092     0.09423  8.51350   21.87 8.85e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

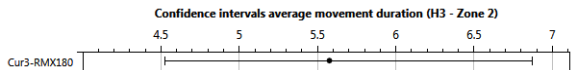
Model residuals

Statistic	Value
Sample skewness	-0.6615
Sample excess kurtosis	0.2188
Passed Shapiro Wilk normality test	Yes (p-value = 0.237 > 0.05)



Analysis average movement duration (H3 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_movement_duration_H3_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals average movement duration (H3 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	5.576	4.523	6.873	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_duration_H3_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 56.6

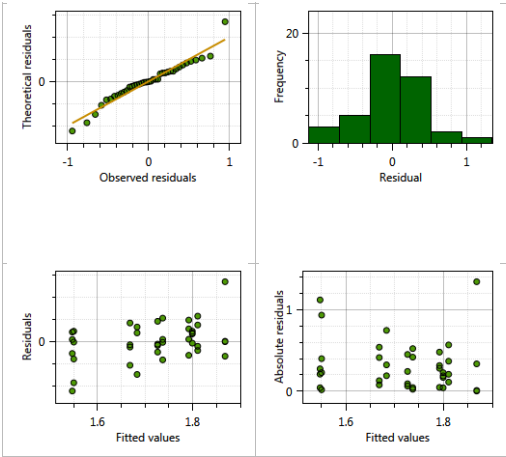
Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.43814 -0.48926 -0.01966  0.49488  2.92464

Random effects:
Groups              Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.000000  0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.03169  0.1780
Residual                                0.21168  0.4601
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  1.71841     0.09279  9.20240   18.52 1.35e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model residuals

Statistic	Value
Sample skewness	0.04414
Sample excess kurtosis	2.082
Passed Shapiro Wilk normality test	Yes (p-value = 0.1537 > 0.05)

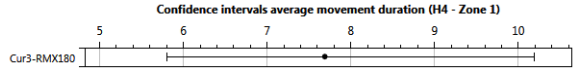


Data points with high residuals

Trial	Arena
Trial 3	26

Analysis average movement duration (H4 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_movement_duration_H4_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	7.689	5.799	10.19	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_duration_H4_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + Genotype_Zone_2:Plant_Zone_2 (1 |
Data: data

REML criterion at convergence: 60.3

Scaled residuals:
Min 1Q Median 3Q Max
-2.4092 -0.3312 0.2779 0.7029 1.2621

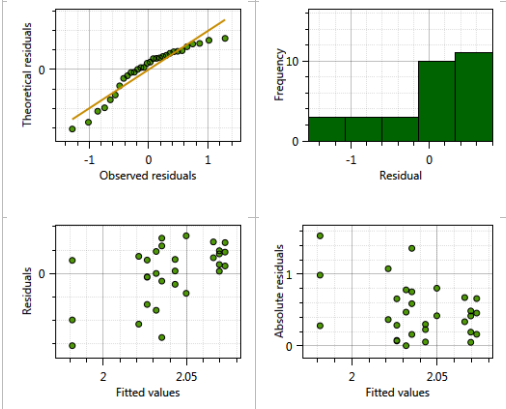
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.00000 0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.01058 0.1029
Residual 0.40685 0.6378
Number of obs: 30, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 2.0397 0.1212 7.5908 16.83 2.77e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

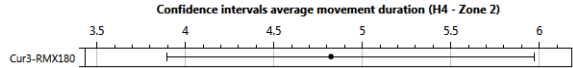
Model residuals

Statistic	Value
Sample skewness	-1.017
Sample excess kurtosis	0.2583
Passed Shapiro Wilk normality test	No (p-value = 0.009072 < 0.05)



Analysis average movement duration (H4 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_movement_duration_H4_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	4.822	3.893	5.972	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_duration_H4_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + Genotype_Zone_2:Plant_Zone_2 (1 |
Data: data

REML criterion at convergence: 51.7

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-2.28263	-0.38914	-0.06957	0.48030	2.07853

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.03251	0.1803
Residual		0.19803	0.4450

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

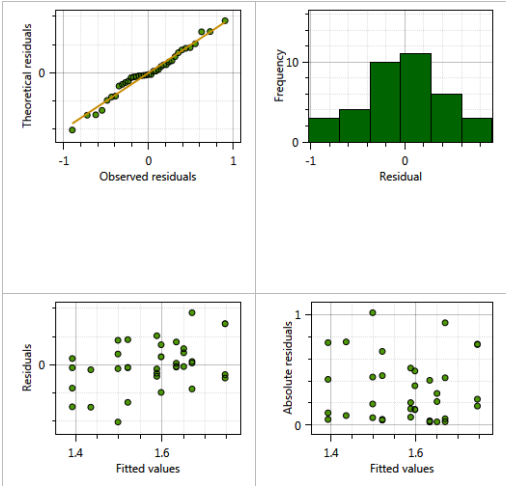
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	1.57323	0.09313	8.18312	16.89	1.19e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

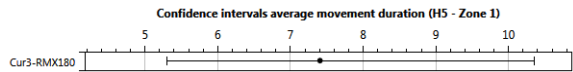
Model residuals

Statistic	Value
Sample skewness	-0.1715
Sample excess kurtosis	0.3177
Passed Shapiro Wilk normality test	Yes (p-value = 0.6172 > 0.05)



Analysis average movement duration (H5 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_movement_duration_H5_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	7.406	5.296	10.36	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_duration_H5_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 69.8

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-3.3014	-0.4290	0.1387	0.5239	1.9390

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.06795	0.2607
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.00000	0.0000
Residual		0.48014	0.6929

Number of obs: 31, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

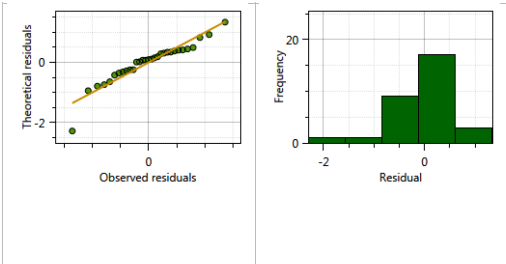
Fixed effects:

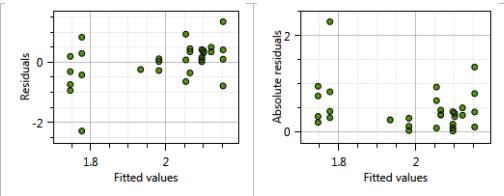
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	2.0023	0.1505	9.9666	13.31	1.14e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

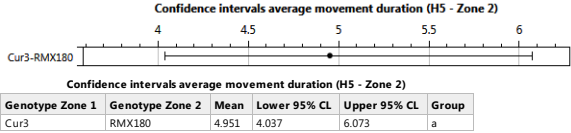
Statistic	Value
Sample skewness	-1.213
Sample excess kurtosis	3.883
Passed Shapiro Wilk normality test	No (p-value = 0.01541 < 0.05)





Analysis average movement duration (H5 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_movement_duration_H5_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_duration_H5_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + Genotype_Zone_2:Plant_Zone_2
Data: data

REML criterion at convergence: 52.8

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-2.6244	-0.3874	0.0524	0.5940	1.9198

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.003813	0.06175
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.007120	0.08438
Residual		0.203604	0.45122

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

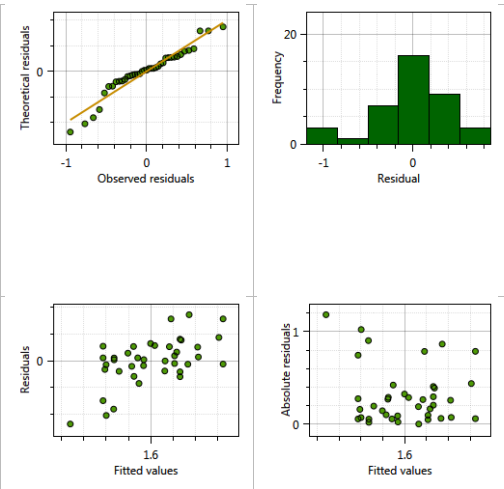
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	1.5997	0.0795	5.0089	20.12	5.52e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

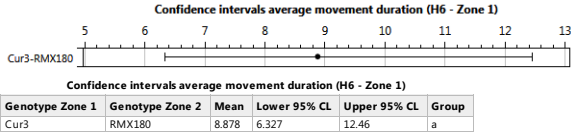
Model residuals

Statistic	Value
Sample skewness	-0.6648
Sample excess kurtosis	1.261
Passed Shapiro Wilk normality test	No (p-value = 0.02959 < 0.05)



Analysis average movement duration (H6 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_movement_duration_H6_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_duration_H6_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + Genotype_Zone_2:Plant_Zone_2
Data: data

REML criterion at convergence: 52.6

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-2.1390	-0.2929	0.1075	0.6883	1.1694

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0839	0.2897
Residual		0.3280	0.5727

Number of obs: 27, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

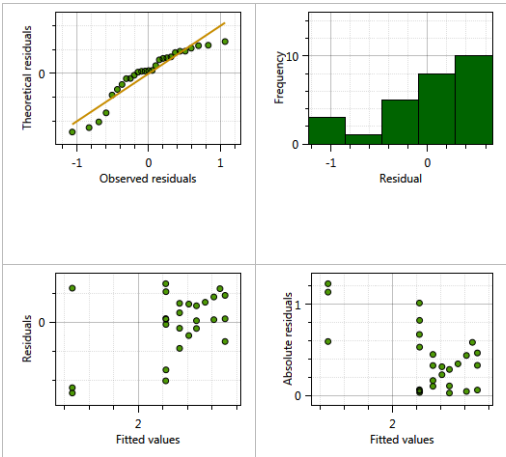
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	2.1835	0.1466	7.9148	14.89	4.53e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

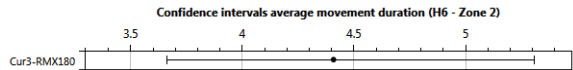
Model residuals

Statistic	Value
Sample skewness	-1.029
Sample excess kurtosis	0.325
Passed Shapiro Wilk normality test	No (p-value = 0.00886 < 0.05)



Analysis average movement duration (H6 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_movement_duration_H6_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	4.408	3.661	5.309	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_duration_H6_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 51.4

Scaled residuals:
Min 1Q Median 3Q Max
-2.7340 -0.3644 0.1449 0.7350 1.5292

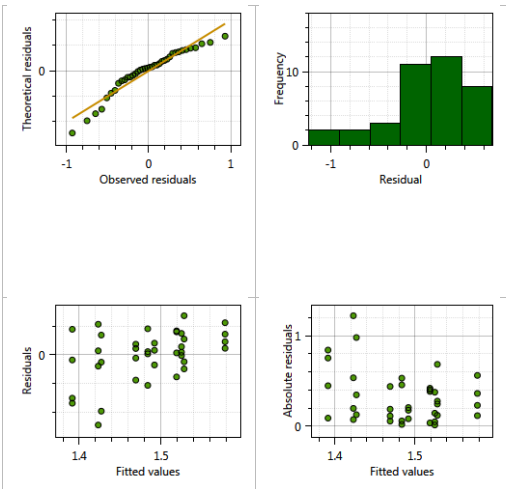
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 1.491e-02 1.221e-01
Genotype_Zone_2:Plant_Zone_2 (Intercept) 3.176e-17 5.636e-09
Residual 2.005e-01 4.478e-01
Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 1.48349 0.08234 9.13848 18.02 1.88e-08 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

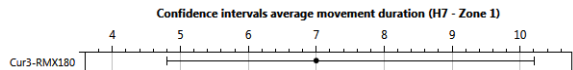
Model residuals

Statistic	Value
Sample skewness	-1.022
Sample excess kurtosis	0.941
Passed Shapiro Wilk normality test	No (p-value = 0.01887 < 0.05)



Analysis average movement duration (H7 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_movement_duration_H7_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals average movement duration (H7 - Zone 1)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	6.998	4.796	10.21	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_duration_H7_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 67.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.0856	-0.1677	0.1866	0.6752	0.9303

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.04877	0.2208
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Residual		0.58270	0.7633

Number of obs: 28, groups: Genotype_Zone_2:Plant_Zone_2, 10; Genotype_Zone_1:Plant_Zone_1, 9

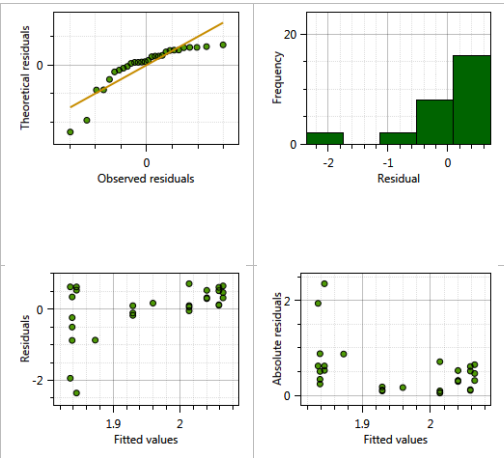
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	1.9457	0.1622	7.5679	11.99	3.41e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

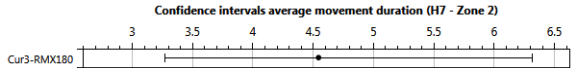
Model residuals

Statistic	Value
Sample skewness	-1.959
Sample excess kurtosis	3.958
Passed Shapiro Wilk normality test	No (p-value = 5.029E-05 < 0.05)



Analysis average movement duration (H7 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_movement_duration_H7_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals average movement duration (H7 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	4.544	3.268	6.318	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_duration_H7_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 56.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.05501	-0.36560	0.09657	0.51678	1.75502

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.12344	0.3513
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.05984	0.2446
Residual		0.13721	0.3704

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

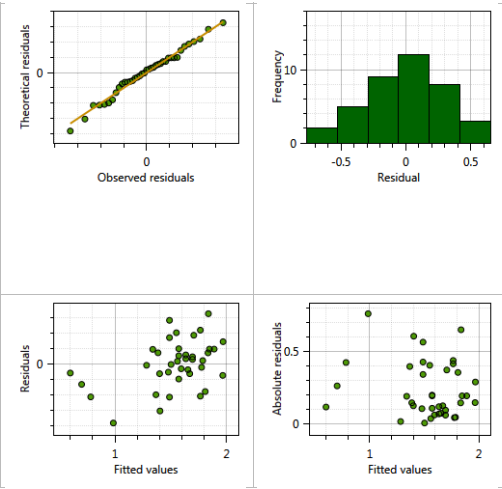
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	1.5138	0.1479	10.0151	10.23	1.27e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

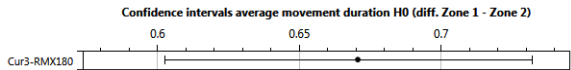
Model residuals

Statistic	Value
Sample skewness	-0.2549
Sample excess kurtosis	0.1397
Passed Shapiro Wilk normality test	Yes (p-value = 0.9078 > 0.05)



Analysis average movement duration H0 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_movement_duration_H0_Zone_1,Average_movement_duration_H0_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals average movement duration H0 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.6706	0.6024	0.7322	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 54.7

Scaled residuals:
Min 1Q Median 3Q Max
-2.58825 -0.45201 0.05375 0.56104 1.74825

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.02322 0.1524
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.04864 0.2205
Residual 1.15077 1.0727
Number of obs: 32, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

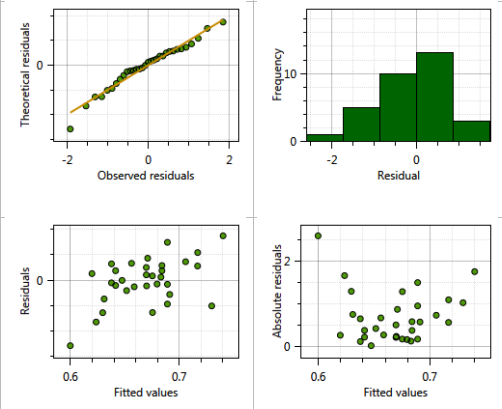
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 0.7107 0.1227 6.4610 5.793 0.000892 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 1.073

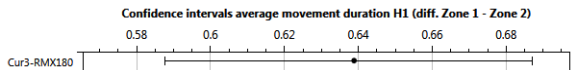
Model residuals

Statistic	Value
Sample skewness	-0.6083
Sample excess kurtosis	0.9254
Passed Shapiro Wilk normality test	Yes (p-value = 0.565 > 0.05)



Analysis average movement duration H1 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_movement_duration_H1_Zone_1,Average_movement_duration_H1_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals average movement duration H1 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.6388	0.5875	0.6871	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data

```
Weights: wi

REML criterion at convergence: 54.8

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.93435 -0.56250  0.03949  0.47558  2.69152

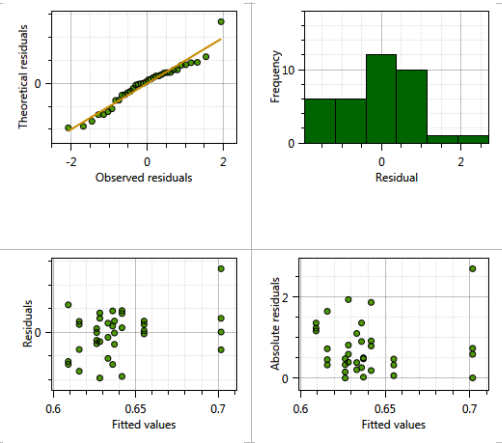
Random effects:
Groups              Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0000   0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.0356   0.1887
Residual                                0.8479   0.9208
Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error      df t value Pr(>|t|)
(Intercept)   0.57029    0.09813  10.80963   5.812 0.000126 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.9208
```

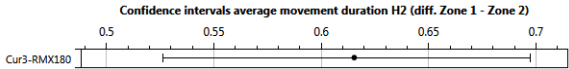
Model residuals

Statistic	Value
Sample skewness	0.1141
Sample excess kurtosis	0.9819
Passed Shapiro Wilk normality test	Yes (p-value = 0.175 > 0.05)



Analysis average movement duration H2 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_movement_duration_H2_Zone_1,Average_movement_duration_H2_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.6153	0.5261	0.6974	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 56.6

Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.1096 -0.6887 -0.1613  0.5369  1.8817

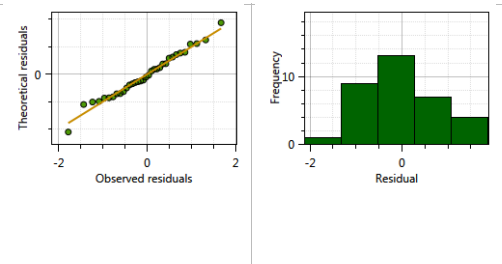
Random effects:
Groups              Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.13771   0.3711
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.06699   0.2588
Residual                                0.57225   0.7565
Number of obs: 34, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

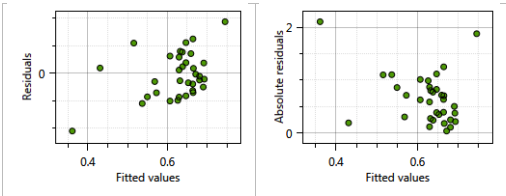
Fixed effects:
              Estimate Std. Error      df t value Pr(>|t|)
(Intercept)   0.4697    0.1598  8.4067   2.94  0.0177 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.7565
```

Model residuals

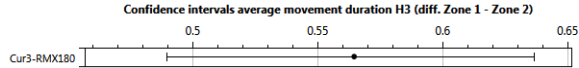
Statistic	Value
Sample skewness	0.0691
Sample excess kurtosis	0.2271
Passed Shapiro Wilk normality test	Yes (p-value = 0.9254 > 0.05)





Analysis average movement duration H3 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_movement_duration_H3_Zone_1Average_movement_duration_H3_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals average movement duration H3 (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5645	0.4895	0.6368	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 61.3

Scaled residuals:
Min 1Q Median 3Q Max
-3.0961 -0.6862 0.1729 0.5624 1.3294

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.05245 0.2290
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.03165 0.1779
Residual 1.02464 1.0122
Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

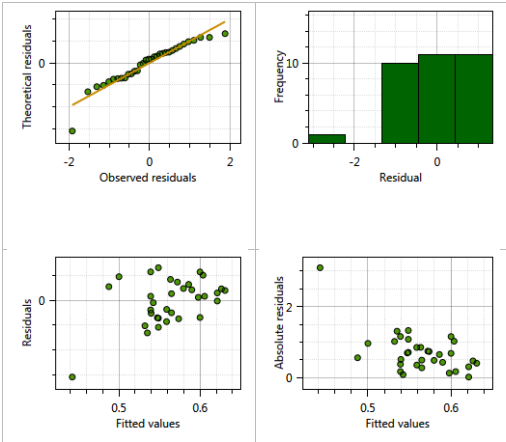
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 0.2596 0.1296 7.5869 2.003 0.082 .

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 1.012

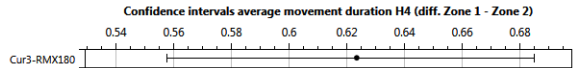
Model residuals

Statistic	Value
Sample skewness	-1.122
Sample excess kurtosis	2.532
Passed Shapiro Wilk normality test	No (p-value = 0.0246 < 0.05)



Analysis average movement duration H4 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_movement_duration_H4_Zone_1Average_movement_duration_H4_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals average movement duration H4 (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.6234	0.5575	0.685	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 43.5

Scaled residuals:
Min 1Q Median 3Q Max
-2.2587 -0.6971 -0.0515 0.6876 1.3251

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.01023 0.1012
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.04806 0.2192
Residual 0.70061 0.8370
Number of obs: 28, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

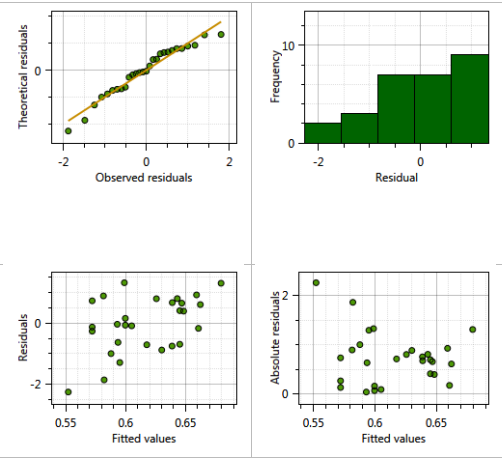
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)

```
(Intercept) 0.5040 0.1154 6.9751 4.369 0.00331 **
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.837
```

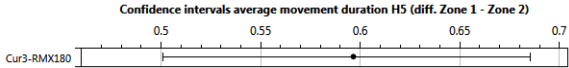
Model residuals

Statistic	Value
Sample skewness	-0.6245
Sample excess kurtosis	-0.04019
Passed Shapiro Wilk normality test	Yes (p-value = 0.2488 > 0.05)



Analysis average movement duration H5 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_movement_duration_H5_Zone_1,Average_movement_duration_H5_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5965	0.5007	0.6855	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 65.4

Scaled residuals:
  Min       1Q   Median       3Q      Max
-1.53472 -0.58918  0.04135  0.41041  2.31526

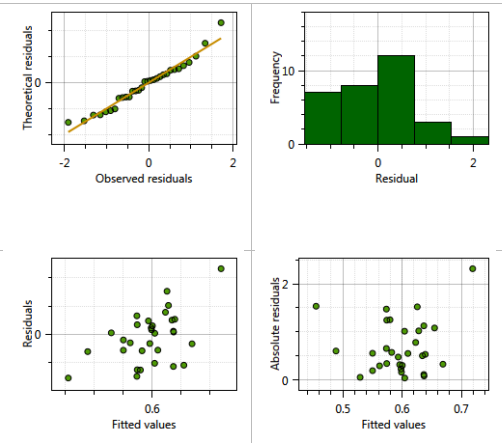
Random effects:
Groups              Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.07423  0.2725
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.06207  0.2491
Residual              1.11148  1.0543
Number of obs: 31, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  0.3910     0.1571  5.7610  2.489  0.0488 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 1.054
```

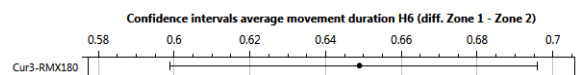
Model residuals

Statistic	Value
Sample skewness	0.5062
Sample excess kurtosis	0.5888
Passed Shapiro Wilk normality test	Yes (p-value = 0.4223 > 0.05)



Analysis average movement duration H6 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_movement_duration_H6_Zone_1,Average_movement_duration_H6_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.6489	0.5988	0.6959	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 43.6

Scaled residuals:
  Min       1Q   Median       3Q      Max
-2.8100 -0.8525 -0.2171  0.6705  1.4620

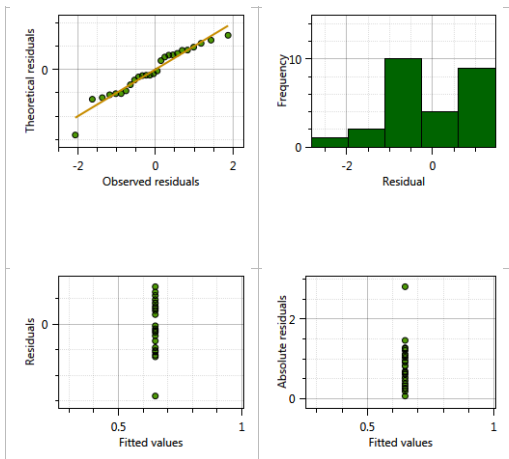
Random effects:
Groups              Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.000    0.000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.000    0.000
Residual                        1.026    1.013
Number of obs: 26, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   0.6142     0.1038 25.0000   5.917 3.56e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 1.013
```

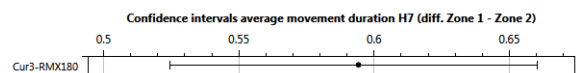
Model residuals

Statistic	Value
Sample skewness	-0.6151
Sample excess kurtosis	0.5375
Passed Shapiro Wilk normality test	Yes (p-value = 0.2301 > 0.05)



Analysis average movement duration H7 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_movement_duration_H7_Zone_1,Average_movement_duration_H7_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5942	0.5244	0.6604	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 51.8

Scaled residuals:
  Min       1Q   Median       3Q      Max
-2.03475 -0.75653  0.06589  0.62285  1.33171

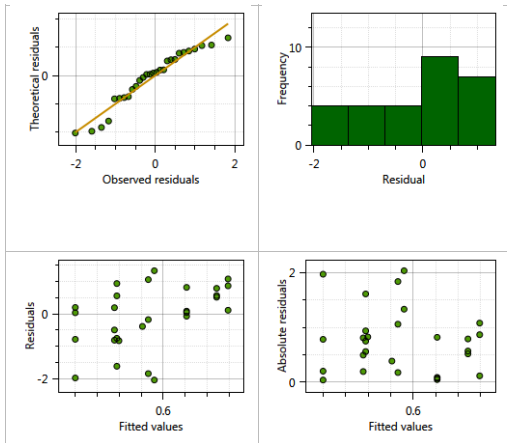
Random effects:
Groups              Name                Variance Std.Dev.
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.03561  0.1887
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.00000  0.0000
Residual                        1.03753  1.0186
Number of obs: 28, groups: Genotype_Zone_2:Plant_Zone_2, 10; Genotype_Zone_1:Plant_Zone_1, 9

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   0.3814     0.1223  7.7119   3.12  0.0149 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 1.019
```

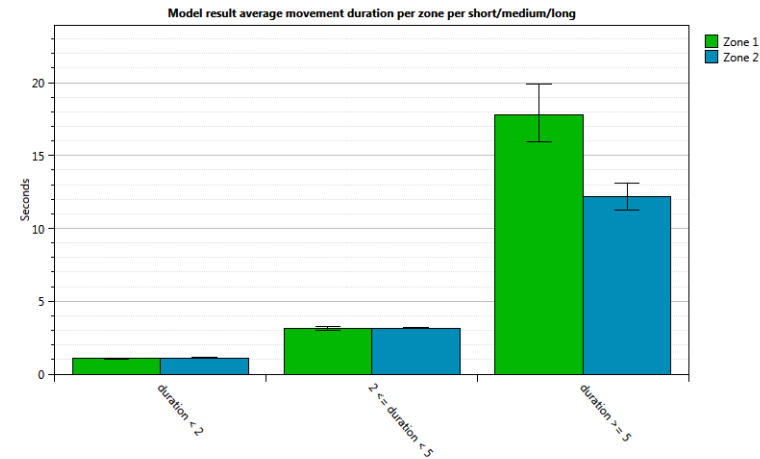
Model residuals

Statistic	Value
Sample skewness	-0.6426
Sample excess kurtosis	-0.3784
Passed Shapiro Wilk normality test	Yes (p-value = 0.08009 > 0.05)



Average movement duration per zone per short/medium/long

Selected zones	Zone 1, Zone 2
Event duration categories	duration < 2, 2 <= duration < 5, duration >= 5
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

Behaviour statistic	Cur3-RMX180	Remark
Average movement duration duration < 2 (diff. Zone 1 - Zone 2)	p=0.07 [-0.0612, 0.00252]	CR
Average movement duration 2 <= duration < 5 (diff. Zone 1 - Zone 2)	p=0.497 [-0.0299, 0.0148]	CR
Average movement duration duration >= 5 (diff. Zone 1 - Zone 2)	p=4.86E-11**** [0.286, 0.446]	CR

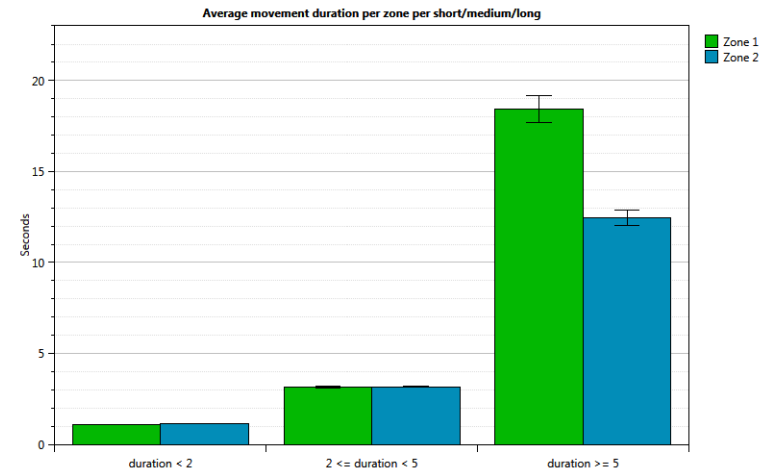
CR = Check residuals

The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Average movement duration (duration < 2 - Zone 1)	1.08 [1.05, 1.12]	CR
Average movement duration (2 <= duration < 5 - Zone 1)	3.14 [3.03, 3.25]	CR
Average movement duration (duration >= 5 - Zone 1)	17.8 [15.9, 19.9]	CR
Average movement duration (duration < 2 - Zone 2)	1.12 [1.11, 1.13]	CR
Average movement duration (2 <= duration < 5 - Zone 2)	3.17 [3.12, 3.21]	CR
Average movement duration (duration >= 5 - Zone 2)	12.2 [11.3, 13.1]	CR

CR = Check residuals

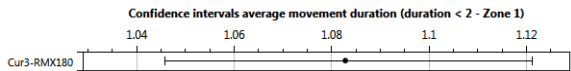
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean duration < 2 - Zone 1	StdErr duration < 2 - Zone 1	Mean 2 <= duration < 5 - Zone 1	StdErr 2 <= duration < 5 - Zone 1	Mean duration >= 5 - Zone 1	StdErr duration >= 5 - Zone 1	Mean duration < 2 - Zone 2	StdErr duration < 2 - Zone 2	Mean 2 <= duration < 5 - Zone 2	StdErr 2 <= duration < 5 - Zone 2	Mean duration >= 5 - Zone 2	StdErr duration >= 5 - Zone 2
Cur3	RMX180	Neutral	1.09	0.01	3.15	0.04	18.43	0.74	1.12	0.01	3.17	0.01	12.47	0.44

Analysis average movement duration (duration < 2 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_movement_duration_duration_2_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	1.083	1.046	1.121	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_duration_duration_2_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: -57.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-5.5648	-0.1121	0.1486	0.4022	1.0470

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.00000	0.0000
Residual		0.01126	0.1061

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

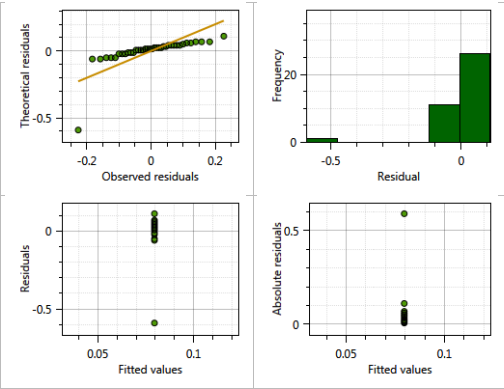
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.07955	0.01721	37.00000	4.622	4.5e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

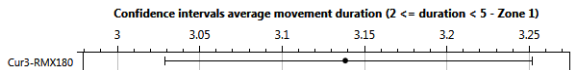
Model residuals

Statistic	Value
Sample skewness	-4.853
Sample excess kurtosis	27.3
Passed Shapiro Wilk normality test	No (p-value = 2.652E-10 < 0.05)



Analysis average movement duration (2 <= duration < 5 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_movement_duration_2_duration_5_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	3.138	3.029	3.252	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_duration_2_duration_5_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: -80.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.8937	-0.2465	0.1146	0.4597	1.1135

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	9.157e-04	3.026e-02
Genotype_Zone_2:Plant_Zone_2	(Intercept)	7.527e-18	2.743e-09
Residual		5.279e-03	7.265e-02

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

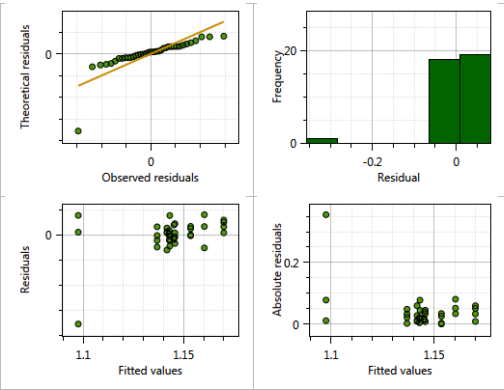
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	1.1437	0.0152	7.3862	75.23	6.3e-12 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

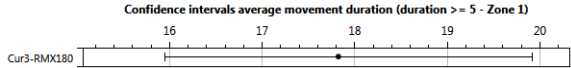
Model residuals

Statistic	Value
Sample skewness	-3.756
Sample excess kurtosis	19.32
Passed Shapiro Wilk normality test	No (p-value = 2.53E-08 < 0.05)



Analysis average movement duration (duration >= 5 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_movement_duration_duration_5_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals average movement duration (duration >= 5 - Zone 1)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	17.82	15.95	19.92	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_duration_duration_5_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 13.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.8970	-0.3255	0.0750	0.6054	1.9852

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	3.968e-03	6.299e-02
Genotype_Zone_2:Plant_Zone_2	(Intercept)	1.830e-17	4.278e-09
Residual		7.462e-02	2.732e-01

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

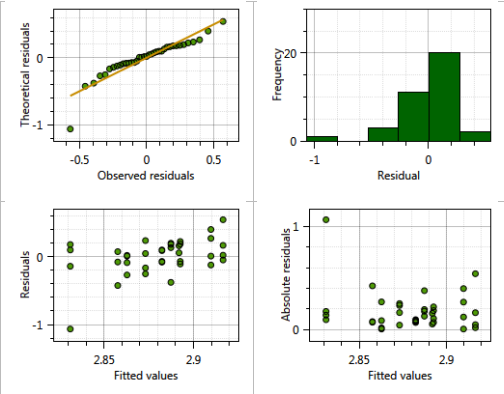
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	2.88047	0.04923	9.07376	58.51	5.21e-13 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

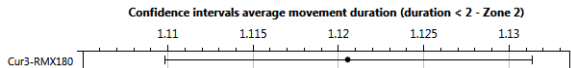
Model residuals

Statistic	Value
Sample skewness	-1.658
Sample excess kurtosis	6.199
Passed Shapiro Wilk normality test	No (p-value = 0.0007474 < 0.05)



Analysis average movement duration (duration < 2 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_movement_duration_duration_2_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals average movement duration (duration < 2 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	1.121	1.11	1.131	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_duration_duration_2_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: -155.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.87044	-0.77681	-0.01624	0.57981	3.13871

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000000	0.00000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000000	0.00000

Residual 0.0008818 0.02969
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

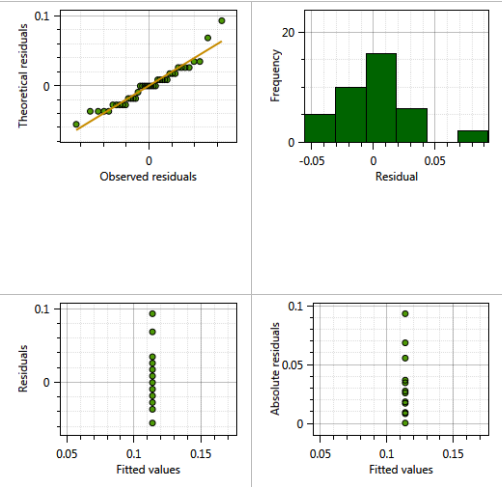
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.113811	0.004755	38.000000	23.93	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

Statistic	Value
Sample skewness	0.8466
Sample excess kurtosis	1.613
Passed Shapiro Wilk normality test	No (p-value = 0.04088 < 0.05)

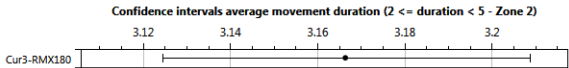


Data points with high residuals

Trial	Arena
Trial 3	12

Analysis average movement duration (2 <= duration < 5 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_movement_duration_2_duration_5_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	3.166	3.124	3.209	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_duration_2_duration_5_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: -161.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.6439	-0.3677	0.2898	0.5166	2.2532

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	1.095e-04	0.010462
Genotype_Zone_2:Plant_Zone_2	(Intercept)	1.956e-05	0.004423
Residual		6.612e-04	0.025714

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

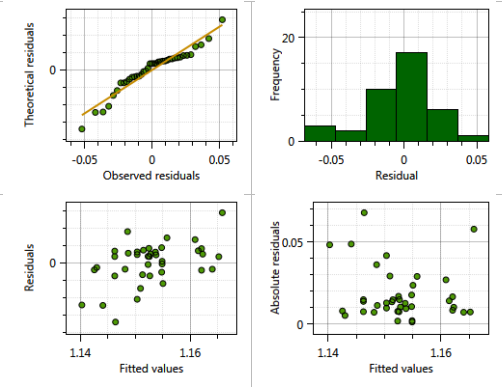
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	1.152572	0.005469	6.104668	210.7	5.05e-13 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

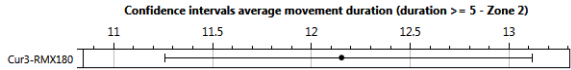
Statistic	Value
Sample skewness	-0.6762
Sample excess kurtosis	1.359
Passed Shapiro Wilk normality test	No (p-value = 0.03554 < 0.05)



Analysis average movement duration (duration >= 5 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_movement_duration_duration_5_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
----------------	---

Transformation	Natural logarithm
----------------	-------------------



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	12.15	11.26	13.12	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_movement_duration_duration_5_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 1.8

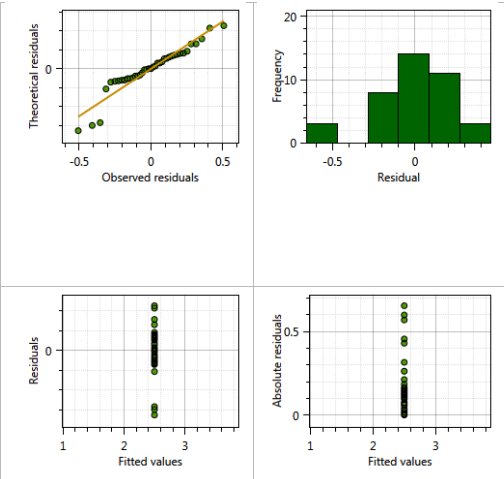
Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.76907 -0.43929  0.00618  0.59035  1.92841

Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.000e+00  0.000e+00
Genotype_Zone_2:Plant_Zone_2 (Intercept)  1.797e-18  1.341e-09
Residual                                5.575e-02  2.361e-01
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error      df t value Pr(>|t|)
(Intercept)  2.49751    0.03781 38.0000    66.06  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

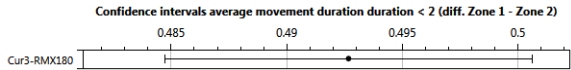
Model residuals

Statistic	Value
Sample skewness	-0.9093
Sample excess kurtosis	1.911
Passed Shapiro Wilk normality test	No (p-value = 0.005292 < 0.05)



Analysis average movement duration duration < 2 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_movement_duration_duration_2_Zone_1,Average_movement_duration_duration_2_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4927	0.4847	0.5006	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: -64.1

Scaled residuals:
    Min       1Q   Median       3Q      Max
-5.3319 -0.2400  0.1203  0.3977  1.2362

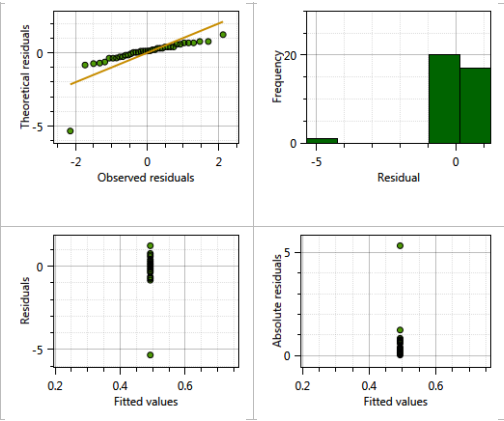
Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.000000  0.00000
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.000000  0.00000
Residual                                0.005179  0.07197
Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error      df t value Pr(>|t|)
(Intercept) -0.02932    0.01571 37.0000   -1.866   0.07 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.07197
```

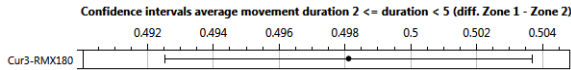
Model residuals

Statistic	Value
Sample skewness	-4.192
Sample excess kurtosis	22.28
Passed Shapiro Wilk normality test	No (p-value = 4.365E-09 < 0.05)



Analysis average movement duration 2 <= duration < 5 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_movement_duration_2_duration_5_Zone_1,Average_movement_duration_2_duration_5_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals average movement duration 2 <= duration < 5 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4981	0.4925	0.5037	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: -90.2

Scaled residuals:
  Min       1Q   Median       3Q      Max
-4.4632 -0.3452  0.0885  0.5939  1.3655

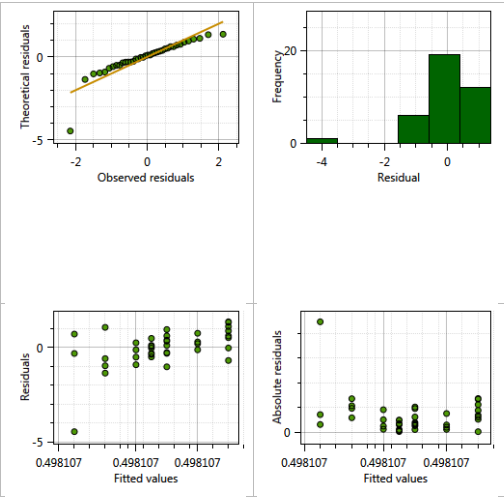
Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 5.231e-17 7.233e-09
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.000e+00 0.000e+00
Residual                          7.322e-03 8.557e-02
Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept) -0.007572   0.011039  37.000000  -0.686   0.497

Dispersion: 0.08557
```

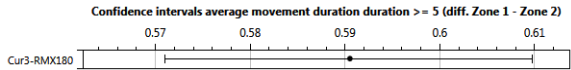
Model residuals

Statistic	Value
Sample skewness	-2.353
Sample excess kurtosis	9.782
Passed Shapiro Wilk normality test	No (p-value = 2.157E-05 < 0.05)



Analysis average movement duration duration >= 5 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_movement_duration_duration_5_Zone_1,Average_movement_duration_duration_5_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals average movement duration duration >= 5 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5905	0.571	0.6098	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
```

Weights: wi

REML criterion at convergence: 4

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.7442	-0.7658	-0.0311	0.6109	3.4373

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00e+00	0.000e+00
Genotype_Zone_2:Plant_Zone_2	(Intercept)	2.14e-18	1.463e-09
Residual		4.38e-01	6.618e-01

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

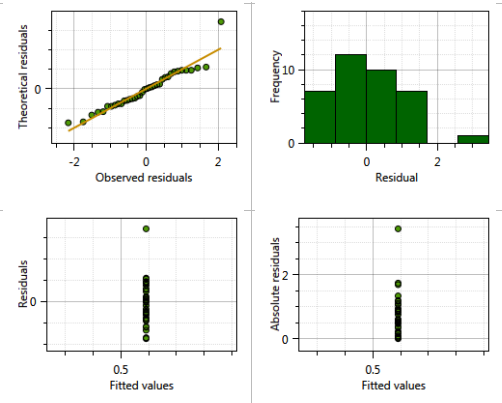
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.3661	0.0396	36.0000	9.244	4.86e-11 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.6618

Model residuals

Statistic	Value
Sample skewness	0.9662
Sample excess kurtosis	2.647
Passed Shapiro Wilk normality test	No (p-value = 0.02424 < 0.05)

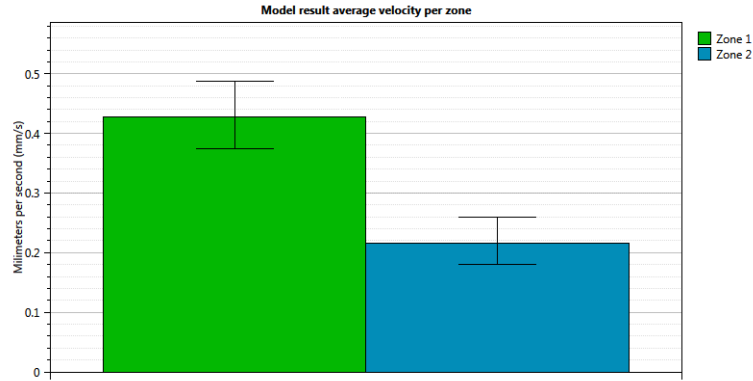


Data points with high residuals

Trial	Arena
Trial 3	24

Average velocity per zone

Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

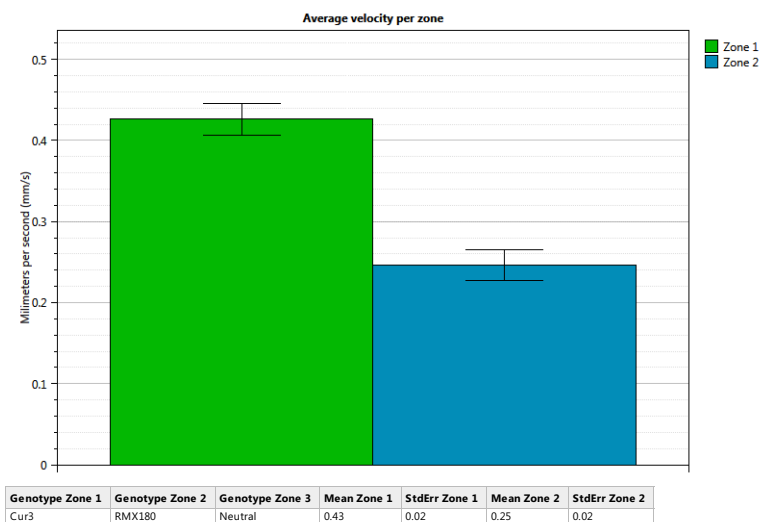
Behaviour statistic	Cur3-RMX180
Average velocity (diff. Zone 1 - Zone 2)	p=0.000461*** [0.316, 0.774]

The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Average velocity (Zone 1)	0.427 [0.374, 0.488]	CR
Average velocity (Zone 2)	0.216 [0.18, 0.26]	

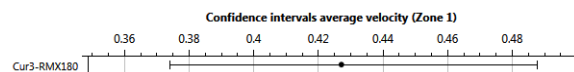
CR = Check residuals

Data summary



Analysis average velocity (Zone 1)

Analysis model	Linear mixed model fit by REML: Average_velocity_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4271	0.374	0.4878	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_velocity_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: -4.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.0731	-0.5542	0.1016	0.5345	1.7247

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.004477	0.06691
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.022924	0.15141
Residual		0.031427	0.17728

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

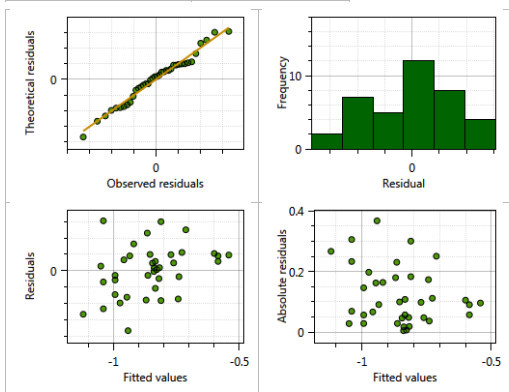
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.85070	0.05984	10.23402	-14.22	4.53e-08 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

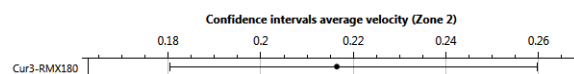
Model residuals

Statistic	Value
Sample skewness	-0.1527
Sample excess kurtosis	-0.04382
Passed Shapiro Wilk normality test	Yes (p-value = 0.6667 > 0.05)



Analysis average velocity (Zone 2)

Analysis model	Linear mixed model fit by REML: Average_velocity_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2164	0.1803	0.2598	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_velocity_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 67.9

Scaled residuals:

Min1QMedian3QMax

-2.6012-0.65080.18360.72171.7502

Random effects:

Groups

Name

Variance

Std.Dev.

Genotype_Zone_1:Plant_Zone_1 (Intercept)0.00000.0000

Genotype_Zone_2:Plant_Zone_2 (Intercept)0.00000.0000

Residual0.31730.5633

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

Estimate

Std. Error

df

t value

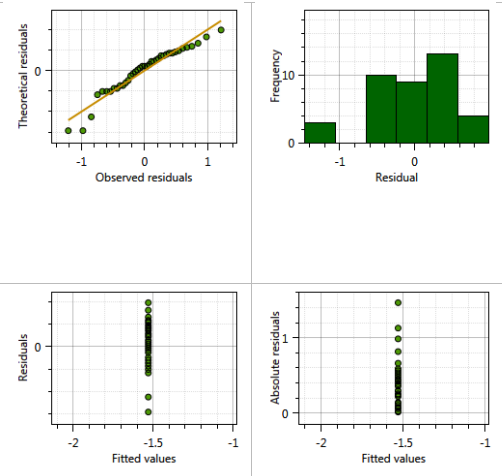
Pr(>|t|)

(Intercept)-1.530540.0901938.00000-16.97<2e-16***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

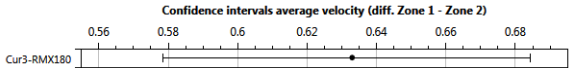
Model residuals

Statistic	Value
Sample skewness	-0.8895
Sample excess kurtosis	0.8517
Passed Shapiro Wilk normality test	No (p-value = 0.03232 < 0.05)



Analysis average velocity (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_velocity_Zone_1,Average_velocity_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.633	0.5784	0.6844	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 61.5

Scaled residuals:
Min1QMedian3QMax
-1.94683-0.598150.023920.645072.29962

Random effects:
GroupsNameVarianceStd.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)0.000000.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept)0.045710.2138
Residual0.033810.1839
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

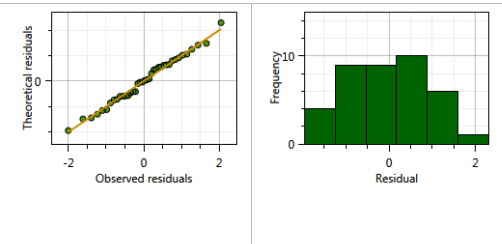
Fixed effects:
EstimateStd. Errordf t valuePr(>|t|)
(Intercept)0.54500.10098.83655.40.000461***

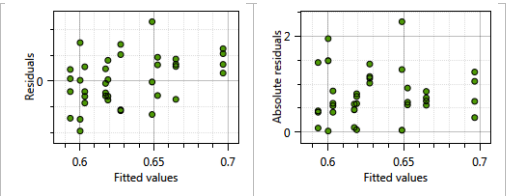
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.1839

Model residuals

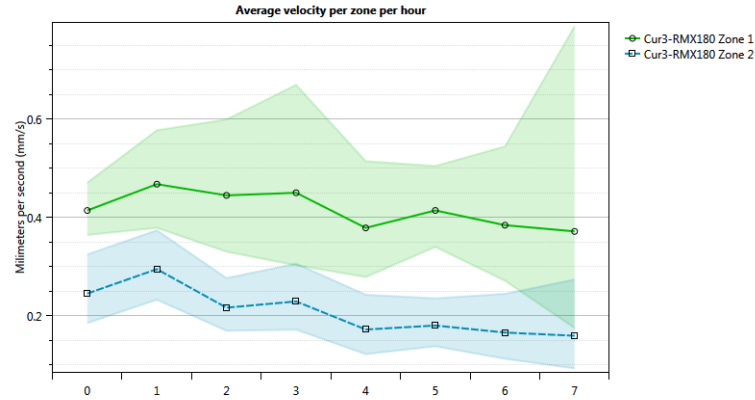
Statistic	Value
Sample skewness	0.06683
Sample excess kurtosis	-0.3361
Passed Shapiro Wilk normality test	Yes (p-value = 0.9519 > 0.05)





Average velocity per zone per hour

Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

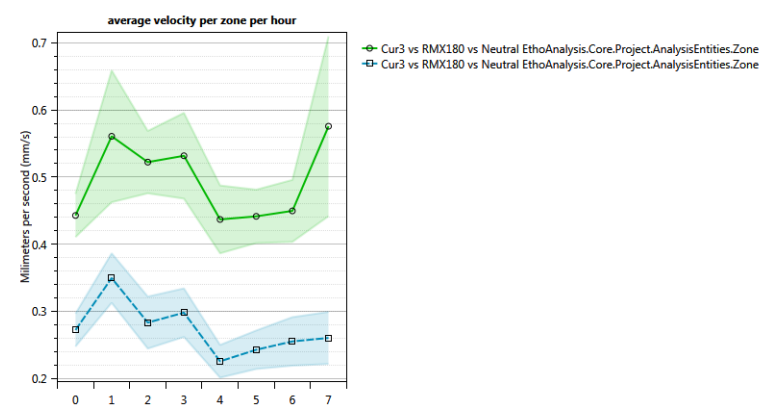
Behaviour statistic	Cur3-RMX180
Average velocity H0 (diff. Zone 1 - Zone 2)	p=0.0213* [0.0881, 0.854]
Average velocity H1 (diff. Zone 1 - Zone 2)	p=0.102 [-0.0954, 0.897]
Average velocity H2 (diff. Zone 1 - Zone 2)	p=2.46E-06**** [0.379, 0.801]
Average velocity H3 (diff. Zone 1 - Zone 2)	p=0.0362* [0.0358, 0.796]
Average velocity H4 (diff. Zone 1 - Zone 2)	p=0.0193* [0.117, 1.02]
Average velocity H5 (diff. Zone 1 - Zone 2)	p=0.0151* [0.119, 0.853]
Average velocity H6 (diff. Zone 1 - Zone 2)	p=0.0243* [0.0513, 0.599]
Average velocity H7 (diff. Zone 1 - Zone 2)	p=0.12 [-0.168, 1.19]

The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Average velocity (H0 - Zone 1)	0.414 [0.364, 0.471]	
Average velocity (H0 - Zone 2)	0.245 [0.185, 0.325]	
Average velocity (H1 - Zone 1)	0.467 [0.379, 0.577]	CR
Average velocity (H1 - Zone 2)	0.295 [0.232, 0.374]	
Average velocity (H2 - Zone 1)	0.445 [0.33, 0.599]	
Average velocity (H2 - Zone 2)	0.216 [0.169, 0.277]	
Average velocity (H3 - Zone 1)	0.45 [0.303, 0.67]	
Average velocity (H3 - Zone 2)	0.229 [0.171, 0.306]	
Average velocity (H4 - Zone 1)	0.379 [0.279, 0.514]	
Average velocity (H4 - Zone 2)	0.172 [0.122, 0.243]	CR
Average velocity (H5 - Zone 1)	0.414 [0.34, 0.504]	CR
Average velocity (H5 - Zone 2)	0.18 [0.138, 0.235]	
Average velocity (H6 - Zone 1)	0.384 [0.271, 0.544]	
Average velocity (H6 - Zone 2)	0.166 [0.112, 0.245]	
Average velocity (H7 - Zone 1)	0.371 [0.175, 0.788]	
Average velocity (H7 - Zone 2)	0.159 [0.0927, 0.274]	

CR = Check residuals

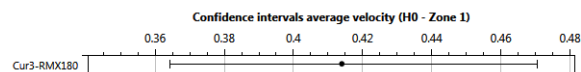
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean H0 - Zone 1	StdErr H0 - Zone 1	Mean H0 - Zone 2	StdErr H0 - Zone 2	Mean H1 - Zone 1	StdErr H1 - Zone 1	Mean H1 - Zone 2	StdErr H1 - Zone 2	Mean H2 - Zone 1	StdErr H2 - Zone 1	Mean H2 - Zone 2	StdErr H2 - Zone 2	Mean H3 - Zone 1	StdErr H3 - Zone 1	Mean H3 - Zone 2	StdErr H3 - Zone 2	Mean H4 - Zone 1	StdErr H4 - Zone 1	Mean H4 - Zone 2	StdErr H4 - Zone 2	Mean H5 - Zone 1	StdErr H5 - Zone 1	Mean H5 - Zone 2	StdErr H5 - Zone 2	Mean H6 - Zone 1	StdErr H6 - Zone 1	Mean H6 - Zone 2	StdErr H6 - Zone 2
Cur3	RMX180	Neutral	0.44	0.03	0.27	0.02	0.56	0.1	0.35	0.04	0.52	0.05	0.28	0.04	0.53	0.06	0.3	0.04	0.44	0.05	0.23	0.02	0.44	0.04	0.24	0.03	0.45	0.05	0.26	0.04

Analysis average velocity (H0 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_velocity_H0_Zone_1 ~ 1 + (1 Genotype_Zone_1 Plant_Zone_1) + (1 Genotype_Zone_2 Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.414	0.3642	0.4706	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_velocity_H0_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 29.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.62571	-0.71220	-0.09493	0.57710	2.60090

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		0.1307	0.3615

Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

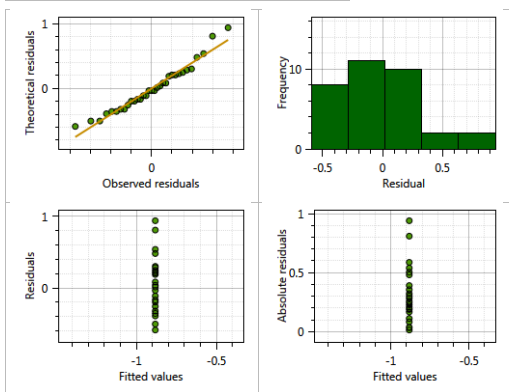
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.88197	0.06293	32.00000	-14.02	3.31e-15 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

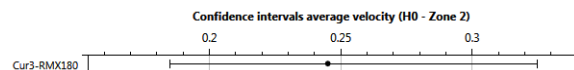
Model residuals

Statistic	Value
Sample skewness	0.7131
Sample excess kurtosis	0.4729
Passed Shapiro Wilk normality test	Yes (p-value = 0.2496 > 0.05)



Analysis average velocity (H0 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_velocity_H0_Zone_2 ~ 1 + (1 Genotype_Zone_1 Plant_Zone_1) + (1 Genotype_Zone_2 Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.245	0.1848	0.3248	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_velocity_H0_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 50.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.69464	-0.54395	0.01485	0.47986	1.98368

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.01577	0.1256
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.07427	0.2725
Residual		0.16316	0.4039

Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

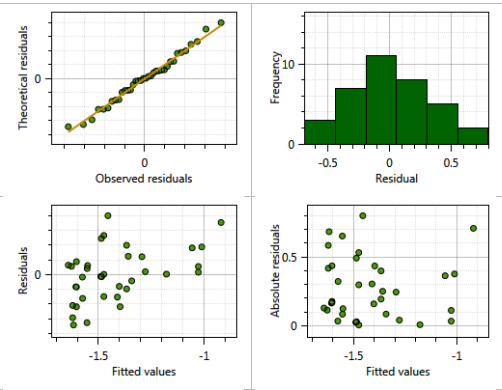
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.4065	0.1171	6.4290	-12.01	1.22e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

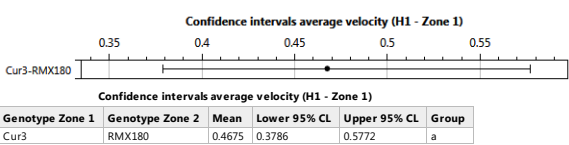
Model residuals

Statistic	Value
Sample skewness	0.1321
Sample excess kurtosis	-0.1797
Passed Shapiro Wilk normality test	Yes (p-value = 0.9061 > 0.05)



Analysis average velocity (H1 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_velocity_H1_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_velocity_H1_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 53.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.6158	-0.5356	-0.1470	0.4007	4.2011

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	2.512e-19	5.012e-10
Genotype_Zone_2:Plant_Zone_2	(Intercept)	1.969e-02	1.403e-01
Residual		2.262e-01	4.756e-01

Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

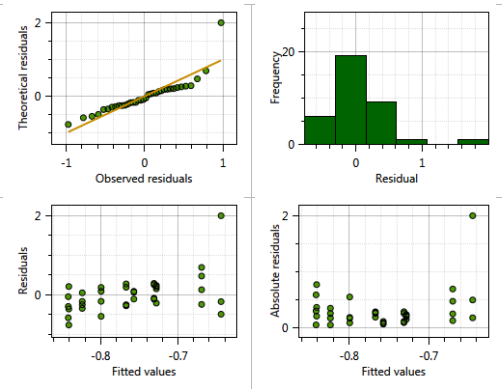
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.7604	0.0910	7.8029	-8.356	3.69e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

Statistic	Value
Sample skewness	2.276
Sample excess kurtosis	9.447
Passed Shapiro Wilk normality test	No (p-value = 3.284E-05 < 0.05)

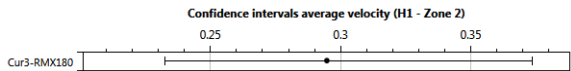


Data points with high residuals

Trial	Arena
Trial 3	12

Analysis average velocity (H1 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_velocity_H1_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2947	0.2324	0.3737	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_velocity_H1_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 67

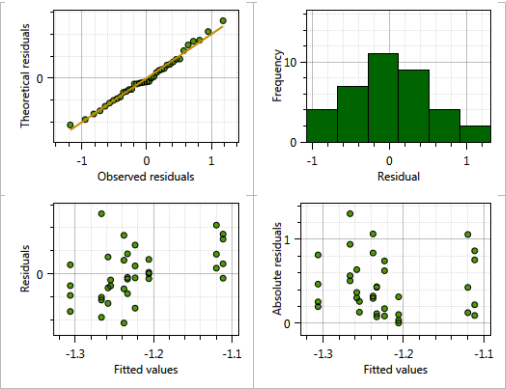
Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.8731 -0.5678 -0.1508  0.5533  2.2971

Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  5.167e-17  7.188e-09
Genotype_Zone_2:Plant_Zone_2 (Intercept)  2.043e-02  1.429e-01
Residual                                3.231e-01  5.684e-01
Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error        df t value Pr(>|t|)
(Intercept)   -1.2218      0.1039    8.4496   -11.76 1.58e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

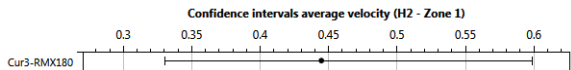
Model residuals

Statistic	Value
Sample skewness	0.3035
Sample excess kurtosis	-0.1333
Passed Shapiro Wilk normality test	Yes (p-value = 0.915 > 0.05)



Analysis average velocity (H2 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_velocity_H2_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4447	0.3301	0.599	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_velocity_H2_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 63.9

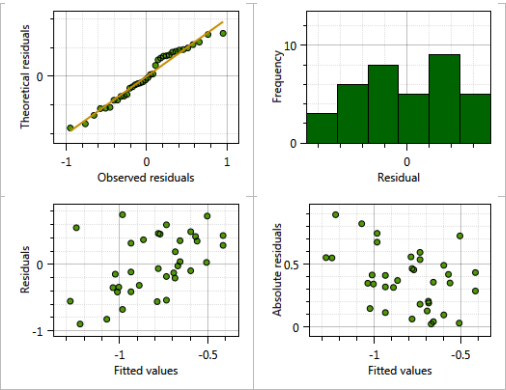
Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.7899 -0.6867 -0.0854  0.7646  1.4923

Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.04191  0.2047
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.06173  0.2485
Residual                                0.25105  0.5010
Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error        df t value Pr(>|t|)
(Intercept)   -0.8104      0.1323    9.2794   -6.126 0.000153 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

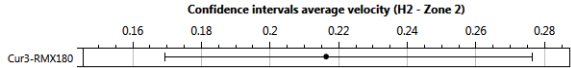
Model residuals

Statistic	Value
Sample skewness	-0.1718
Sample excess kurtosis	-0.9494
Passed Shapiro Wilk normality test	Yes (p-value = 0.2771 > 0.05)



Analysis average velocity (H2 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_velocity_H2_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2163	0.1692	0.2765	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_velocity_H2_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 83.7

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.2930	-0.5911	-0.1066	0.3982	2.1067

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		0.5419	0.7361

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

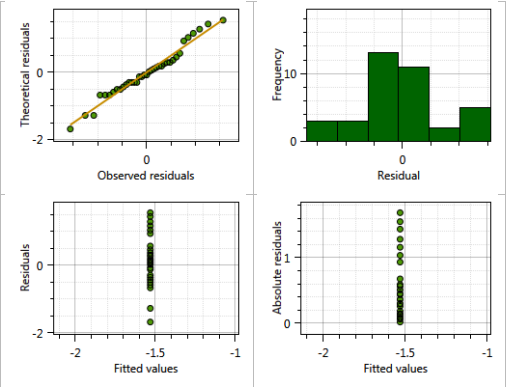
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.531	0.121	36.000	-12.65	8.19e-15 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

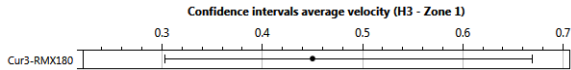
Model residuals

Statistic	Value
Sample skewness	0.1489
Sample excess kurtosis	0.2146
Passed Shapiro Wilk normality test	Yes (p-value = 0.4503 > 0.05)



Analysis average velocity (H3 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_velocity_H3_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.45	0.3025	0.6695	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_velocity_H3_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 63.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.12104	-0.45402	0.09116	0.53058	1.72437

Random effects:

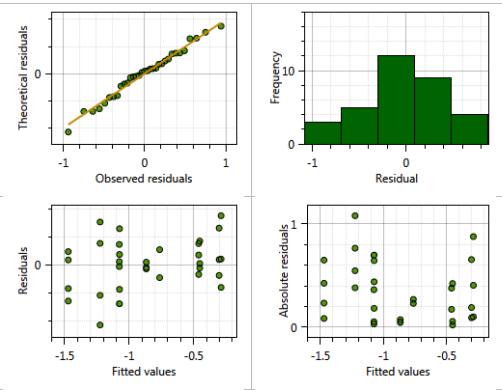
Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.2303	0.4799

Residual 0.2578 0.5078
Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -0.7984 0.1763 9.2523 -4.528 0.00133 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

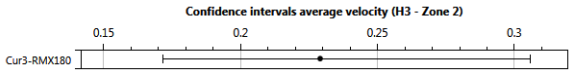
Model residuals

Statistic	Value
Sample skewness	-0.2425
Sample excess kurtosis	-0.07554
Passed Shapiro Wilk normality test	Yes (p-value = 0.8875 > 0.05)



Analysis average velocity (H3 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_velocity_H3_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.229	0.1715	0.3059	a

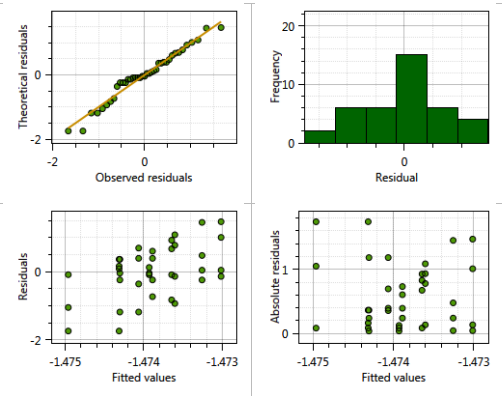
Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_velocity_H3_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data
REML criterion at convergence: 91.8
Scaled residuals:
Min 1Q Median 3Q Max
-2.26168 -0.31273 -0.05163 0.56670 1.90964
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0002197 0.01482
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.0000000 0.00000
Residual 0.5949911 0.77136
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -1.4739 0.1236 7.3602 -11.92 4.46e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

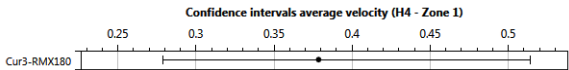
Model residuals

Statistic	Value
Sample skewness	-0.3572
Sample excess kurtosis	0.1168
Passed Shapiro Wilk normality test	Yes (p-value = 0.3109 > 0.05)



Analysis average velocity (H4 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_velocity_H4_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.3785	0.2786	0.5142	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_velocity_H4_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 55.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.90706	-0.33262	0.09275	0.42585	2.04749

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.05304	0.2303
Residual		0.30924	0.5561

Number of obs: 30, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

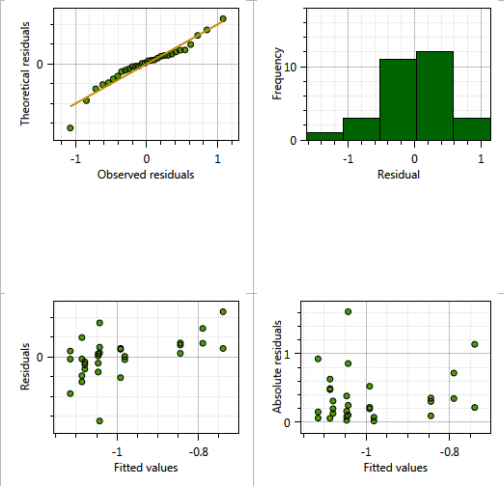
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.9715	0.1259	6.1396	-7.716	0.00022 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

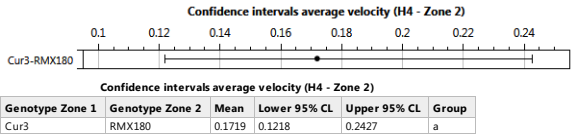
Model residuals

Statistic	Value
Sample skewness	-0.7258
Sample excess kurtosis	2.438
Passed Shapiro Wilk normality test	Yes (p-value = 0.1461 > 0.05)



Analysis average velocity (H4 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_velocity_H4_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_velocity_H4_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 91.7

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.2171	-0.7438	0.3471	0.7403	1.3912

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.06441	0.2538
Residual		0.62500	0.7906

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

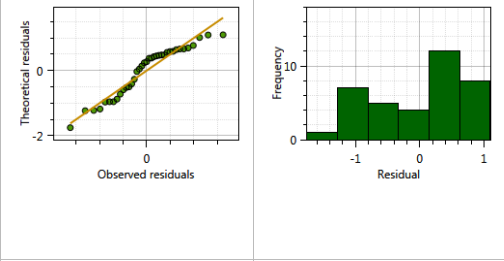
Fixed effects:

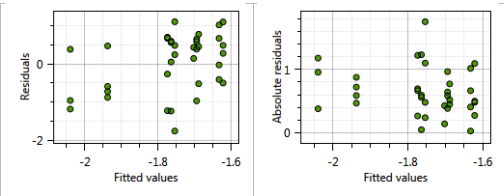
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.7607	0.1533	9.3037	-11.49	8.36e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

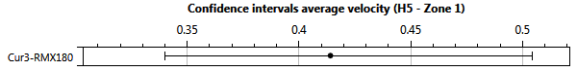
Statistic	Value
Sample skewness	-0.5548
Sample excess kurtosis	-0.8162
Passed Shapiro Wilk normality test	No (p-value = 0.01441 < 0.05)





Analysis average velocity (H5 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_velocity_H5_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals average velocity (H5 - Zone 1)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.414	0.3398	0.5045	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_velocity_H5_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 39.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.8587	-0.2832	0.1598	0.4430	2.1816

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.01219	0.1104
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.00000	0.0000
Residual		0.19330	0.4397

Number of obs: 30, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

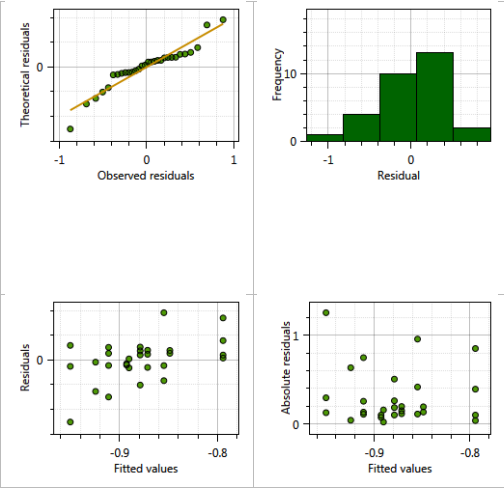
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.88178	0.08793	9.41978	-10.03	2.47e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

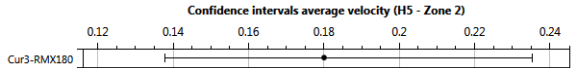
Model residuals

Statistic	Value
Sample skewness	-0.5711
Sample excess kurtosis	2.302
Passed Shapiro Wilk normality test	No (p-value = 0.03003 < 0.05)



Analysis average velocity (H5 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_velocity_H5_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals average velocity (H5 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.18	0.1377	0.2354	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_velocity_H5_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 97

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.16750	-0.59587	0.06523	0.83827	1.60757

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000e+00	0.000e+00
Genotype_Zone_2:Plant_Zone_2	(Intercept)	3.473e-15	5.893e-08
Residual		6.835e-01	8.267e-01

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

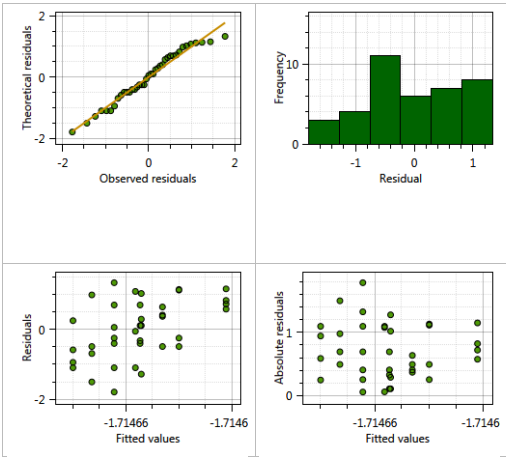
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.7147	0.1324	38.0000	-12.95	1.63e-15 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

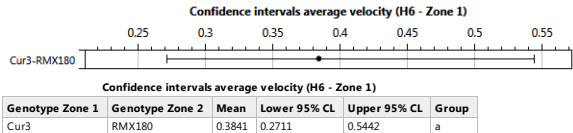
Model residuals

Statistic	Value
Sample skewness	-0.245
Sample excess kurtosis	-0.8185
Passed Shapiro Wilk normality test	Yes (p-value = 0.27 > 0.05)



Analysis average velocity (H6 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_velocity_H6_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.3841	0.2711	0.5442	a

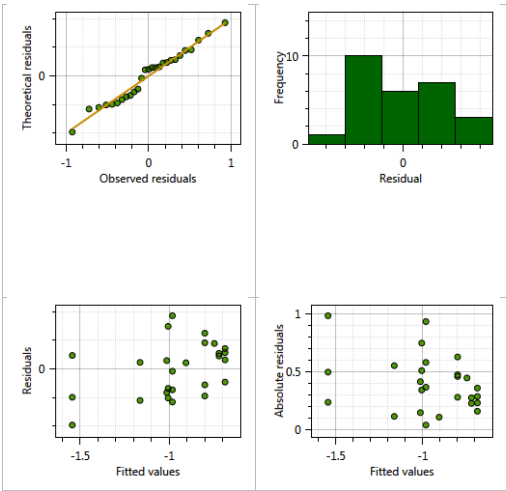
Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_velocity_H6_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data
REML criterion at convergence: 49.4
Scaled residuals:
Min IQ Median 3Q Max
-1.9123 -0.7587 0.2224 0.5453 1.8144
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0000 0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.1247 0.3531
Residual 0.2631 0.5129
Number of obs: 27, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -0.9569 0.1528 8.5314 -6.263 0.000185 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

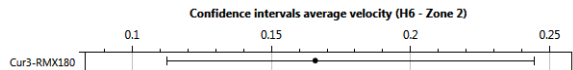
Model residuals

Statistic	Value
Sample skewness	-0.03375
Sample excess kurtosis	-0.5358
Passed Shapiro Wilk normality test	Yes (p-value = 0.6358 > 0.05)



Analysis average velocity (H6 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_velocity_H6_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals average velocity (H6 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1657	0.1123	0.2445	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_velocity_H6_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 108.7

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.6973	-0.9920	0.2281	0.7182	1.7617

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.03609	0.1900
Residual		0.96996	0.9849

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

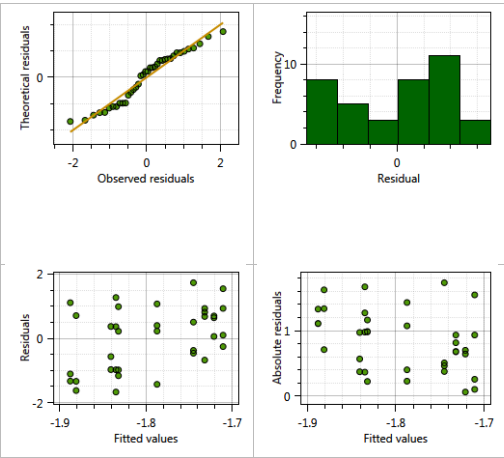
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.7973	0.1708	8.6357	-10.52	3.23e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

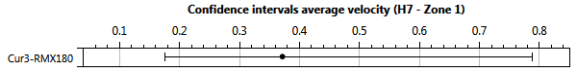
Model residuals

Statistic	Value
Sample skewness	-0.1812
Sample excess kurtosis	-1.188
Passed Shapiro Wilk normality test	Yes (p-value = 0.06215 > 0.05)



Analysis average velocity (H7 - Zone 1)

Analysis model	Linear mixed model fit by REML: Average_velocity_H7_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals average velocity (H7 - Zone 1)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.3715	0.175	0.7884	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_velocity_H7_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 66.5

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.8832	-0.4049	-0.1386	0.2900	1.4995

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.5650	0.7517
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.3269	0.5717
Residual		0.2030	0.4506

Number of obs: 28, groups: Genotype_Zone_2:Plant_Zone_2, 10; Genotype_Zone_1:Plant_Zone_1, 9

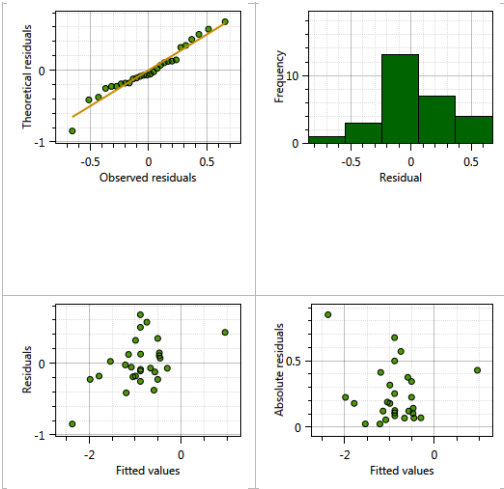
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.9903	0.3207	7.2718	-3.088	0.0168 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

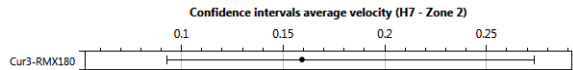
Model residuals

Statistic	Value
Sample skewness	-0.0192
Sample excess kurtosis	0.8524
Passed Shapiro Wilk normality test	Yes (p-value = 0.4259 > 0.05)



Analysis average velocity (H7 - Zone 2)

Analysis model	Linear mixed model fit by REML: Average_velocity_H7_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1592	0.09266	0.2737	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Average_velocity_H7_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 110.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.37109	-0.71195	-0.02461	0.70421	1.79367

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.1809	0.4254
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.2193	0.4683
Residual		0.7070	0.8408

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

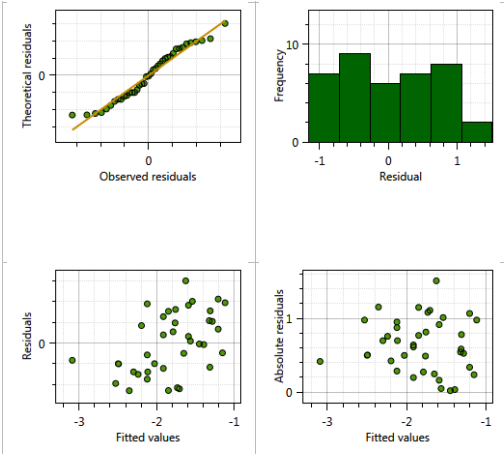
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.8374	0.2414	9.5404	-7.61	2.38e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

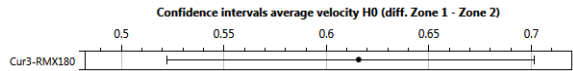
Model residuals

Statistic	Value
Sample skewness	0.08375
Sample excess kurtosis	-1.123
Passed Shapiro Wilk normality test	Yes (p-value = 0.1304 > 0.05)



Analysis average velocity H0 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_velocity_H0_Zone_1,Average_velocity_H0_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.6157	0.522	0.7015	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

```
REML criterion at convergence: 60.9

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.6789 -0.3560  0.0781  0.4209  2.0716

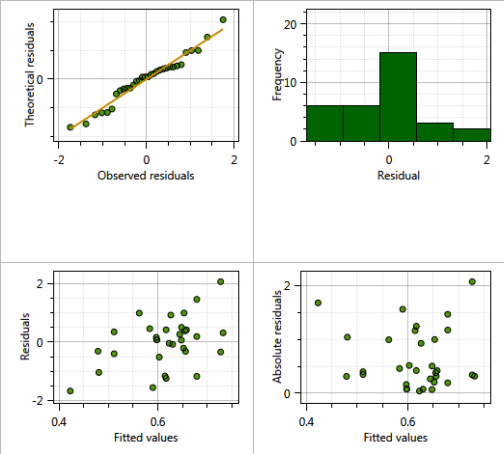
Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.08577  0.2929
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.11463  0.3386
Residual                                0.03749  0.1936
Number of obs: 32, groups:  Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    0.4713     0.1692  8.9458   2.785   0.0213 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.1936
```

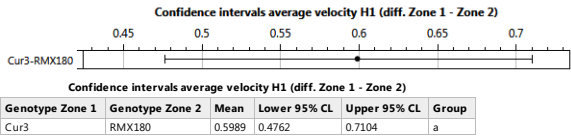
Model residuals

Statistic	Value
Sample skewness	0.004093
Sample excess kurtosis	0.3483
Passed Shapiro Wilk normality test	Yes (p-value = 0.4491 > 0.05)



Analysis average velocity H1 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_velocity_H1_Zone_1,Average_velocity_H1_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
  Data: data
Weights: wi

REML criterion at convergence: 90.1

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.9801 -0.5415  0.2071  0.6024  2.1941

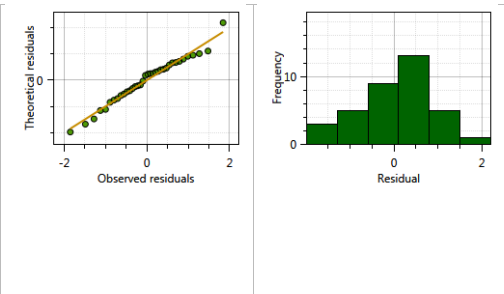
Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.04567  0.2137
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.32453  0.5697
Residual                                0.08779  0.2963
Number of obs: 36, groups:  Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

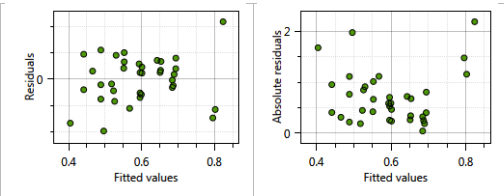
Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    0.4010     0.2227  9.9656   1.801   0.102

Dispersion: 0.2963
```

Model residuals

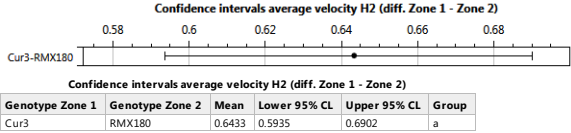
Statistic	Value
Sample skewness	-0.1612
Sample excess kurtosis	0.2992
Passed Shapiro Wilk normality test	Yes (p-value = 0.7532 > 0.05)





Analysis average velocity H2 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_velocity_H2_Zone_1,Average_velocity_H2_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 68.1

Scaled residuals:
  Min       1Q   Median       3Q      Max
-2.5512 -0.6119  0.2946  0.7444  1.5983

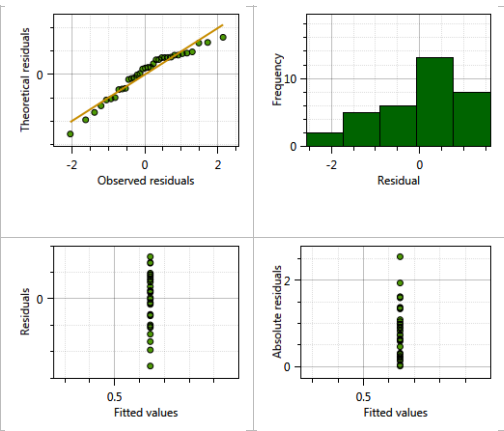
Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.00000 0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.00000 0.0000
Residual              0.07124 0.2669
Number of obs: 34, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   0.5897     0.1038 33.0000   5.682 2.46e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.2669
```

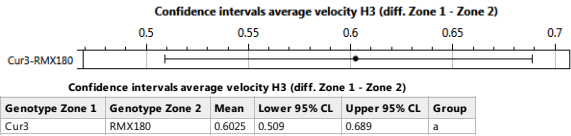
Model residuals

Statistic	Value
Sample skewness	-0.7948
Sample excess kurtosis	0.12
Passed Shapiro Wilk normality test	Yes (p-value = 0.06692 > 0.05)



Analysis average velocity H3 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_velocity_H3_Zone_1,Average_velocity_H3_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 73.8

Scaled residuals:
  Min       1Q   Median       3Q      Max
-1.86057 -0.69197  0.04667  0.47987  2.47300

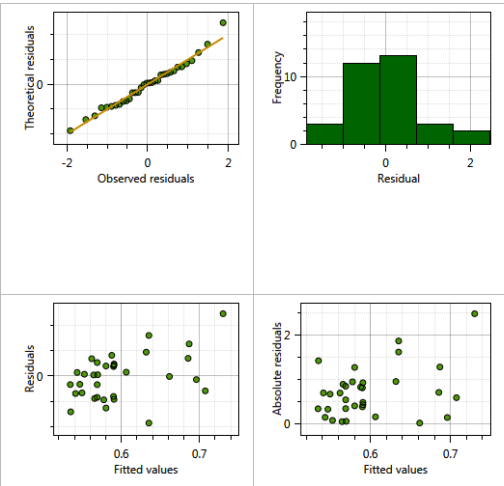
Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.02191 0.1480
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.11535 0.3396
Residual              0.07441 0.2728
Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   0.4157     0.1597 6.7893   2.604  0.0362 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Dispersion: 0.2728

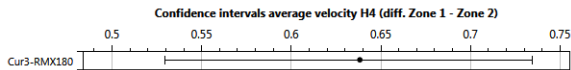
Model residuals

Statistic	Value
Sample skewness	0.4513
Sample excess kurtosis	0.6495
Passed Shapiro Wilk normality test	Yes (p-value = 0.8346 > 0.05)



Analysis average velocity H4 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_velocity_H4_Zone_1,Average_velocity_H4_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.6383	0.5293	0.7346	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 54.9

Scaled residuals:
Min IQ Median 3Q Max
-1.43169 -0.70729 -0.04817 0.79386 1.45180

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0000 0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.3022 0.5497
Residual 0.0367 0.1916
Number of obs: 28, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

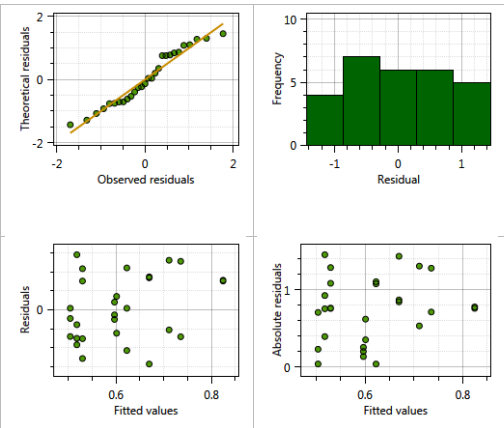
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 0.5678 0.1976 8.5666 2.874 0.0193 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.1916

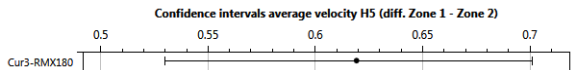
Model residuals

Statistic	Value
Sample skewness	0.0772
Sample excess kurtosis	-1.253
Passed Shapiro Wilk normality test	Yes (p-value = 0.1609 > 0.05)



Analysis average velocity H5 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_velocity_H5_Zone_1,Average_velocity_H5_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals average velocity H5 (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.6192	0.5297	0.7012	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 69.9

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.92297 -0.74933  0.02265  0.93100  1.45334

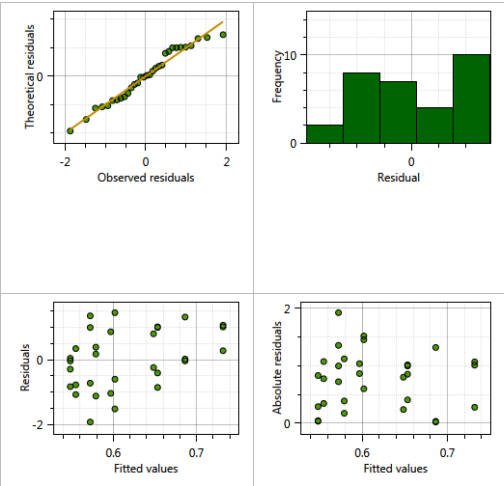
Random effects:
Groups              Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 1.793e-17 4.234e-09
Genotype_Zone_2:Plant_Zone_2 (Intercept) 1.356e-01 3.682e-01
Residual                                6.217e-02 2.493e-01
Number of obs: 31, groups:  Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   0.4860     0.1618  8.8542   3.003  0.0151 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.2493
```

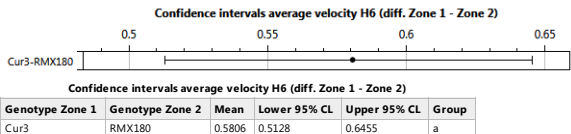
Model residuals

Statistic	Value
Sample skewness	-0.1819
Sample excess kurtosis	-0.904
Passed Shapiro Wilk normality test	Yes (p-value = 0.2958 > 0.05)



Analysis average velocity H6 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_velocity_H6_Zone_1,Average_velocity_H6_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 43.8

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.3126 -0.5480 -0.0038  0.3286  2.1739

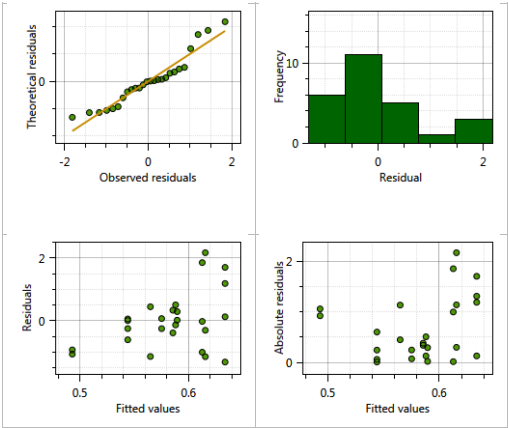
Random effects:
Groups              Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.06451  0.2540
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.00000  0.0000
Residual                                0.04136  0.2034
Number of obs: 26, groups:  Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   0.3253     0.1239 10.5634   2.626  0.0243 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.2034
```

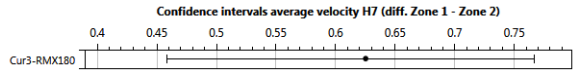
Model residuals

Statistic	Value
Sample skewness	0.7925
Sample excess kurtosis	0.3862
Passed Shapiro Wilk normality test	Yes (p-value = 0.05105 > 0.05)



Analysis average velocity H7 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Average_velocity_H7_Zone_1,Average_velocity_H7_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.6252	0.4581	0.7669	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 77

Scaled residuals:
Min 1Q Median 3Q Max
-1.44866 -0.70709 0.02056 0.66250 1.92638

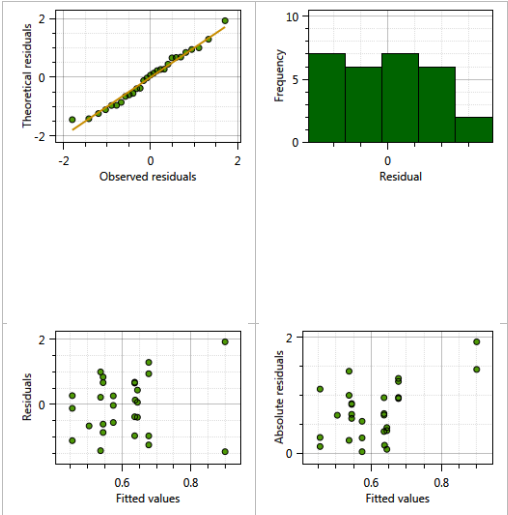
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.61434 0.7838
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.00000 0.0000
Residual 0.08907 0.2985
Number of obs: 28, groups: Genotype_Zone_2:Plant_Zone_2, 10; Genotype_Zone_1:Plant_Zone_1, 9

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 0.5115 0.2935 7.8231 1.742 0.12

Dispersion: 0.2985

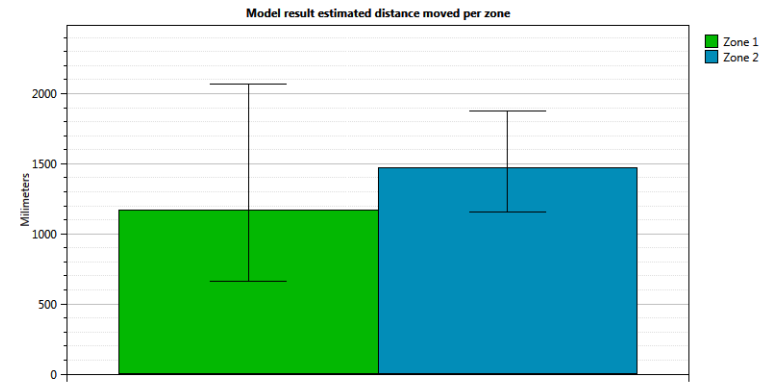
Model residuals

Statistic	Value
Sample skewness	0.197
Sample excess kurtosis	-0.5832
Passed Shapiro Wilk normality test	Yes (p-value = 0.7284 > 0.05)



Estimated distance moved per zone

Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

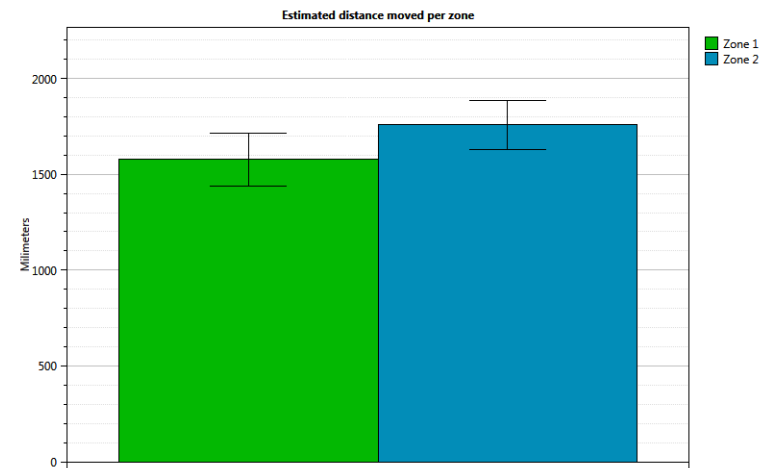
Behaviour statistic	Cur3-RMX180
Estimated distance moved (diff. Zone 1 - Zone 2)	p=0.118 [-0.263, 0.0356]

The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Estimated distance moved (Zone 1)	1.17E+03 [662, 2.07E+03]	CR
Estimated distance moved (Zone 2)	1.47E+03 [1.16E+03, 1.87E+03]	CR

CR = Check residuals

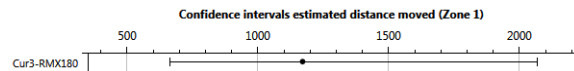
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean Zone 1	StdErr Zone 1	Mean Zone 2	StdErr Zone 2
Cur3	RMX180	Neutral	1577.46	139.13	1758.24	128.9

Analysis estimated distance moved (Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_distance_moved_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	1171	662.3	2070	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_distance_moved_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 128.1

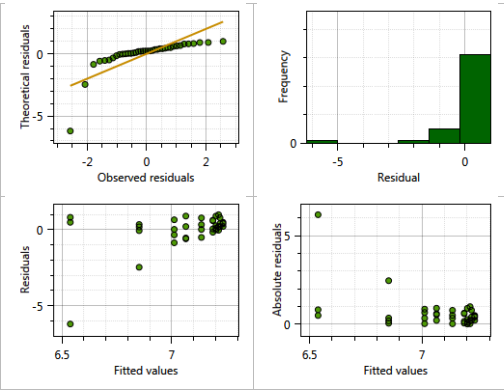
Scaled residuals:
    Min       1Q   Median       3Q      Max
-4.9667 -0.0176  0.1762  0.3949  0.7958

Random effects:
Groups              Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 1.685e-01 4.105e-01
Genotype_Zone_2:Plant_Zone_2 (Intercept) 3.053e-13 5.526e-07
Residual                                1.559e+00 1.248e+00
Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   7.0654      0.2408 6.9897  29.34 1.41e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

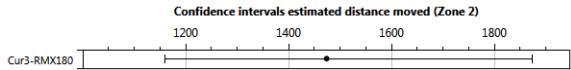
Model residuals

Statistic	Value
Sample skewness	-4.077
Sample excess kurtosis	19.77
Passed Shapiro Wilk normality test	No (p-value = 1.791E-09 < 0.05)



Analysis estimated distance moved (Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_distance_moved_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals estimated distance moved (Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	1474	1159	1874	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_distance_moved_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 88.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.2494	-0.1954	0.1764	0.6102	1.2767

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		0.5495	0.7413

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

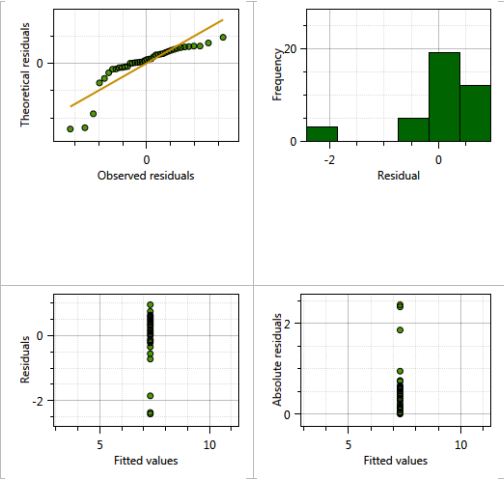
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	7.2957	0.1187	38.0000	61.46	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

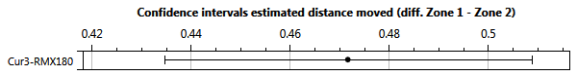
Model residuals

Statistic	Value
Sample skewness	-2.114
Sample excess kurtosis	4.807
Passed Shapiro Wilk normality test	No (p-value = 1.675E-06 < 0.05)



Analysis estimated distance moved (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_distance_moved_Zone_1,Estimated_distance_moved_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals estimated distance moved (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4716	0.4346	0.5089	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

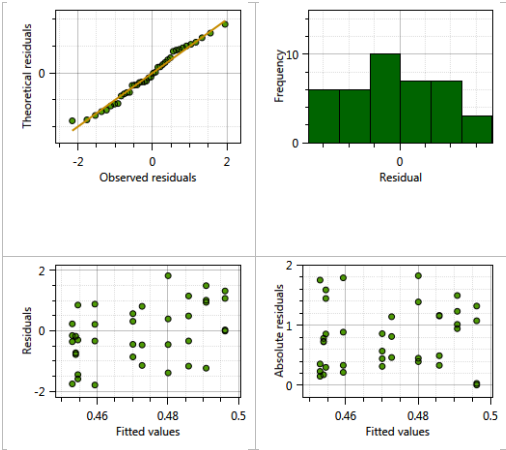
REML criterion at convergence: 40.1

Scaled residuals:

Min	1Q	Median	3Q	Max	
-1.7858	-0.7553	-0.1765	0.6902	1.8209	
Random effects:					
Groups	Name	Variance	Std.Dev.		
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.01347	0.1161		
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.00000	0.0000		
Residual		92.81723	9.6342		
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10					
Fixed effects:					
	Estimate	Std. Error	df	t value Pr(> t)	
(Intercept)	-0.11372	0.06544	8.52961	-1.738	0.118
Dispersion: 9.634					

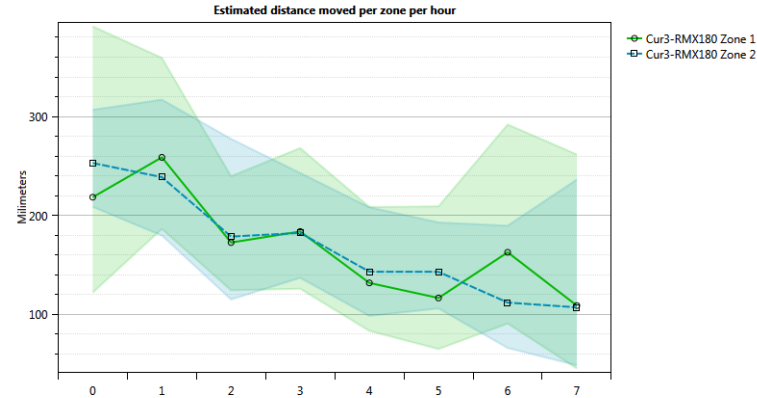
Model residuals

Statistic	Value
Sample skewness	0.04159
Sample excess kurtosis	-0.8493
Passed Shapiro Wilk normality test	Yes (p-value = 0.5684 > 0.05)



Estimated distance moved per zone per hour

Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

Behaviour statistic	Cur3-RMX180
Estimated distance moved H0 (diff. Zone 1 - Zone 2)	p=0.771 [-0.385, 0.294]
Estimated distance moved H1 (diff. Zone 1 - Zone 2)	p=0.309 [-0.0891, 0.273]
Estimated distance moved H2 (diff. Zone 1 - Zone 2)	p=0.422 [-0.386, 0.184]
Estimated distance moved H3 (diff. Zone 1 - Zone 2)	p=0.226 [-0.295, 0.0718]
Estimated distance moved H4 (diff. Zone 1 - Zone 2)	p=0.076 [-0.57, 0.0356]
Estimated distance moved H5 (diff. Zone 1 - Zone 2)	p=0.0637 [-0.645, 0.0246]
Estimated distance moved H6 (diff. Zone 1 - Zone 2)	p=0.615 [-0.309, 0.185]
Estimated distance moved H7 (diff. Zone 1 - Zone 2)	p=0.121 [-0.709, 0.1]

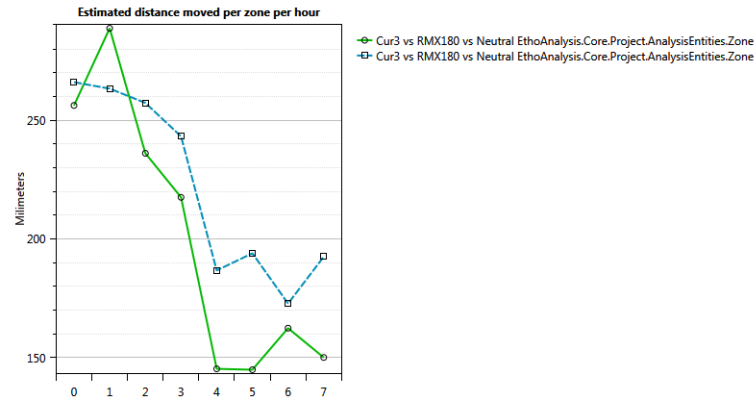
The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Estimated distance moved (H0 - Zone 1)	218 [122, 391]	CR
Estimated distance moved (H0 - Zone 2)	253 [209, 307]	CR
Estimated distance moved (H1 - Zone 1)	259 [186, 359]	CR
Estimated distance moved (H1 - Zone 2)	239 [180, 317]	
Estimated distance moved (H2 - Zone 1)	173 [124, 240]	
Estimated distance moved (H2 - Zone 2)	179 [115, 277]	CR
Estimated distance moved (H3 - Zone 1)	184 [126, 268]	CR
Estimated distance moved (H3 - Zone 2)	182 [137, 243]	CR
Estimated distance moved (H4 - Zone 1)	132 [83.3, 209]	CR
Estimated distance moved (H4 - Zone 2)	143	CR

Statistic	Cur3-RMX180	Remark
	[98.4, 208]	
Estimated distance moved (H5 - Zone 1)	117	CR
	[65, 209]	
Estimated distance moved (H5 - Zone 2)	143	CR
	[106, 193]	
Estimated distance moved (H6 - Zone 1)	163	CR
	[90.8, 292]	
Estimated distance moved (H6 - Zone 2)	112	CR
	[66.1, 190]	
Estimated distance moved (H7 - Zone 1)	109	CR
	[45.3, 262]	
Estimated distance moved (H7 - Zone 2)	107	
	[48.5, 236]	

CR = Check residuals

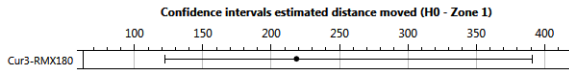
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean H0 - Zone 1	StdErr H0 - Zone 1	Mean H0 - Zone 2	StdErr H0 - Zone 2	Mean H1 - Zone 1	StdErr H1 - Zone 1	Mean H1 - Zone 2	StdErr H1 - Zone 2	Mean H2 - Zone 1	StdErr H2 - Zone 1	Mean H2 - Zone 2	StdErr H2 - Zone 2	Mean H3 - Zone 1	StdErr H3 - Zone 1	Mean H3 - Zone 2	StdErr H3 - Zone 2	Mean H4 - Zone 1	StdErr H4 - Zone 1	Mean H4 - Zone 2	StdErr H4 - Zone 2	Mean H5 - Zone 1	StdErr H5 - Zone 1	Mean H5 - Zone 2	StdErr H5 - Zone 2	Mean H6 - Zone 1	StdErr H6 - Zone 1	Mean H6 - Zone 2	StdErr H6 - Zone 2
Cur3	RMX180	Neutral	256.21	31.53	266.01	24.32	288.72	27.56	263.29	23.91	236.05	37.32	257.28	36.3	217.5	32.08	243.18	25.53	145.21	21.94	186.67	21.44	144.85	23.12	193.91	21.15	162.35	29.98	172.73	24

Analysis estimated distance moved (H0 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_distance_moved_H0_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	218.5	122	391.2	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_distance_moved_H0_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 100.3

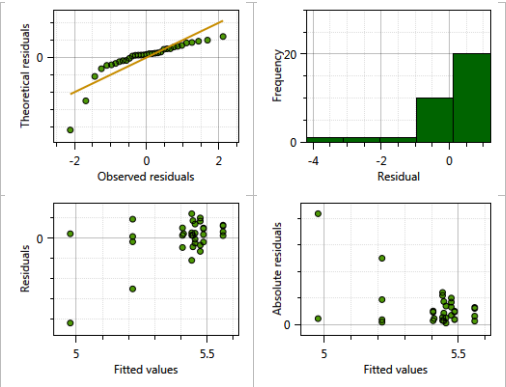
Scaled residuals:
    Min       1Q   Median       3Q      Max
-3.9617 -0.1803  0.1699  0.4781  1.1422

Random effects:
              Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.115    0.3391
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.000    0.0000
Residual                                1.113    1.0551
Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    5.3867      0.2148 4.2566   25.08 8.7e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

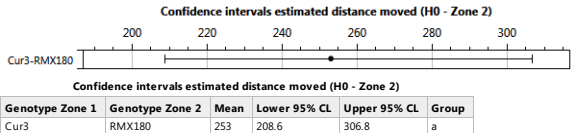
Model residuals

Statistic	Value
Sample skewness	-2.663
Sample excess kurtosis	9.052
Passed Shapiro Wilk normality test	No (p-value = 2.432E-06 < 0.05)



Analysis estimated distance moved (H0 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_distance_moved_H0_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_distance_moved_H0_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 63.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.1187	-0.4613	0.2648	0.6072	1.8444

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.00
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.00
Residual		0.3249	0.57

Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

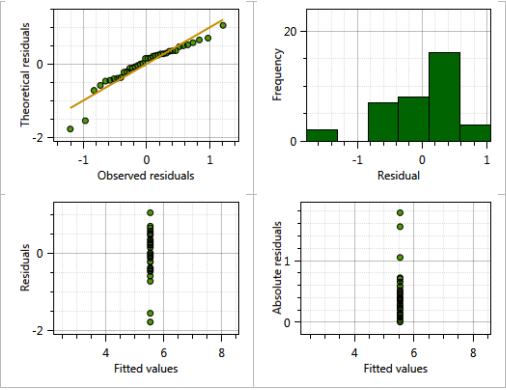
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	5.533	0.095	35.000	58.25	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

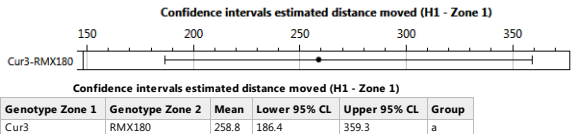
Model residuals

Statistic	Value
Sample skewness	-1.263
Sample excess kurtosis	2.618
Passed Shapiro Wilk normality test	No (p-value = 0.006754 < 0.05)



Analysis estimated distance moved (H1 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_distance_moved_H1_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_distance_moved_H1_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 86.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.5739	-0.2362	0.1018	0.6252	1.3282

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.03107	0.1763
Residual		0.60489	0.7777

Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

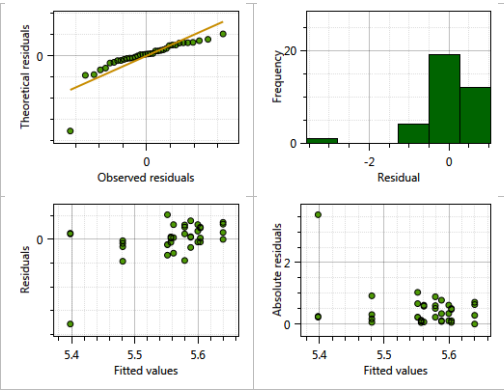
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	5.5560	0.1413	7.6656	39.33	4.02e-10 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

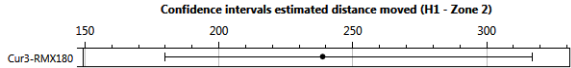
Model residuals

Statistic	Value
Sample skewness	-2.99
Sample excess kurtosis	13.26
Passed Shapiro Wilk normality test	No (p-value = 1.21E-06 < 0.05)



Analysis estimated distance moved (H1 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_distance_moved_H1_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	238.7	179.7	317.1	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_distance_moved_H1_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + Genotype_Zone_2:Plant_Zone_2
Data: data

REML criterion at convergence: 61.9

Scaled residuals:
Min 1Q Median 3Q Max
-2.15986 -0.41324 0.06628 0.79050 1.54690

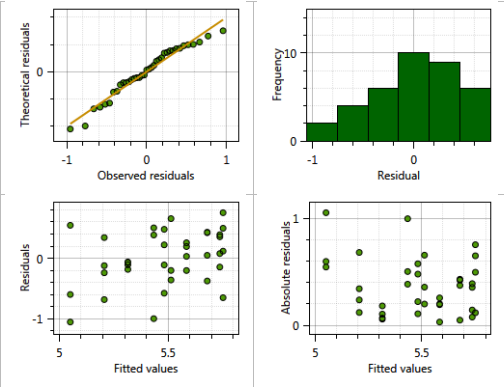
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.00000 0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.09136 0.3023
Residual 0.23711 0.4869
Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 5.4754 0.1249 8.7323 43.83 1.53e-11 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

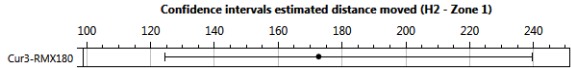
Model residuals

Statistic	Value
Sample skewness	-0.5353
Sample excess kurtosis	-0.2199
Passed Shapiro Wilk normality test	Yes (p-value = 0.2313 > 0.05)



Analysis estimated distance moved (H2 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_distance_moved_H2_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	172.7	124.4	239.7	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_distance_moved_H2_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + Genotype_Zone_2:Plant_Zone_2
Data: data

REML criterion at convergence: 100.8

Scaled residuals:
Min 1Q Median 3Q Max
-2.59146 -0.53581 -0.07171 0.69220 1.84331

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 6.620e-18 2.573e-09
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.000e+00 0.000e+00

Residual 9.404e-01 9.697e-01
Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

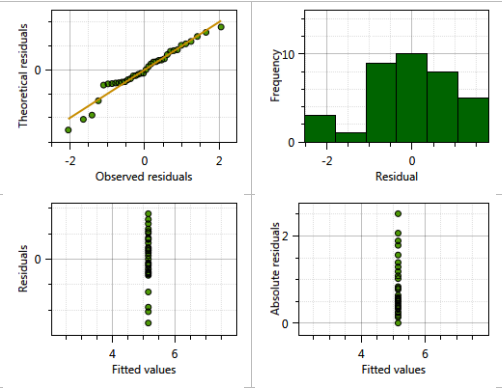
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	5.1513	0.1616	35.0000	31.87	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

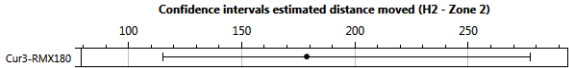
Model residuals

Statistic	Value
Sample skewness	-0.5504
Sample excess kurtosis	0.5751
Passed Shapiro Wilk normality test	Yes (p-value = 0.2346 > 0.05)



Analysis estimated distance moved (H2 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_distance_moved_H2_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	178.7	115.1	277.5	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_distance_moved_H2_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 112.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.7003	-0.4566	0.1796	0.4341	1.4601

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.04597	0.2144
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.00000	0.0000
Residual		1.17772	1.0852

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

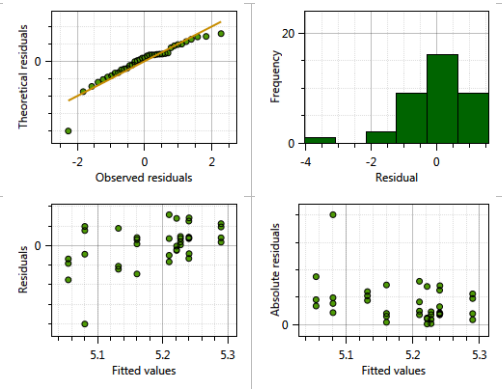
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	5.186	0.191	8.037	27.15	3.41e-09 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

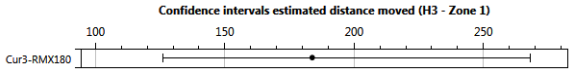
Model residuals

Statistic	Value
Sample skewness	-1.49
Sample excess kurtosis	4.306
Passed Shapiro Wilk normality test	No (p-value = 0.002968 < 0.05)



Analysis estimated distance moved (H3 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_distance_moved_H3_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	183.8	125.9	268.2	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated distance moved_H3_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 92.7

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.8705	-0.2986	0.2767	0.5079	1.6481

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.002828	0.05318
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000000	0.00000
Residual		0.948611	0.97397

Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

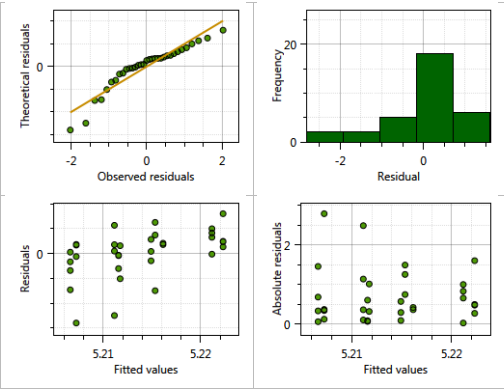
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	5.2138	0.1704	10.3416	30.59	1.75e-11 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

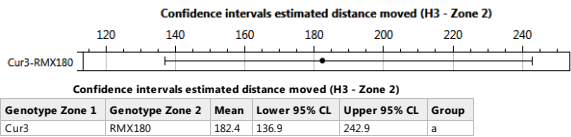
Model residuals

Statistic	Value
Sample skewness	-1.26
Sample excess kurtosis	1.911
Passed Shapiro Wilk normality test	No (p-value = 0.005167 < 0.05)



Analysis estimated distance moved (H3 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_distance_moved_H3_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated distance moved_H3_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 102.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.7743	-0.6314	0.2484	0.6434	1.3842

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		0.7826	0.8846

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

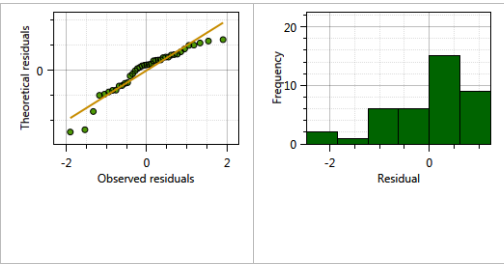
Fixed effects:

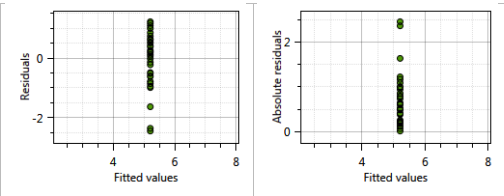
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	5.2060	0.1417	38.0000	36.75	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

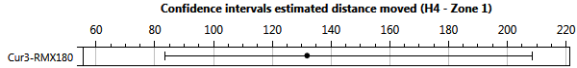
Statistic	Value
Sample skewness	-1.093
Sample excess kurtosis	1.141
Passed Shapiro Wilk normality test	No (p-value = 0.005416 < 0.05)





Analysis estimated distance moved (H4 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_distance_moved_H4_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals estimated distance moved (H4 - Zone 1)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	131.8	83.31	208.6	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_distance_moved_H4_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + Genotype_Zone_2:Plant_Zone_2 (1 |
Data: data

REML criterion at convergence: 85.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.0853	-0.6331	0.3688	0.6644	1.3381

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.09509	0.3084
Residual		0.90917	0.9535

Number of obs: 30, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

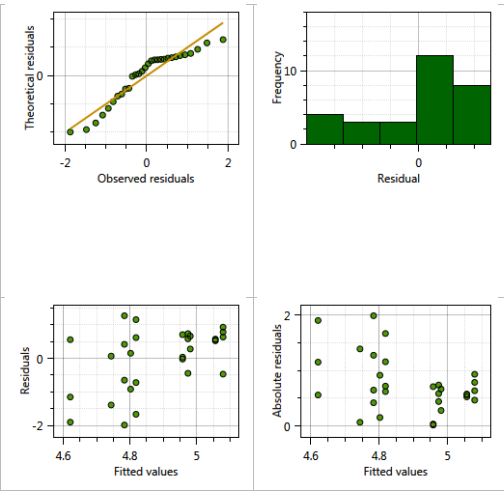
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	4.8815	0.2008	8.4297	24.32	4.19e-09 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

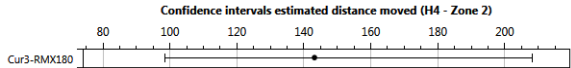
Model residuals

Statistic	Value
Sample skewness	-0.8455
Sample excess kurtosis	-0.3288
Passed Shapiro Wilk normality test	No (p-value = 0.007712 < 0.05)



Analysis estimated distance moved (H4 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_distance_moved_H4_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals estimated distance moved (H4 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	143.2	98.4	208.3	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_distance_moved_H4_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + Genotype_Zone_2:Plant_Zone_2 (1 |
Data: data

REML criterion at convergence: 103.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.0942	-0.3470	0.1552	0.7085	1.3049

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.02137	0.1462
Residual		0.91363	0.9558

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

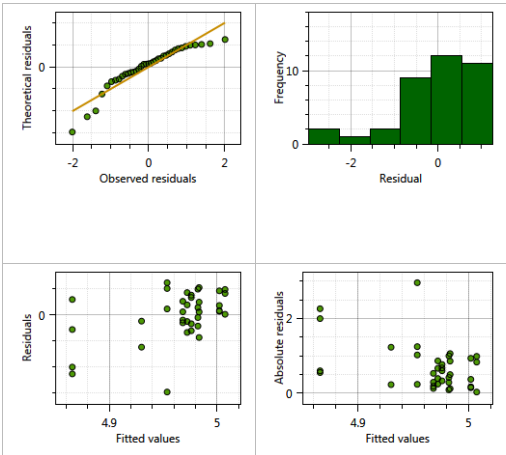
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	4.964	0.164	8.409	30.27	7.01e-10 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

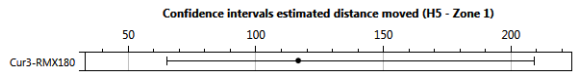
Model residuals

Statistic	Value
Sample skewness	-1.356
Sample excess kurtosis	2.108
Passed Shapiro Wilk normality test	No (p-value = 0.001666 < 0.05)



Analysis estimated distance moved (H5 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_distance_moved_H5_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	116.6	64.97	209.3	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_distance_moved_H5_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 99

Scaled residuals:
Min IQ Median 3Q Max
-2.4575 -0.5480 0.3394 0.6662 1.3577

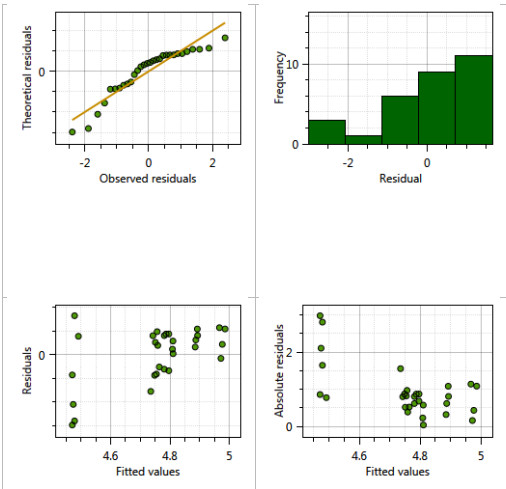
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.00819 0.0905
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.12572 0.3546
Residual 1.47026 1.2125
Number of obs: 30, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 4.7588 0.2513 7.5969 18.94 1.14e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

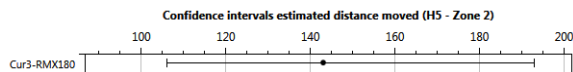
Model residuals

Statistic	Value
Sample skewness	-1.166
Sample excess kurtosis	0.8167
Passed Shapiro Wilk normality test	No (p-value = 0.002991 < 0.05)



Analysis estimated distance moved (H5 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_distance_moved_H5_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals estimated distance moved (H5 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	143	106	193	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated distance moved_H5_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 105.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.0017	-0.3730	0.1801	0.6830	1.4729

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	2.114e-16	1.454e-08
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000e+00	0.000e+00
Residual		8.552e-01	9.247e-01

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

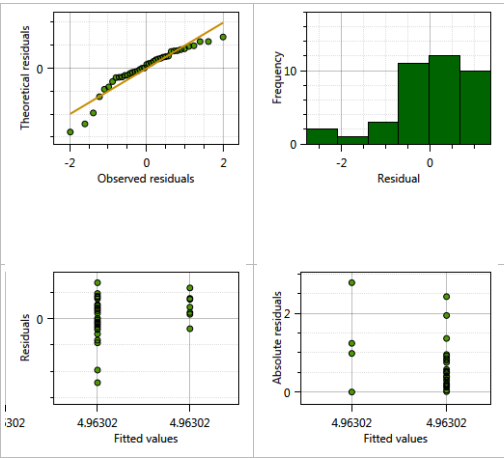
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	4.9630	0.1481	38.0000	33.52	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

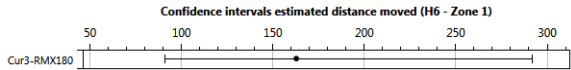
Model residuals

Statistic	Value
Sample skewness	-1.264
Sample excess kurtosis	1.926
Passed Shapiro Wilk normality test	No (p-value = 0.002997 < 0.05)



Analysis estimated distance moved (H6 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated distance moved_H6_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals estimated distance moved (H6 - Zone 1)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	162.8	90.76	292	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated distance moved_H6_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 79.1

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.7607	-0.7254	0.1658	0.7891	1.3278

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.2419	0.4918
Residual		0.9006	0.9490

Number of obs: 27, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

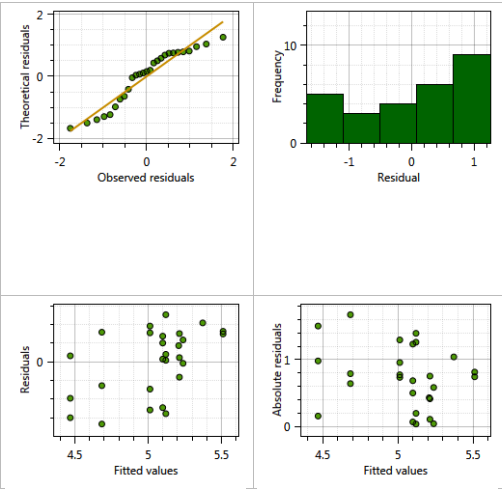
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	5.0924	0.2455	6.7810	20.75	2.18e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

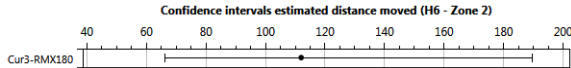
Model residuals

Statistic	Value
Sample skewness	-0.5699
Sample excess kurtosis	-0.9727
Passed Shapiro Wilk normality test	No (p-value = 0.02698 < 0.05)



Analysis estimated distance moved (H6 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_distance_moved_H6_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	112	66.07	189.7	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_distance_moved_H6_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + Genotype_Zone_2:Plant_Zone_2
Data: data

REML criterion at convergence: 118.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.97685	-0.30123	0.07863	0.69421	1.34660

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.04894	0.2212
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.12303	0.3508
Residual		1.15242	1.0735

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

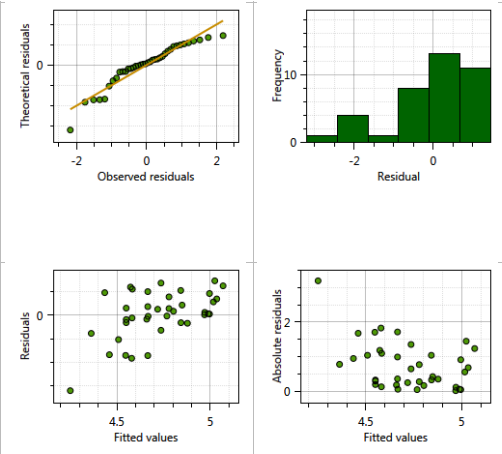
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	4.7181	0.2183	6.3386	21.61	3.55e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

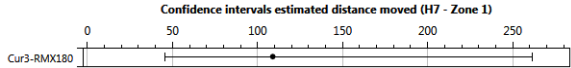
Model residuals

Statistic	Value
Sample skewness	-1.086
Sample excess kurtosis	1.45
Passed Shapiro Wilk normality test	No (p-value = 0.009372 < 0.05)



Analysis estimated distance moved (H7 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_distance_moved_H7_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	108.9	45.33	261.7	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_distance_moved_H7_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + Genotype_Zone_2:Plant_Zone_2
Data: data

REML criterion at convergence: 115.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.1964	-0.1653	0.2796	0.4892	0.7896

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.1044	0.3231
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Residual		3.6478	1.9099

Number of obs: 28, groups: Genotype_Zone_2:Plant_Zone_2, 10; Genotype_Zone_1:Plant_Zone_1, 9

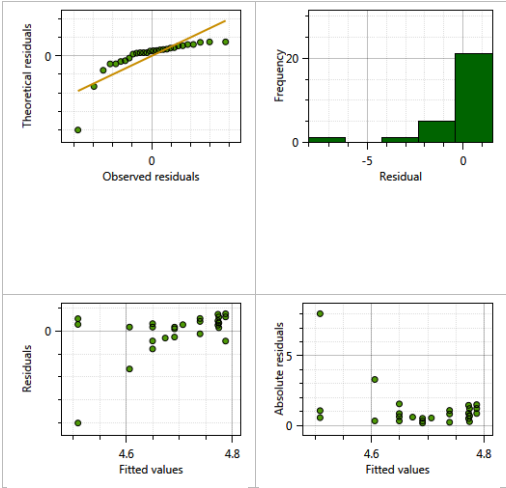
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	4.6905	0.3771	7.6467	12.44	2.4e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

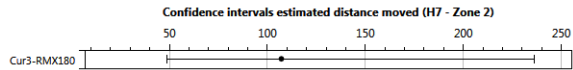
Model residuals

Statistic	Value
Sample skewness	-3.192
Sample excess kurtosis	12.25
Passed Shapiro Wilk normality test	No (p-value = 5.735E-07 < 0.05)



Analysis estimated distance moved (H7 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_distance_moved_H7_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	107.1	48.53	236.3	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_distance_moved_H7_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 115.5

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.20722	-0.38150	-0.05443	0.49600	1.42373

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.7638	0.8740
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.4044	0.6359
Residual		0.5486	0.7406

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

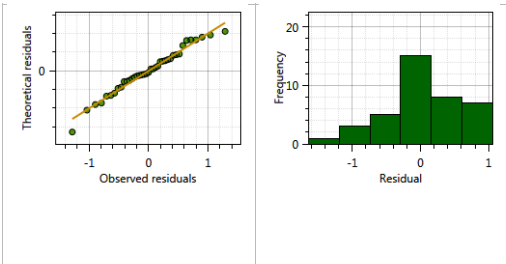
Fixed effects:

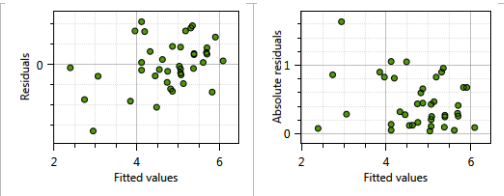
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	4.6737	0.3621	11.6400	12.91	2.98e-08 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

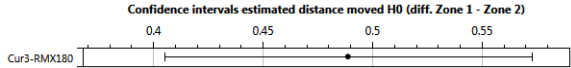
Statistic	Value
Sample skewness	-0.3694
Sample excess kurtosis	0.2502
Passed Shapiro Wilk normality test	Yes (p-value = 0.6084 > 0.05)





Analysis estimated distance moved H0 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_distance_moved_H0_Zone_1,Estimated_distance_moved_H0_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals estimated distance moved H0 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4887	0.405	0.573	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 103.3

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.95027 -0.44139 -0.02179  0.50860  1.92384

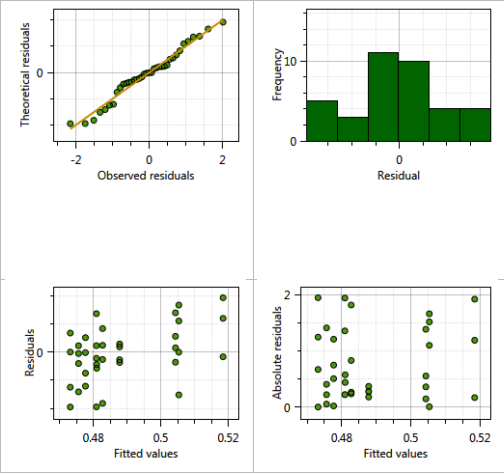
Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.00000  0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.02931  0.1712
Residual                                100.42120 10.0210
Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -0.0453    0.1511   9.4454   -0.3    0.771

Dispersion: 10.02
```

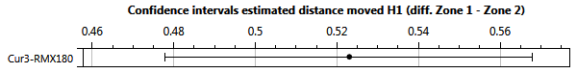
Model residuals

Statistic	Value
Sample skewness	-0.1064
Sample excess kurtosis	-0.2578
Passed Shapiro Wilk normality test	Yes (p-value = 0.4582 > 0.05)



Analysis estimated distance moved H1 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_distance_moved_H1_Zone_1,Estimated_distance_moved_H1_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals estimated distance moved H1 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.523	0.4777	0.5679	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 66.5

Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.2024 -0.6252  0.1305  0.6001  1.7763

Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.00    0.000
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.00    0.000
Residual                                42.92    6.551
Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

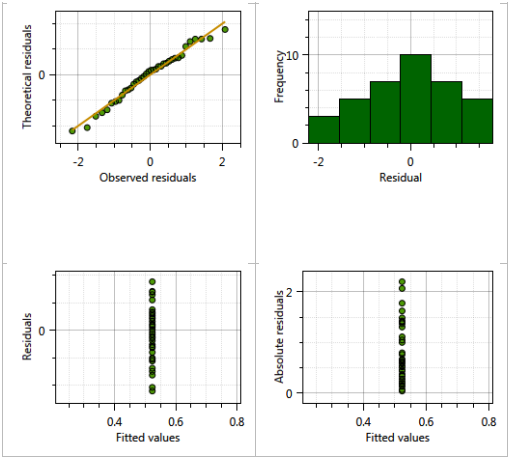
Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
```

(Intercept) 0.09219 0.08939 36.00000 1.031 0.309

Dispersion: 6.551

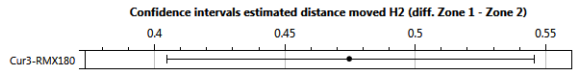
Model residuals

Statistic	Value
Sample skewness	-0.3119
Sample excess kurtosis	-0.4079
Passed Shapiro Wilk normality test	Yes (p-value = 0.6387 > 0.05)



Analysis estimated distance moved H2 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_distance_moved_H2_Zone_1,Estimated_distance_moved_H2_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4747	0.4046	0.5458	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 85.8

Scaled residuals:
Min 1Q Median 3Q Max
-1.7178 -0.6478 -0.2831 0.4326 2.7297

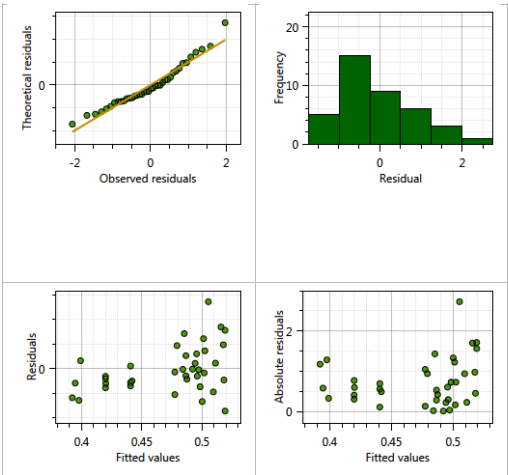
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.06237 0.24974
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.00321 0.05665
Residual 31.90458 5.64841
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -0.1014 0.1182 6.4026 -0.858 0.422

Dispersion: 5.648

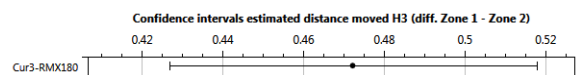
Model residuals

Statistic	Value
Sample skewness	0.8541
Sample excess kurtosis	0.831
Passed Shapiro Wilk normality test	Yes (p-value = 0.1091 > 0.05)



Analysis estimated distance moved H3 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_distance_moved_H3_Zone_1,Estimated_distance_moved_H3_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4721	0.4268	0.518	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 83.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.6511	-0.9781	-0.3743	0.4679	1.9907

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00	0.000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.00	0.000
Residual		36.77	6.064

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

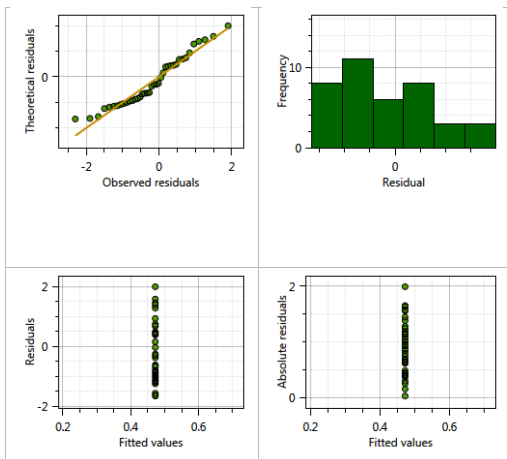
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.11160	0.09062	38.00000	-1.232	0.226

Dispersion: 6.064

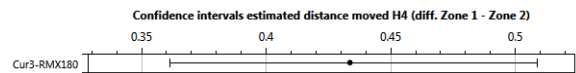
Model residuals

Statistic	Value
Sample skewness	0.5034
Sample excess kurtosis	-0.7466
Passed Shapiro Wilk normality test	Yes (p-value = 0.0503 > 0.05)



Analysis estimated distance moved H4 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_distance_moved_H4_Zone_1,Estimated_distance_moved_H4_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4336	0.3612	0.5089	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 105.5

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.7055	-0.9585	-0.3428	0.7561	1.7761

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.03848	0.1962
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.00000	0.0000
Residual		40.65623	6.3762

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

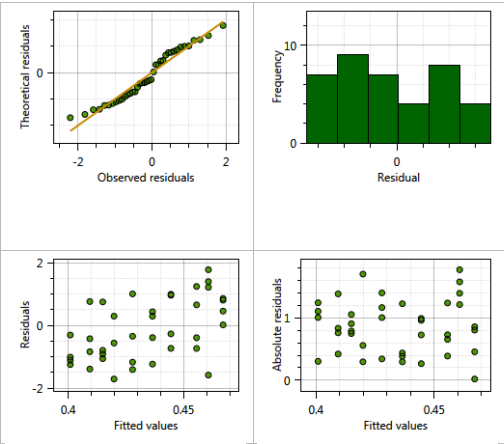
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.2672	0.1302	7.6128	-2.053	0.076 .

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 6.376

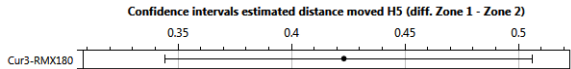
Model residuals

Statistic	Value
Sample skewness	0.2008
Sample excess kurtosis	-1.187
Passed Shapiro Wilk normality test	Yes (p-value = 0.07986 > 0.05)



Analysis estimated distance moved H5 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_distance_moved_H5_Zone_1,Estimated_distance_moved_H5_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.423	0.344	0.5062	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 106.3

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.9066 -0.8878 -0.2225  0.5118  1.9226

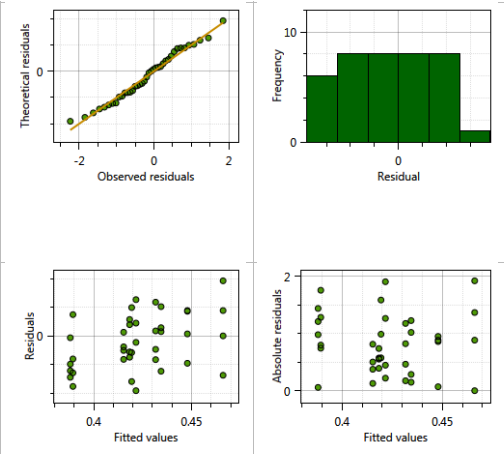
Random effects:
Groups              Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.04214  0.2053
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.00000  0.0000
Residual                                     44.34602  6.6593
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -0.3104    0.1355  5.7516  -2.291  0.0637 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 6.659
```

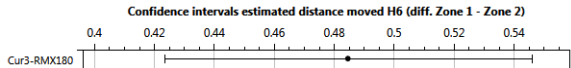
Model residuals

Statistic	Value
Sample skewness	0.1314
Sample excess kurtosis	-0.7983
Passed Shapiro Wilk normality test	Yes (p-value = 0.62 > 0.05)



Analysis estimated distance moved H6 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_distance_moved_H6_Zone_1,Estimated_distance_moved_H6_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4845	0.4234	0.5461	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
```

Weights: wi

REML criterion at convergence: 115.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.3674	-0.7873	-0.3879	0.4950	1.7341

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0	0.000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0	0.000
Residual		48.6	6.971

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

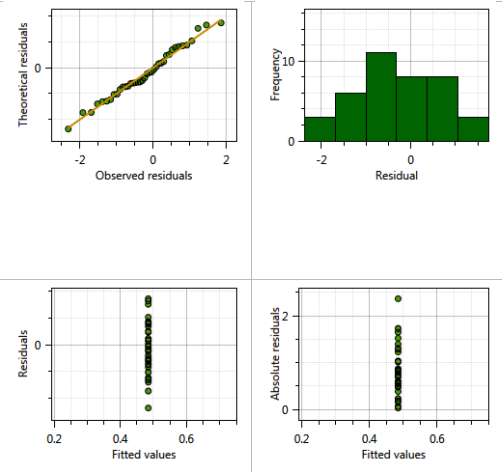
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.06196	0.12202	38.00000	-0.508	0.615

Dispersion: 6.971

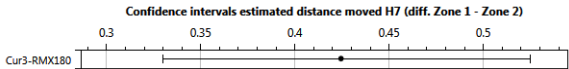
Model residuals

Statistic	Value
Sample skewness	0.1487
Sample excess kurtosis	-0.3696
Passed Shapiro Wilk normality test	Yes (p-value = 0.8069 > 0.05)



Analysis estimated distance moved H7 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_distance_moved_H7_Zone_1,Estimated_distance_moved_H7_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4244	0.3297	0.525	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: ziFormula

Data: data

Weights: wi

REML criterion at convergence: 104.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.6179	-0.8983	-0.2520	0.5270	1.5122

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.05874	0.2424
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.13353	0.3654
Residual		26.11069	5.1099

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

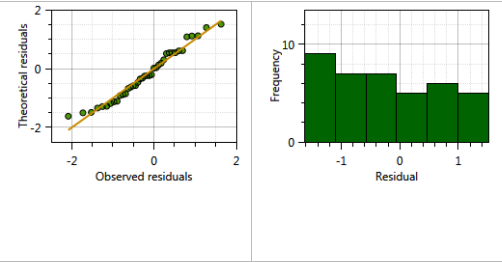
Fixed effects:

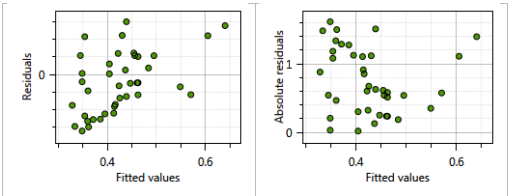
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.3046	0.1761	8.1459	-1.73	0.121

Dispersion: 5.11

Model residuals

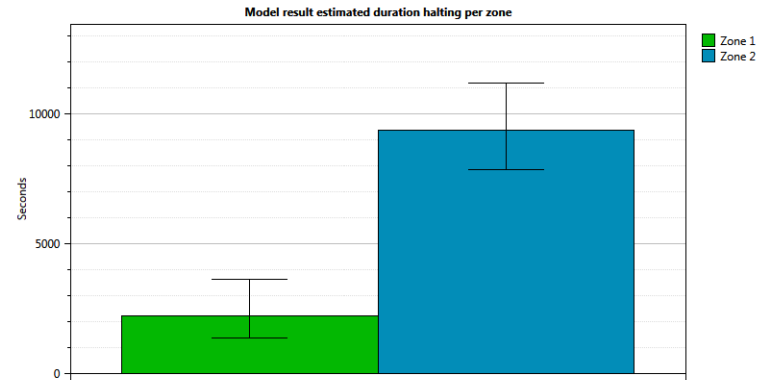
Statistic	Value
Sample skewness	0.2569
Sample excess kurtosis	-0.8603
Passed Shapiro Wilk normality test	Yes (p-value = 0.2355 > 0.05)





Estimated duration halting per zone

Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

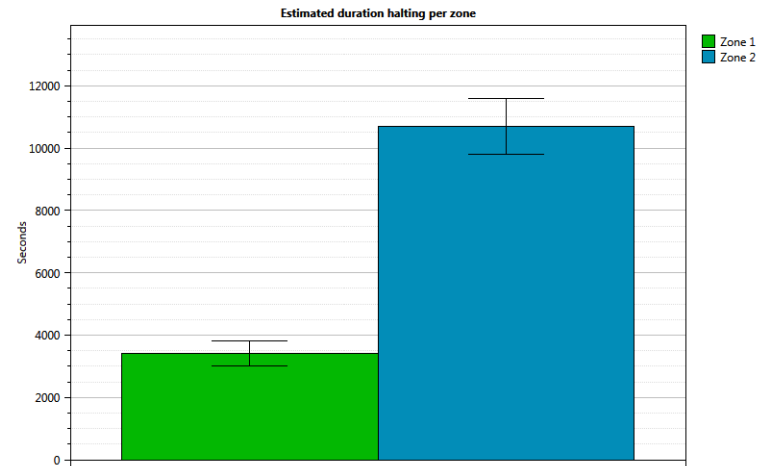
Behaviour statistic	Cur3-RMX180
Estimated duration halting (diff. Zone 1 - Zone 2)	p=0.00476**
	[-1.73, -0.572]

The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Estimated duration halting (Zone 1)	2.21E+03	CR
	[1.34E+03, 3.63E+03]	
Estimated duration halting (Zone 2)	9.35E+03	CR
	[7.83E+03, 1.12E+04]	

CR = Check residuals

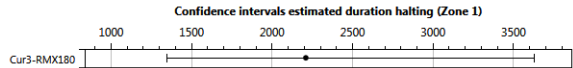
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean Zone 1	StdErr Zone 1	Mean Zone 2	StdErr Zone 2
Cur3	RMX180	Neutral	3406.74	411.96	10696.09	905.43

Analysis estimated duration halting (Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_halting_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	2209	1344	3630	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_halting_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 124.6

Scaled residuals:
  Min       1Q   Median       3Q      Max
-3.5135 -0.3221  0.1740  0.5518  1.2597

Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0000   0.0000
```

Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.1541 0.3925
Residual 1.2899 1.1357
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

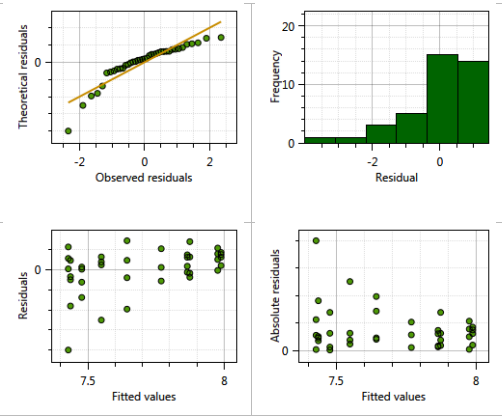
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	7.7004	0.2203	9.2142	34.95	4.13e-11 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

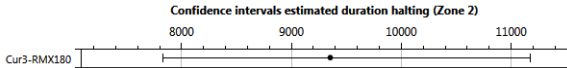
Model residuals

Statistic	Value
Sample skewness	-1.775
Sample excess kurtosis	4.04
Passed Shapiro Wilk normality test	No (p-value = 9.771E-05 < 0.05)



Analysis estimated duration halting (Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_halting_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	9353	7827	1.118E+04	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_halting_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 66

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-3.2870	-0.5380	0.1692	0.4418	1.8595

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	1.577e-20	1.256e-10
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000e+00	0.000e+00
Residual		3.019e-01	5.494e-01

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

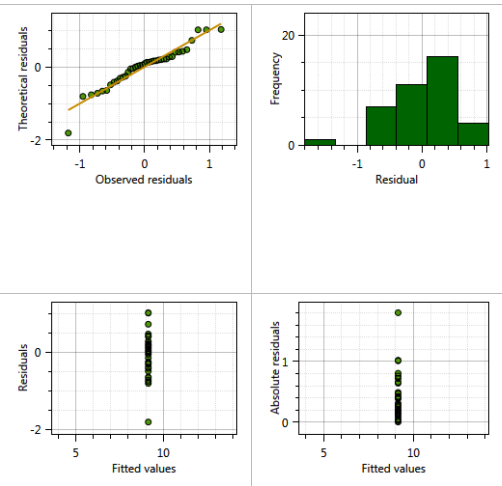
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	9.14342	0.08798	38.00000	103.9	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

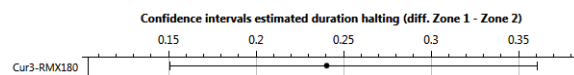
Model residuals

Statistic	Value
Sample skewness	-0.6986
Sample excess kurtosis	2.084
Passed Shapiro Wilk normality test	No (p-value = 0.04147 < 0.05)



Analysis estimated duration halting (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_halting_Zone_1,Estimated_duration_halting_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals estimated duration halting (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2403	0.1506	0.3608	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 120.1

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.52872 -0.56741 -0.02098  0.52707  2.58959

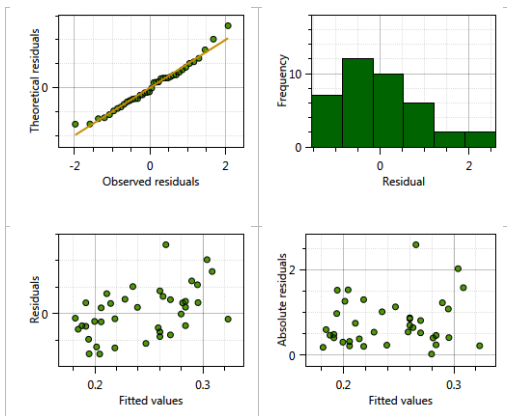
Random effects:
Groups              Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 3.943e-02 0.1986
Genotype_Zone_2:Plant_Zone_2 (Intercept) 1.466e-01 0.3829
Residual                                2.681e+03 51.7748
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -1.1510     0.2139   4.2746  -5.381  0.00476 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 51.77
```

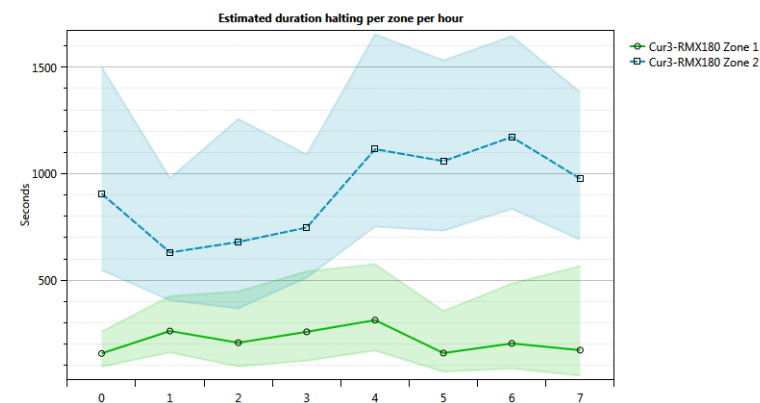
Model residuals

Statistic	Value
Sample skewness	0.5106
Sample excess kurtosis	0.3007
Passed Shapiro Wilk normality test	Yes (p-value = 0.4928 > 0.05)



Estimated duration halting per zone per hour

Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

Behaviour statistic	Cur3-RMX180	Remark
Estimated duration halting H0 (diff. Zone 1 - Zone 2)	p=8.57E-06*** [-2.02, -0.878]	CR
Estimated duration halting H1 (diff. Zone 1 - Zone 2)	p=0.0355* [-1.22, -0.0535]	CR
Estimated duration halting H2 (diff. Zone 1 - Zone 2)	p=0.0922 [-2.12, 0.166]	
Estimated duration halting H3 (diff. Zone 1 - Zone 2)	p=0.0362* [-1.75, -0.0734]	CR
Estimated duration halting H4 (diff. Zone 1 - Zone 2)	p=0.0377* [-1.77, -0.0765]	CR
Estimated duration halting H5 (diff. Zone 1 - Zone 2)	p=0.00532** [-1.94, -0.508]	CR
Estimated duration halting H6 (diff. Zone 1 - Zone 2)	p=0.00431** [-2.66, -0.685]	CR
Estimated duration halting H7 (diff. Zone 1 - Zone 2)	p=0.00316** [-2.51, -0.72]	CR

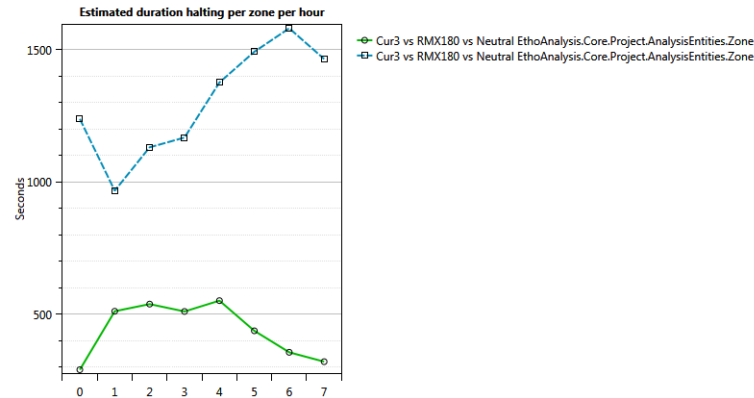
CR = Check residuals

The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Estimated duration halting (H0 - Zone 1)	157 [94.7, 259]	CR
Estimated duration halting (H0 - Zone 2)	907 [548, 1.5E+03]	
Estimated duration halting (H1 - Zone 1)	262 [161, 426]	CR
Estimated duration halting (H1 - Zone 2)	631 [406, 980]	
Estimated duration halting (H2 - Zone 1)	207 [95.7, 448]	CR
Estimated duration halting (H2 - Zone 2)	680 [368, 1.26E+03]	
Estimated duration halting (H3 - Zone 1)	258 [123, 542]	CR
Estimated duration halting (H3 - Zone 2)	748 [513, 1.09E+03]	
Estimated duration halting (H4 - Zone 1)	313 [170, 575]	CR
Estimated duration halting (H4 - Zone 2)	1.12E+03 [752, 1.65E+03]	
Estimated duration halting (H5 - Zone 1)	158 [70.6, 356]	CR
Estimated duration halting (H5 - Zone 2)	1.06E+03 [732, 1.53E+03]	
Estimated duration halting (H6 - Zone 1)	204 [85.6, 485]	CR
Estimated duration halting (H6 - Zone 2)	1.17E+03 [835, 1.65E+03]	
Estimated duration halting (H7 - Zone 1)	172 [52.2, 567]	CR
Estimated duration halting (H7 - Zone 2)	977 [690, 1.38E+03]	

CR = Check residuals

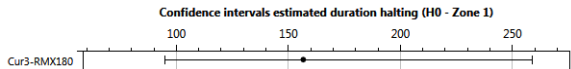
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean H0 - Zone 1	StdErr H0 - Zone 1	Mean H0 - Zone 2	StdErr H0 - Zone 2	Mean H1 - Zone 1	StdErr H1 - Zone 1	Mean H1 - Zone 2	StdErr H1 - Zone 2	Mean H2 - Zone 1	StdErr H2 - Zone 1	Mean H2 - Zone 2	StdErr H2 - Zone 2	Mean H3 - Zone 1	StdErr H3 - Zone 1	Mean H3 - Zone 2	StdErr H3 - Zone 2	Mean H4 - Zone 1	StdErr H4 - Zone 1	Mean H4 - Zone 2	StdErr H4 - Zone 2	Mean H5 - Zone 1	StdErr H5 - Zone 1	Mean H5 - Zone 2	StdErr H5 - Zone 2	Mean H6 - Zone 1	StdErr H6 - Zone 1	
Cur3	RMX180	Neutral	291.2	58.13	1238.57	145.36	512.12	109.81	967.43	125.92	539.12	141.49	1131.43	132.56	511.28	99.56	1168.38	149.95	552.16	133.51	1376.35	142.87	438.18	100.6	1492.45	153.85	356.98	111.39	1581.

Analysis estimated duration halting (H0 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_halting_H0_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	156.6	94.72	259	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_halting_H0_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 121.3

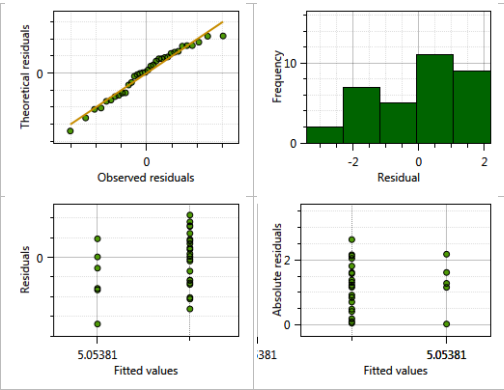
Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.35861 -0.81239  0.07999  0.76496  1.51131

Random effects:
 Groups              Name                Variance Std.Dev.
 Genotype_Zone_1:Plant_Zone_1 (Intercept) 2.409e-16 1.552e-08
 Genotype_Zone_2:Plant_Zone_2 (Intercept) 2.818e-16 1.679e-08
 Residual                    2.077e+00 1.441e+00
Number of obs: 34, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   5.0538      0.2472 33.0000   20.45  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

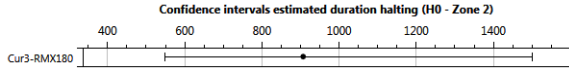
Model residuals

Statistic	Value
Sample skewness	-0.4864
Sample excess kurtosis	-0.5283
Passed Shapiro Wilk normality test	Yes (p-value = 0.2676 > 0.05)



Analysis estimated duration halting (H0 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_halting_H0_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	906.8	547.6	1501	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_halting_H0_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 115.1

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.4002	-0.2869	0.1681	0.6036	1.3422

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.01672	0.1293
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.02089	0.1445
Residual		1.15634	1.0753

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

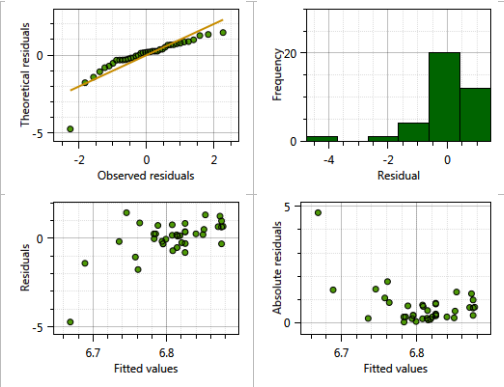
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	6.810	0.185	4.198	36.81	1.98e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

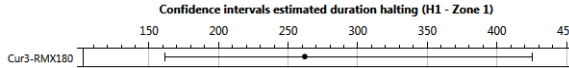
Model residuals

Statistic	Value
Sample skewness	-2.519
Sample excess kurtosis	10.07
Passed Shapiro Wilk normality test	No (p-value = 8.107E-06 < 0.05)



Analysis estimated duration halting (H1 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_halting_H1_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	261.9	161.2	425.6	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_halting_H1_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 128.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.0092	-0.5418	0.1177	0.7546	1.8232

Random effects:

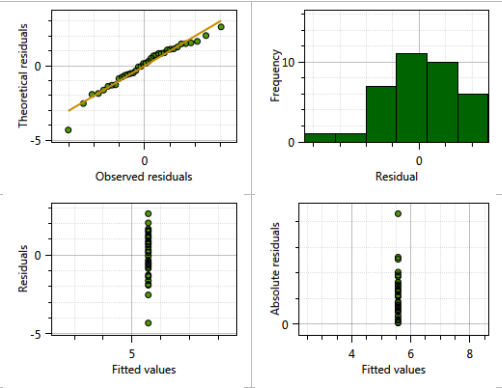
Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000	0.000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000	0.000

Residual 2.059 1.435
Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 5.5680 0.2392 35.0000 23.28 <2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

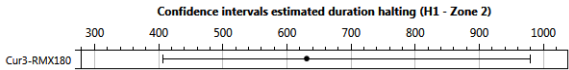
Model residuals

Statistic	Value
Sample skewness	-0.7535
Sample excess kurtosis	0.9482
Passed Shapiro Wilk normality test	Yes (p-value = 0.2887 > 0.05)



Analysis estimated duration halting (H1 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_halting_H1_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	630.7	405.9	980	a

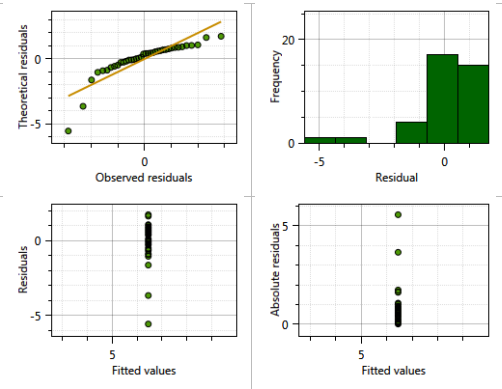
Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_halting_H1_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data
REML criterion at convergence: 130.3
Scaled residuals:
Min 1Q Median 3Q Max
-4.1486 -0.2031 0.2960 0.5615 1.2990
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.000 0.000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.000 0.000
Residual 1.798 1.341
Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 6.4468 0.2175 37.0000 29.64 <2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

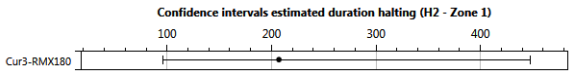
Model residuals

Statistic	Value
Sample skewness	-2.49
Sample excess kurtosis	8.246
Passed Shapiro Wilk normality test	No (p-value = 2.319E-06 < 0.05)



Analysis estimated duration halting (H2 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_halting_H2_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	207	95.68	447.9	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_halting_H2_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 132.4

Scaled residuals:
Min 1Q Median 3Q Max
-2.06685 -0.76585 0.00738 0.74825 1.75024

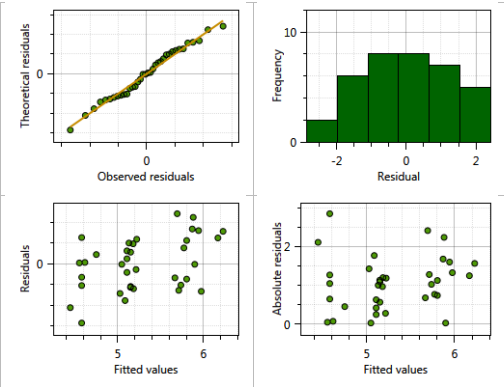
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.54744 0.7399
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.05037 0.2244
Residual 1.90071 1.3787
Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 5.3328 0.3372 8.3689 15.81 1.59e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

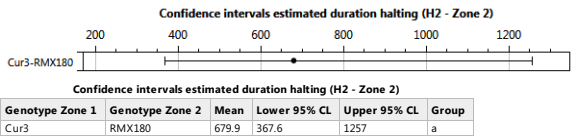
Model residuals

Statistic	Value
Sample skewness	-0.07747
Sample excess kurtosis	-0.6465
Passed Shapiro Wilk normality test	Yes (p-value = 0.7765 > 0.05)



Analysis estimated duration halting (H2 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_halting_H2_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_halting_H2_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 145.3

Scaled residuals:
Min 1Q Median 3Q Max
-4.6586 -0.0686 0.3280 0.4798 0.9525

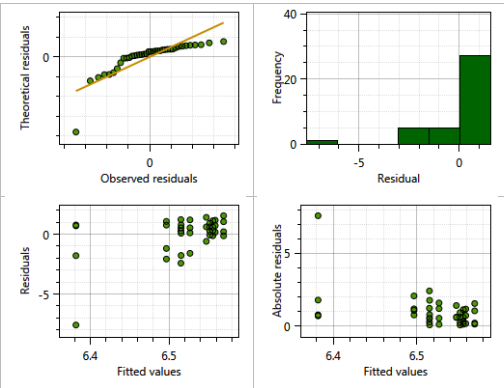
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.00000 0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.04701 0.2168
Residual 2.65150 1.6283
Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 6.522 0.273 9.270 23.89 1.21e-09 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

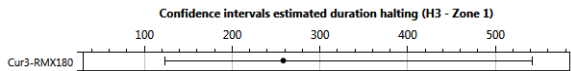
Model residuals

Statistic	Value
Sample skewness	-3.091
Sample excess kurtosis	12.67
Passed Shapiro Wilk normality test	No (p-value = 1.037E-07 < 0.05)



Analysis estimated duration halting (H3 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_halting_H3_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals estimated duration halting (H3 - Zone 1)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	258.1	122.9	542.2	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_halting_H3_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 129.5

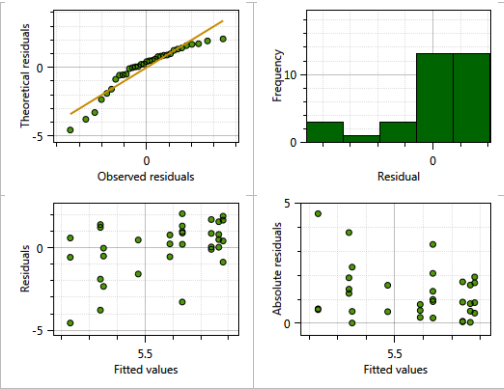
Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.7107 -0.3185  0.2526  0.5901  1.2360

Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.0000   0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.2018   0.4493
Residual                                2.8338   1.6834
Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   5.5535     0.3271  8.8239  16.98 4.84e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

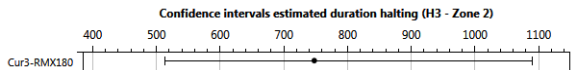
Model residuals

Statistic	Value
Sample skewness	-1.269
Sample excess kurtosis	1.266
Passed Shapiro Wilk normality test	No (p-value = 0.002329 < 0.05)



Analysis estimated duration halting (H3 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_halting_H3_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals estimated duration halting (H3 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	747.7	512.8	1090	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_halting_H3_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 123

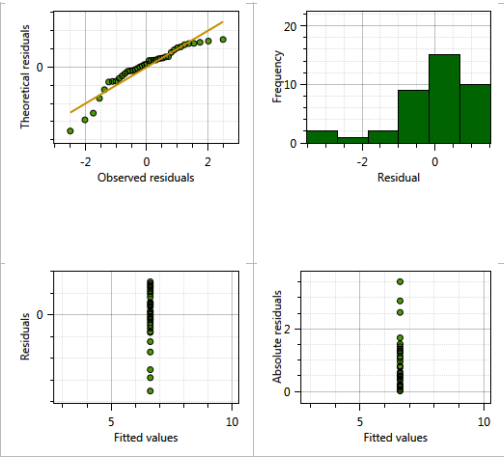
Scaled residuals:
    Min       1Q   Median       3Q      Max
-3.0200 -0.3606  0.1466  0.5928  1.3059

Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.000   0.000
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.000   0.000
Residual                                1.354   1.163
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   6.6170     0.1863 38.0000   35.52 <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

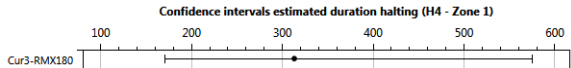
Model residuals

Statistic	Value
Sample skewness	-1.28
Sample excess kurtosis	1.828
Passed Shapiro Wilk normality test	No (p-value = 0.001648 < 0.05)



Analysis estimated duration halting (H4 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_halting_H4_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	313	170.3	575.4	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_halting_H4_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 109.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.2846	-0.4234	0.1660	0.7482	1.4785

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	1.190e+15	3.450e+08
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000e+00	0.000e+00
Residual		2.562e+00	1.601e+00

Number of obs: 29, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

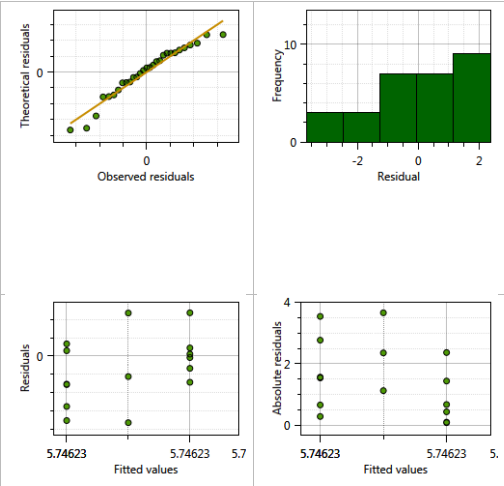
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	5.7462	0.2972	28.0000	19.33	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

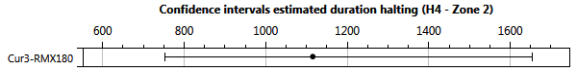
Model residuals

Statistic	Value
Sample skewness	-0.7149
Sample excess kurtosis	0.1012
Passed Shapiro Wilk normality test	Yes (p-value = 0.1527 > 0.05)



Analysis estimated duration halting (H4 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_halting_H4_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	1115	751.9	1655	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_halting_H4_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 98.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.3190	-0.2917	0.1053	0.5543	1.2091

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.1076	0.3281
Residual		0.7287	0.8536

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

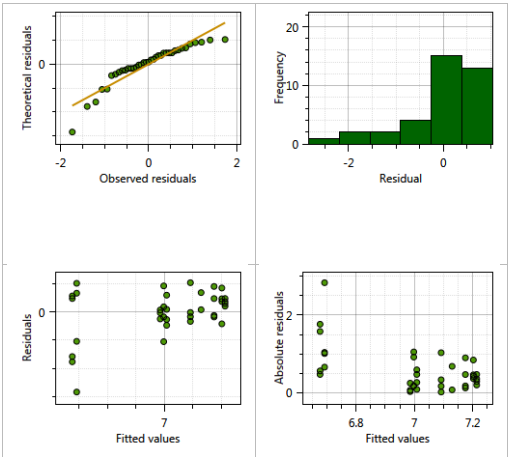
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	7.0170	0.1752	9.3122	40.05	9.62e-12 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

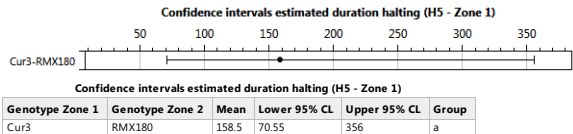
Model residuals

Statistic	Value
Sample skewness	-1.568
Sample excess kurtosis	3.249
Passed Shapiro Wilk normality test	No (p-value = 0.0005907 < 0.05)



Analysis estimated duration halting (H5 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_halting_H5_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_halting_H5_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 136

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.8418	-0.9246	0.3110	0.7377	1.3042

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000	0.000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000	0.000
Residual		4.867	2.206

Number of obs: 31, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

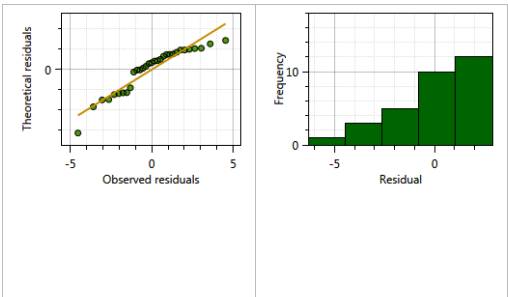
Fixed effects:

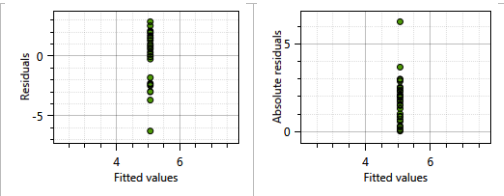
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	5.0656	0.3962	30.0000	12.78	1.13e-13 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

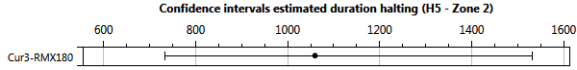
Statistic	Value
Sample skewness	-1.016
Sample excess kurtosis	0.5299
Passed Shapiro Wilk normality test	No (p-value = 0.005691 < 0.05)





Analysis estimated duration halting (H5 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_halting_H5_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals estimated duration halting (H5 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	1059	732.4	1532	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_halting_H5_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 111.1

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.4053	-0.5114	0.4624	0.6561	1.1663

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.01862	0.1365
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.00000	0.0000
Residual		0.97176	0.9858

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

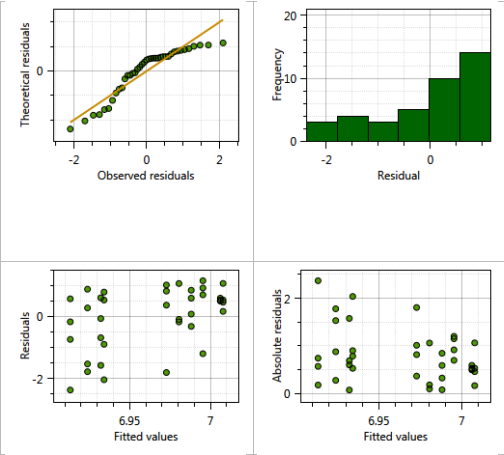
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	6.9654	0.1637	9.2042	42.56	6.95e-12 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

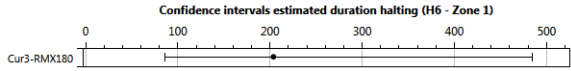
Model residuals

Statistic	Value
Sample skewness	-1.012
Sample excess kurtosis	-0.09354
Passed Shapiro Wilk normality test	No (p-value = 0.0003484 < 0.05)



Analysis estimated duration halting (H6 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_halting_H6_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals estimated duration halting (H6 - Zone 1)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	203.7	85.61	484.8	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_halting_H6_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 99.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.9606	-0.4628	0.0174	0.5498	1.3994

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.1225	0.3500
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.4207	0.6486
Residual		1.9137	1.3834

Number of obs: 27, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

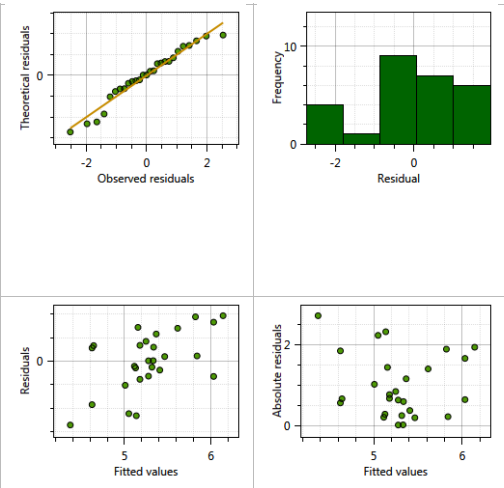
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	5.317	0.362	6.588	14.69	2.8e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

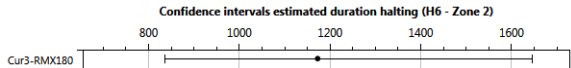
Model residuals

Statistic	Value
Sample skewness	-0.499
Sample excess kurtosis	-0.2463
Passed Shapiro Wilk normality test	Yes (p-value = 0.3156 > 0.05)



Analysis estimated duration halting (H6 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_halting_H6_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	1173	835.2	1646	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_halting_H6_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 111

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.7085	-0.5702	0.3798	0.5913	1.0640

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000	0.000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000	0.000
Residual		1.066	1.032

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

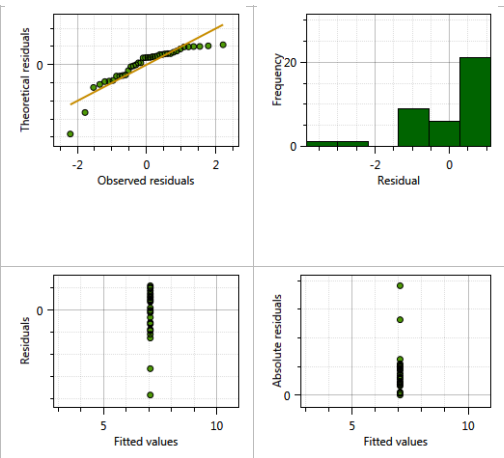
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	7.0669	0.1675	37.0000	42.2	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

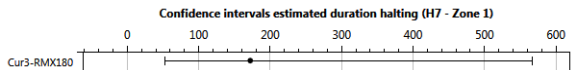
Model residuals

Statistic	Value
Sample skewness	-1.858
Sample excess kurtosis	4.53
Passed Shapiro Wilk normality test	No (p-value = 3.766E-05 < 0.05)



Analysis estimated duration halting (H7 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_halting_H7_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals estimated duration halting (H7 - Zone 1)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	172.1	52.21	567.2	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_halting_H7_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 110.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.5840	-0.3872	0.2228	0.6594	1.3677

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.9808	0.9903
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.5706	0.7554
Residual		2.4893	1.5777

Number of obs: 27, groups: Genotype_Zone_2:Plant_Zone_2, 10; Genotype_Zone_1:Plant_Zone_1, 9

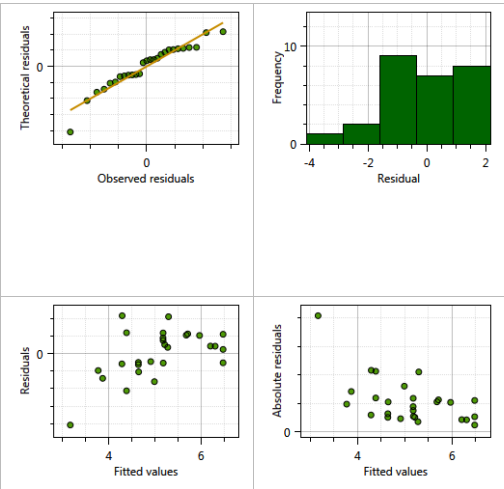
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	5.1480	0.5184	8.1088	9.93	8.13e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

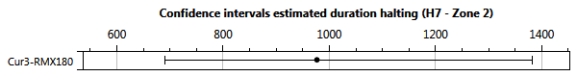
Model residuals

Statistic	Value
Sample skewness	-0.9615
Sample excess kurtosis	1.729
Passed Shapiro Wilk normality test	Yes (p-value = 0.08814 > 0.05)



Analysis estimated duration halting (H7 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_halting_H7_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals estimated duration halting (H7 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	976.6	689.8	1383	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_halting_H7_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 116.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.3522	-0.8055	0.4677	0.7073	1.1876

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00	0.000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.00	0.000
Residual		1.15	1.072

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

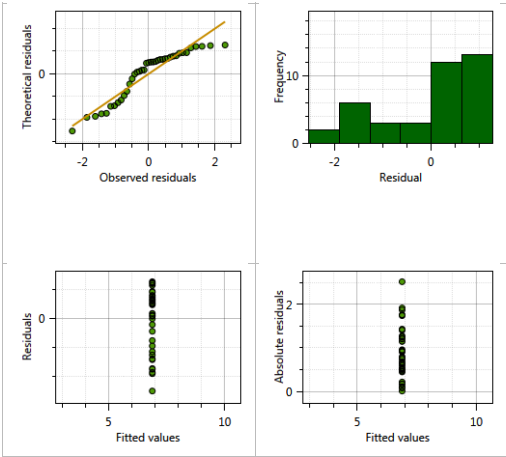
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	6.8841	0.1717	38.0000	40.09	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

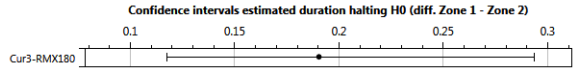
Model residuals

Statistic	Value
Sample skewness	-0.818
Sample excess kurtosis	-0.581
Passed Shapiro Wilk normality test	No (p-value = 0.000724 < 0.05)



Analysis estimated duration halting H0 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_halting_H0_Zone_1,Estimated_duration_halting_H0_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1904	0.1173	0.2937	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 158.8

Scaled residuals:
Min IQ Median 3Q Max
-1.0772 -0.6598 -0.1135 0.5231 2.8293

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0 0.00
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.0 0.00
Residual 729.4 27.01
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

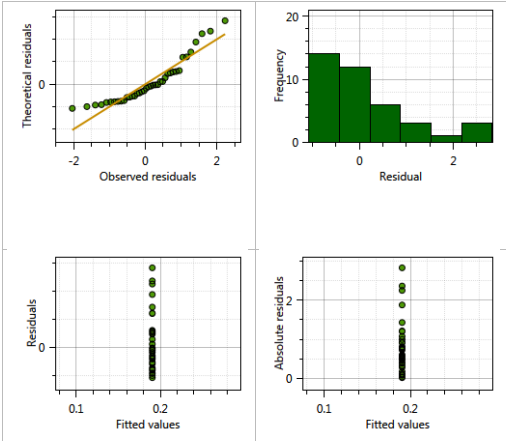
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -1.4477 0.2817 38.0000 -5.14 8.57e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 27.01

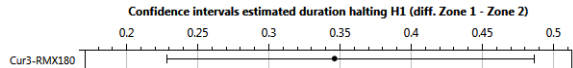
Model residuals

Statistic	Value
Sample skewness	1.209
Sample excess kurtosis	0.8446
Passed Shapiro Wilk normality test	No (p-value = 0.0005149 < 0.05)



Analysis estimated duration halting H1 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_halting_H1_Zone_1,Estimated_duration_halting_H1_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.3461	0.228	0.4866	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data

Weights: wi

REML criterion at convergence: 149.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.4740	-0.7853	-0.2031	0.6852	2.7470

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.03403	0.1845
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.00000	0.0000
Residual		833.80678	28.8757

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

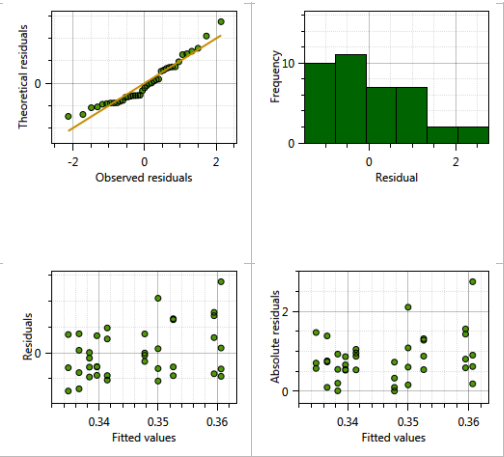
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.6364	0.2595	9.4384	-2.452	0.0355 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 28.88

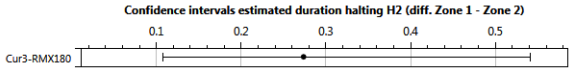
Model residuals

Statistic	Value
Sample skewness	0.8246
Sample excess kurtosis	0.2167
Passed Shapiro Wilk normality test	No (p-value = 0.02922 < 0.05)



Analysis estimated duration halting H2 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_halting_H2_Zone_1,Estimated_duration_halting_H2_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2736	0.1072	0.5415	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: ziFormula

Data: data

Weights: wi

REML criterion at convergence: 164.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.5599	-0.6154	-0.3300	0.5153	1.8816

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	1.1710	1.0821
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.4454	0.6674
Residual		648.1894	25.4596

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

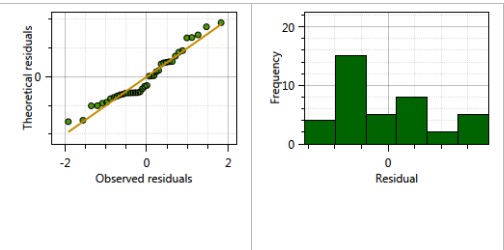
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.9766	0.4738	6.3809	-2.061	0.0822 .

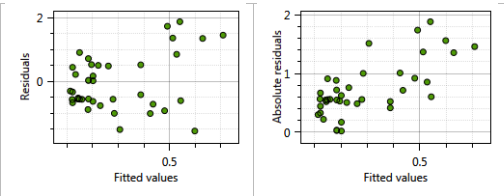
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 25.46

Model residuals

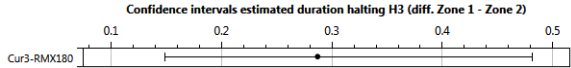
Statistic	Value
Sample skewness	0.5465
Sample excess kurtosis	-0.4083
Passed Shapiro Wilk normality test	Yes (p-value = 0.0574 > 0.05)





Analysis estimated duration halting H3 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_halting_H3_Zone_1,Estimated_duration_halting_H3_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.287	0.1484	0.4817	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 153.1

Scaled residuals:
Min 1Q Median 3Q Max
-1.4260 -0.7947 -0.1628 0.8222 1.8337

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0000 0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.8052 0.8973
Residual 662.1146 25.7316
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

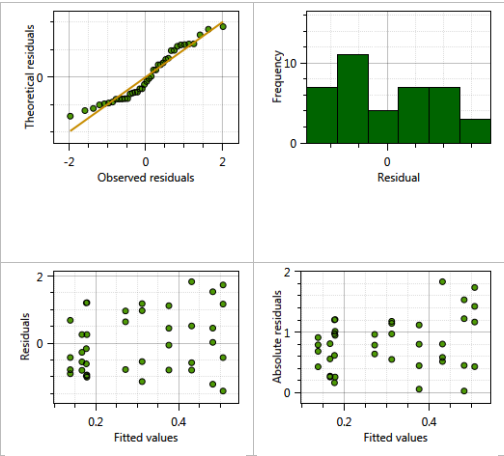
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -0.9101 0.3693 8.9025 -2.465 0.0362 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 25.73

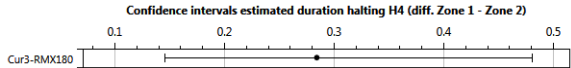
Model residuals

Statistic	Value
Sample skewness	0.3591
Sample excess kurtosis	-1.134
Passed Shapiro Wilk normality test	No (p-value = 0.02699 < 0.05)



Analysis estimated duration halting H4 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_halting_H4_Zone_1,Estimated_duration_halting_H4_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2841	0.1453	0.4809	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 156

Scaled residuals:
Min 1Q Median 3Q Max
-0.9973 -0.7234 -0.4313 0.6547 2.2899

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 8.926e-02 0.2988
Genotype_Zone_2:Plant_Zone_2 (Intercept) 3.435e-01 0.5861
Residual 1.011e+03 31.7903
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

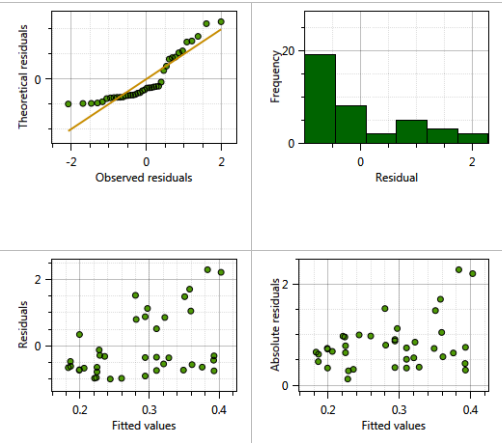
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)

```
(Intercept) -0.9242 0.3336 5.2028 -2.77 0.0377 *
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 31.79
```

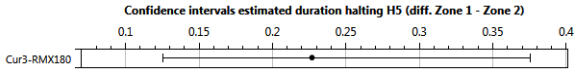
Model residuals

Statistic	Value
Sample skewness	1.14
Sample excess kurtosis	0.1232
Passed Shapiro Wilk normality test	No (p-value = 3.03E-05 < 0.05)



Analysis estimated duration halting H5 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_halting_H5_Zone_1,Estimated_duration_halting_H5_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2269	0.1252	0.3757	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 159.6

Scaled residuals:
    Min       1Q   Median       3Q      Max
-0.9471 -0.7035 -0.3962  0.7043  2.7715

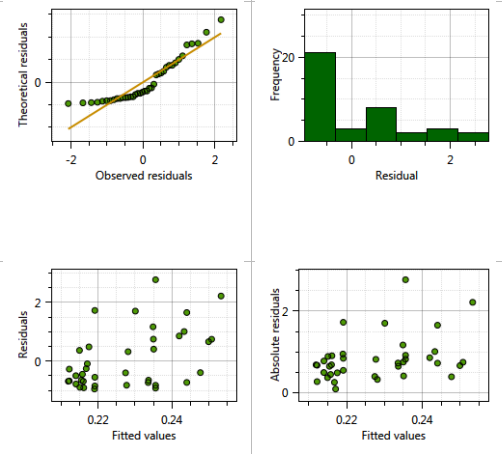
Random effects:
Groups:                               Name      Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 6.783e-02 0.26044
Genotype_Zone_2:Plant_Zone_2 (Intercept) 7.995e-03 0.08941
Residual_                               1.077e+03 32.82052
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -1.2262     0.2993   6.5340  -4.096  0.00532 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 32.82
```

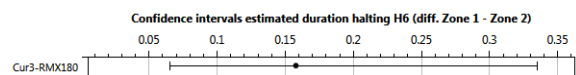
Model residuals

Statistic	Value
Sample skewness	1.097
Sample excess kurtosis	0.3347
Passed Shapiro Wilk normality test	No (p-value = 0.0001362 < 0.05)



Analysis estimated duration halting H6 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_halting_H6_Zone_1,Estimated_duration_halting_H6_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1578	0.06508	0.3352	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 167.9

Scaled residuals:
Min 1Q Median 3Q Max
-1.3164 -0.6540 -0.2286 0.2614 2.4858

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.3311 0.5754
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.7297 0.8542
Residual 746.2009 27.3167
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

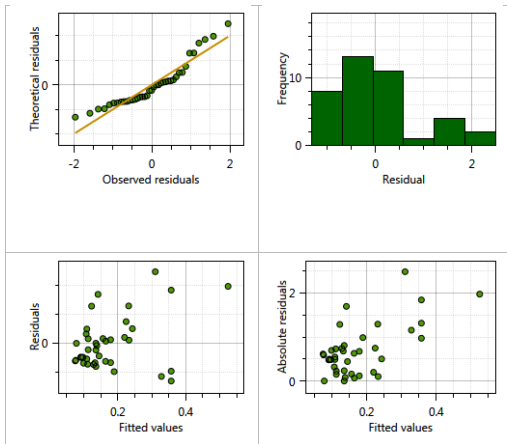
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -1.6747 0.4333 8.4446 -3.865 0.00431 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 27.32

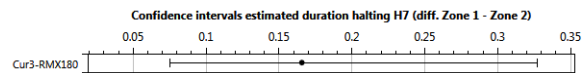
Model residuals

Statistic	Value
Sample skewness	1.11
Sample excess kurtosis	0.711
Passed Shapiro Wilk normality test	No (p-value = 0.001946 < 0.05)



Analysis estimated duration halting H7 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_halting_H7_Zone_1,Estimated_duration_halting_H7_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1657	0.07496	0.3273	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 166.2

Scaled residuals:
Min 1Q Median 3Q Max
-1.1560 -0.6318 -0.4023 0.7911 2.0564

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.06106 0.2471
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.65019 0.8063
Residual 715.10909 26.7415
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

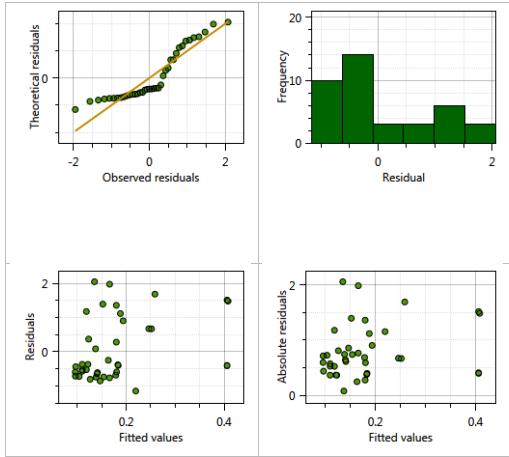
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -1.6166 0.3889 8.0251 -4.157 0.00316 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 26.74

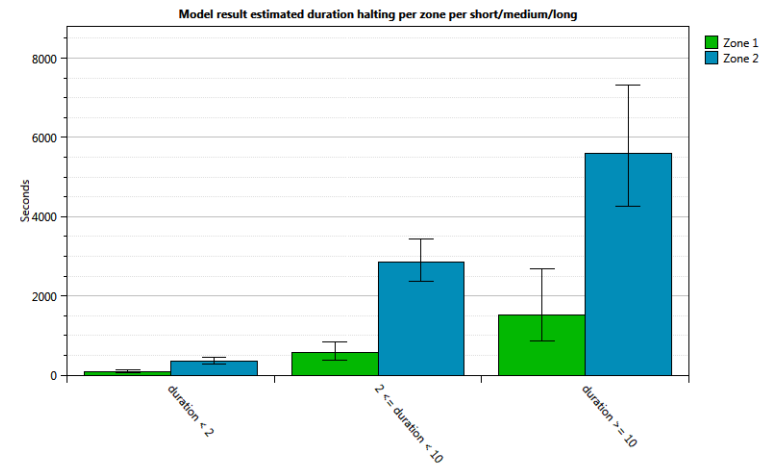
Model residuals

Statistic	Value
Sample skewness	0.8325
Sample excess kurtosis	-0.7594
Passed Shapiro Wilk normality test	No (p-value = 9.521E-05 < 0.05)



Estimated duration halting per zone per short/medium/long

Selected zones	Zone 1, Zone 2
Event duration categories	duration < 2, 2 <= duration < 10, duration >= 10
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

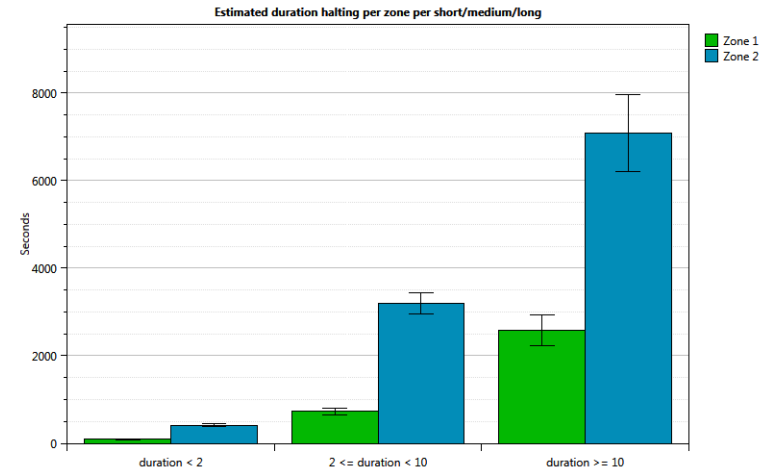
Behaviour statistic	Cur3-RMX180
Estimated duration halting duration < 2 (diff. Zone 1 - Zone 2)	p=1.25E-05**** [-1.89, -1.08]
Estimated duration halting 2 <= duration < 10 (diff. Zone 1 - Zone 2)	p=2.7E-05**** [-1.89, -1.05]
Estimated duration halting duration >= 10 (diff. Zone 1 - Zone 2)	p=0.0129* [-1.71, -0.318]

The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Estimated duration halting (duration < 2 - Zone 1)	80.7 [53.6, 121]	
Estimated duration halting (2 <= duration < 10 - Zone 1)	567 [388, 828]	CR
Estimated duration halting (duration >= 10 - Zone 1)	1.53E+03 [870, 2.67E+03]	CR
Estimated duration halting (duration < 2 - Zone 2)	355 [282, 446]	
Estimated duration halting (2 <= duration < 10 - Zone 2)	2.85E+03 [2.36E+03, 3.44E+03]	
Estimated duration halting (duration >= 10 - Zone 2)	5.59E+03 [4.26E+03, 7.33E+03]	CR

CR = Check residuals

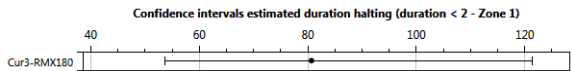
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean duration < 2 - Zone 1	StdErr duration < 2 - Zone 1	Mean 2 <= duration < 10 - Zone 1	StdErr 2 <= duration < 10 - Zone 1	Mean duration >= 10 - Zone 1	StdErr duration >= 10 - Zone 1	Mean duration < 2 - Zone 2	StdErr duration < 2 - Zone 2	Mean 2 <= duration < 10 - Zone 2	StdErr 2 <= duration < 10 - Zone 2	Mean duration >= 10 - Zone 2	StdErr duration >= 10 - Zone 2
Cur3	RMX180	Neutral	92.67	9.18	734.62	77.45	2579.45	352.76	418.18	38.05	3196.86	238.46	7081.04	882.38

Analysis estimated duration halting (duration < 2 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_halting_duration_2_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	80.67	53.59	121.4	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_halting_duration_2_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 79.7

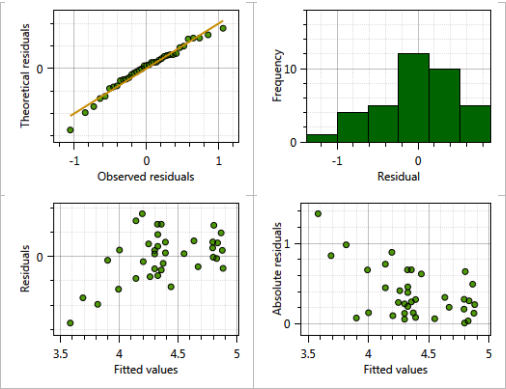
Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.3828 -0.4325  0.1112  0.5255  1.5471

Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.1196   0.3458
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.1088   0.3298
Residual                        0.3307   0.5751
Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    4.3903     0.1792 8.5016   24.5 3.48e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

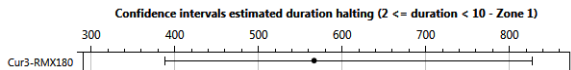
Model residuals

Statistic	Value
Sample skewness	-0.6164
Sample excess kurtosis	0.5363
Passed Shapiro Wilk normality test	Yes (p-value = 0.4762 > 0.05)



Analysis estimated duration halting (2 <= duration < 10 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_halting_2_duration_10_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	566.5	387.8	827.6	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_halting_2_duration_10_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 109.9

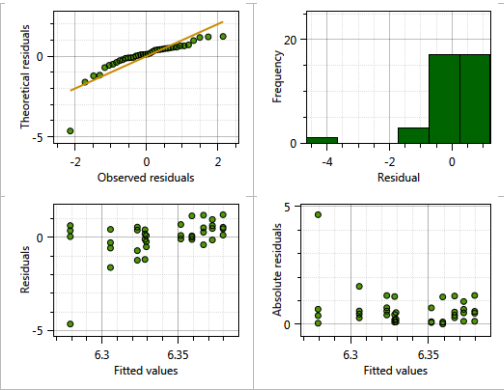
Scaled residuals:
    Min       1Q   Median       3Q      Max
-4.6026 -0.1962  0.1202  0.5080  1.2140

Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.00000   0.000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.01716   0.131
Residual                        1.01804   1.009
Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    6.3395     0.1689 9.4864   37.54 1.22e-11 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

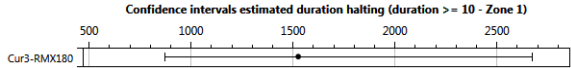
Model residuals

Statistic	Value
Sample skewness	-2.857
Sample excess kurtosis	12.04
Passed Shapiro Wilk normality test	No (p-value = 1.153E-06 < 0.05)



Analysis estimated duration halting (duration >= 10 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_halting_duration_10_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	1525	870.1	2674	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_halting_duration_10_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 129.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.0143	-0.1818	0.1411	0.6014	1.4937

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	2.486e-15	4.986e-08
Genotype_Zone_2:Plant_Zone_2	(Intercept)	2.568e-01	5.068e-01
Residual		1.410e+00	1.187e+00

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

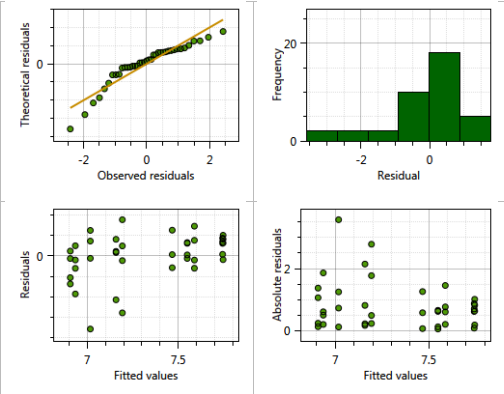
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	7.3300	0.2489	9.1714	29.45	2.13e-10 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

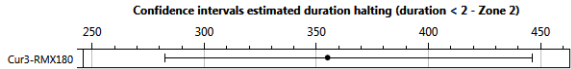
Model residuals

Statistic	Value
Sample skewness	-1.364
Sample excess kurtosis	2.21
Passed Shapiro Wilk normality test	No (p-value = 0.001378 < 0.05)



Analysis estimated duration halting (duration < 2 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_halting_duration_2_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	355	282.3	446.4	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_halting_duration_2_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 72.1

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.65091	-0.68737	-0.09242	0.82437	1.65288

Random effects:

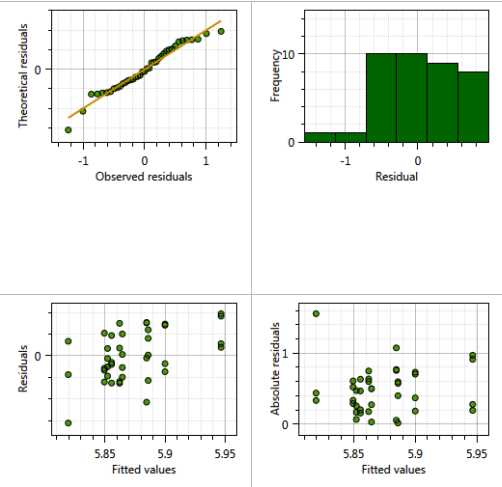
Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.01092	0.1045

Residual 0.34489 0.5873
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 5.87207 0.09971 8.17590 58.89 4.87e-12 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

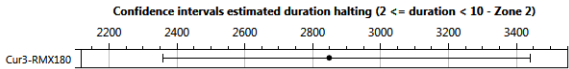
Model residuals

Statistic	Value
Sample skewness	-0.3113
Sample excess kurtosis	-0.08991
Passed Shapiro Wilk normality test	Yes (p-value = 0.3061 > 0.05)



Analysis estimated duration halting (2 <= duration < 10 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_halting_2_duration_10_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	2849	2358	3442	a

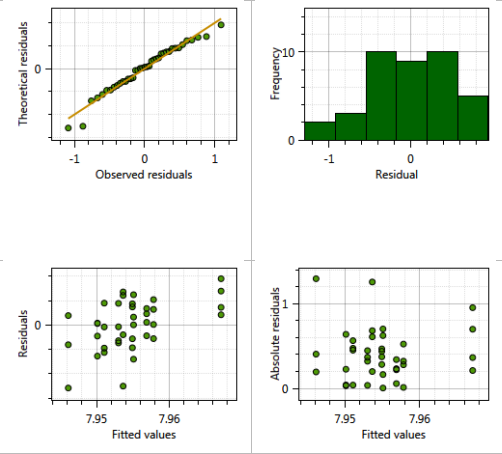
Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_halting_2_duration_10_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data
REML criterion at convergence: 60.2
Scaled residuals:
Min 1Q Median 3Q Max
-2.54816 -0.59345 0.06214 0.72494 1.87553
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.000000 0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.001452 0.0381
Residual 0.257870 0.5078
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 7.95457 0.08221 8.10103 96.76 1.06e-13 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

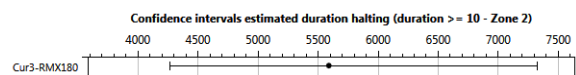
Model residuals

Statistic	Value
Sample skewness	-0.5884
Sample excess kurtosis	0.3941
Passed Shapiro Wilk normality test	Yes (p-value = 0.3285 > 0.05)



Analysis estimated duration halting (duration >= 10 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_halting_duration_10_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	5589	4263	7327	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_halting_duration_10_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 85.6

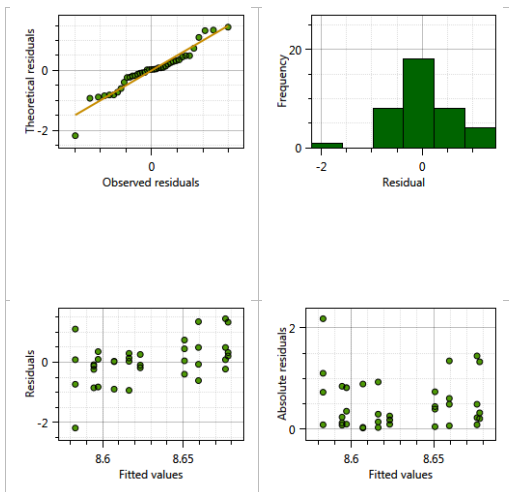
Scaled residuals:
    Min       1Q   Median       3Q      Max
-3.10500 -0.32916  0.04443  0.43979  2.05833

Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0131  0.1144
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.0000  0.0000
Residual                      0.4936  0.7025
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   8.6285     0.1182  8.3238    73 5.58e-13 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

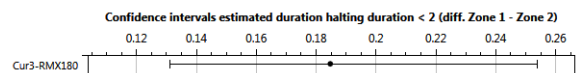
Model residuals

Statistic	Value
Sample skewness	-0.3541
Sample excess kurtosis	1.864
Passed Shapiro Wilk normality test	No (p-value = 0.04264 < 0.05)



Analysis estimated duration halting duration < 2 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_halting_duration_2_Zone_1,Estimated_duration_halting_duration_2_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1847	0.131	0.2539	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 107.7

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.50771 -0.85702  0.03003  0.83140  1.86462

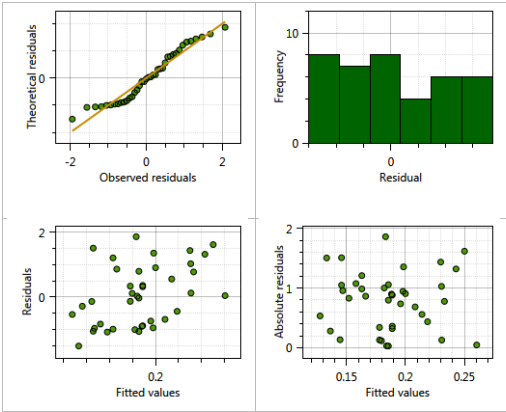
Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.03943  0.1986
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.10516  0.3243
Residual                      53.02243  7.2817
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -1.4848     0.1817  9.6125  -8.172 1.25e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 7.282
```

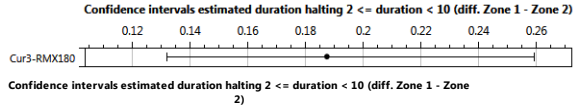
Model residuals

Statistic	Value
Sample skewness	0.2564
Sample excess kurtosis	-1.135
Passed Shapiro Wilk normality test	Yes (p-value = 0.05025 > 0.05)



Analysis estimated duration halting 2 <= duration < 10 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_halting_2_duration_10_Zone_1,Estimated_duration_halting_2_duration_10_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1873	0.1318	0.2593	a

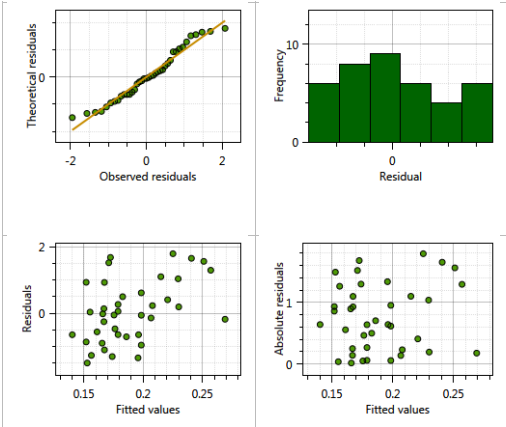
Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi
REML criterion at convergence: 108.5
Scaled residuals:
Min 1Q Median 3Q Max
-1.4935 -0.6422 -0.0164 0.7735 1.7932
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.07264 0.2695
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.06719 0.2592
Residual 449.32871 21.1974
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -1.4674 0.1838 8.7219 -7.984 2.7e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Dispersion: 21.2

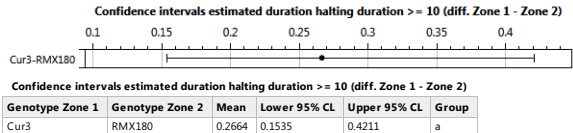
Model residuals

Statistic	Value
Sample skewness	0.2664
Sample excess kurtosis	-0.8793
Passed Shapiro Wilk normality test	Yes (p-value = 0.1628 > 0.05)



Analysis estimated duration halting duration >= 10 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_halting_duration_10_Zone_1,Estimated_duration_halting_duration_10_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2664	0.1535	0.4211	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi
REML criterion at convergence: 130

```
Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.50204 -0.58073  0.01577  0.55464  2.41383

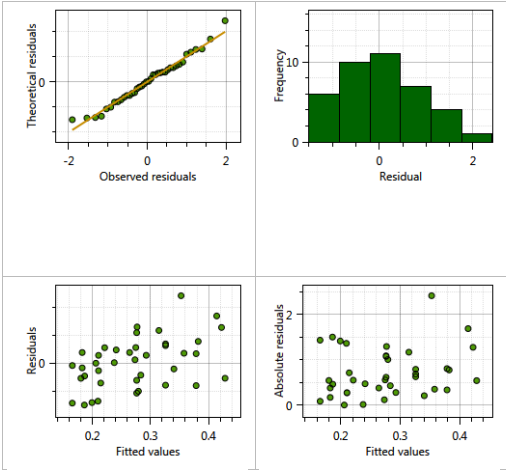
Random effects:
Groups              Name      Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)    0.1537  0.3920
Genotype_Zone_2:Plant_Zone_2 (Intercept)    0.2902  0.5387
Residual                                  2104.1744 45.8713
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   -1.013      0.274   5.249  -3.697  0.0129 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 45.87
```

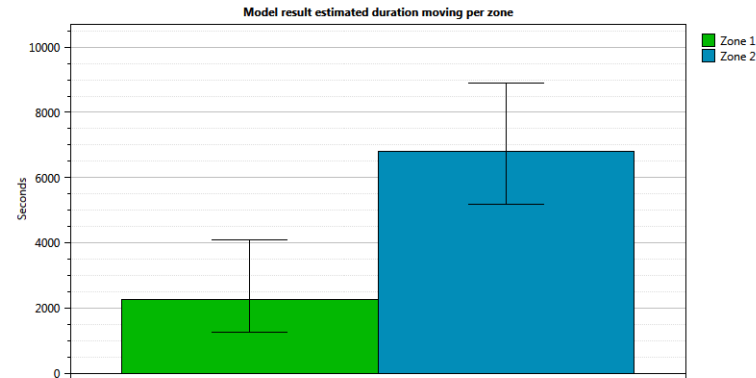
Model residuals

Statistic	Value
Sample skewness	0.3178
Sample excess kurtosis	0.0114
Passed Shapiro Wilk normality test	Yes (p-value = 0.6858 > 0.05)



Estimated duration moving per zone

Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



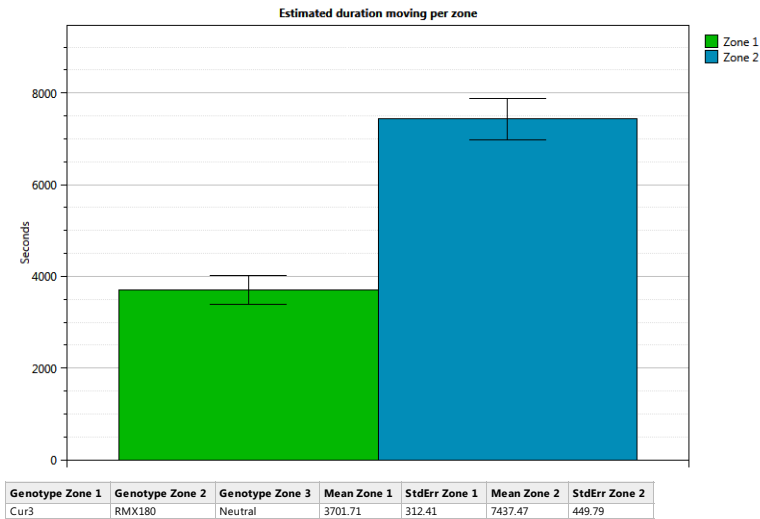
Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.		
Behaviour statistic	Cur3-RMX180	Remark
Estimated duration moving (diff. Zone 1 - Zone 2)	p=0.000403*** [-0.982, -0.408]	CR

CR = Check residuals

The model predictions and 95% confidence intervals for each statistic.		
Statistic	Cur3-RMX180	Remark
Estimated duration moving (Zone 1)	2.27E+03	CR
	[1.26E+03, 4.1E+03]	
Estimated duration moving (Zone 2)	6.8E+03	CR
	[5.19E+03, 8.91E+03]	

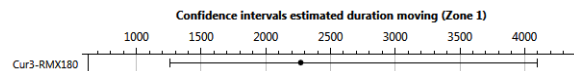
CR = Check residuals

Data summary



Analysis estimated duration moving (Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	2269	1256	4100	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 157.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.2176	0.0521	0.2792	0.4315	0.6887

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000	0.000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000	0.000
Residual		3.331	1.825

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

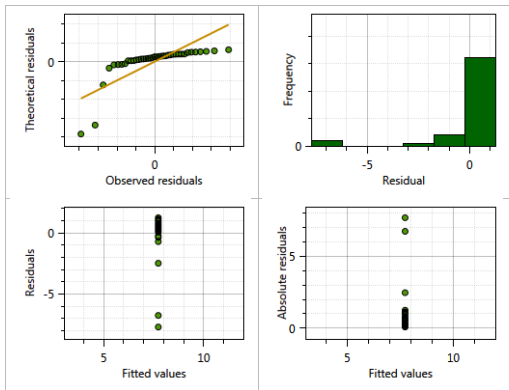
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	7.7271	0.2923	38.0000	26.44	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

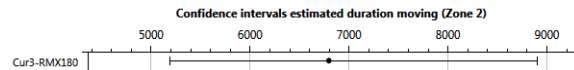
Model residuals

Statistic	Value
Sample skewness	-3.495
Sample excess kurtosis	12.4
Passed Shapiro Wilk normality test	No (p-value = 3.854E-10 < 0.05)



Analysis estimated duration moving (Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	6796	5186	8905	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 49.5

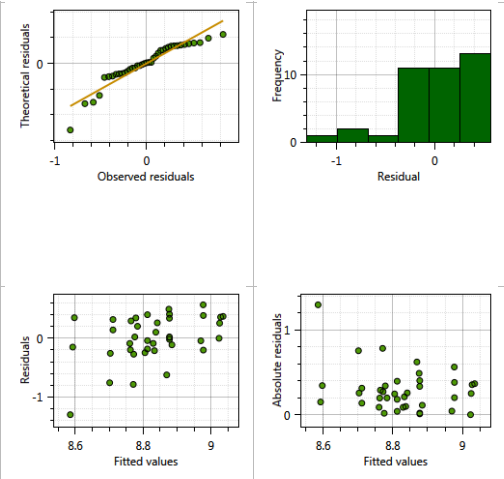
```
Scaled residuals:
  Min       1Q   Median       3Q      Max
-3.15723 -0.46555  0.03048  0.79248  1.37299

Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.001133 0.03366
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.035655 0.18883
Residual                        0.168910 0.41099
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  8.82405    0.08957  3.31508   98.51  7.3e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

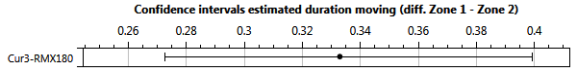
Model residuals

Statistic	Value
Sample skewness	-1.258
Sample excess kurtosis	2.288
Passed Shapiro Wilk normality test	No (p-value = 0.002427 < 0.05)



Analysis estimated duration moving (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_moving_Zone_1,Estimated_duration_moving_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals estimated duration moving (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.3329	0.2725	0.3993	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 82.2

Scaled residuals:
  Min       1Q   Median       3Q      Max
-1.46735 -0.78687 -0.05515  0.82239  1.55168

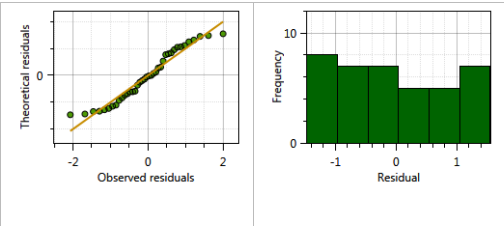
Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 8.769e-03 0.09364
Genotype_Zone_2:Plant_Zone_2 (Intercept) 5.188e-02 0.22777
Residual                        9.356e+02 30.58728
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

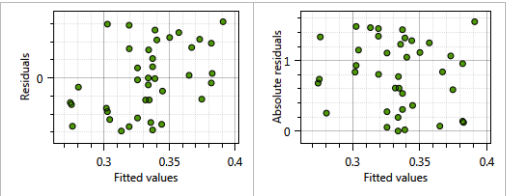
Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -0.6951    0.1265  8.8687  -5.494 0.000403 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 30.59
```

Model residuals

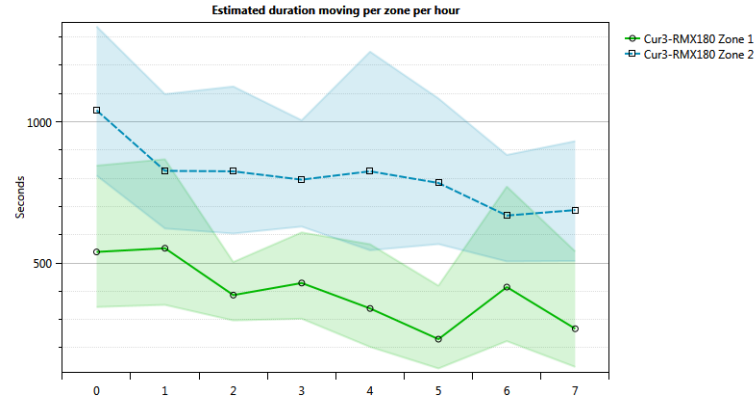
Statistic	Value
Sample skewness	0.1232
Sample excess kurtosis	-1.244
Passed Shapiro Wilk normality test	No (p-value = 0.04148 < 0.05)





Estimated duration moving per zone per hour

Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

Behaviour statistic	Cur3-RMX180	Remark
Estimated duration moving H0 (diff. Zone 1 - Zone 2)	p=0.0451* [-0.955, -0.0133]	
Estimated duration moving H1 (diff. Zone 1 - Zone 2)	p=0.0157* [-0.656, -0.073]	
Estimated duration moving H2 (diff. Zone 1 - Zone 2)	p=0.00426** [-1.09, -0.306]	CR
Estimated duration moving H3 (diff. Zone 1 - Zone 2)	p=0.00289** [-1.02, -0.28]	
Estimated duration moving H4 (diff. Zone 1 - Zone 2)	p=0.0127* [-1.66, -0.264]	CR
Estimated duration moving H5 (diff. Zone 1 - Zone 2)	p=0.00138** [-1.55, -0.507]	CR
Estimated duration moving H6 (diff. Zone 1 - Zone 2)	p=0.00339** [-1.2, -0.305]	
Estimated duration moving H7 (diff. Zone 1 - Zone 2)	p=0.00891** [-1.42, -0.28]	CR

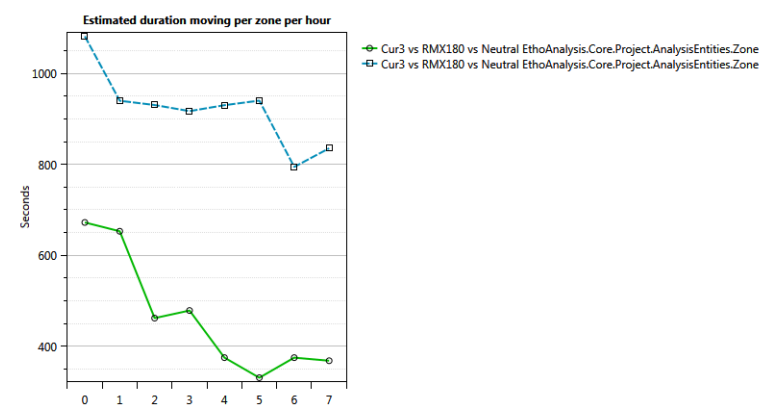
CR = Check residuals

The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Estimated duration moving (H0 - Zone 1)	539 [344, 845]	CR
Estimated duration moving (H0 - Zone 2)	1.04E+03 [810, 1.34E+03]	CR
Estimated duration moving (H1 - Zone 1)	552 [352, 868]	CR
Estimated duration moving (H1 - Zone 2)	827 [622, 1.1E+03]	CR
Estimated duration moving (H2 - Zone 1)	386 [297, 504]	
Estimated duration moving (H2 - Zone 2)	825 [604, 1.13E+03]	CR
Estimated duration moving (H3 - Zone 1)	429 [303, 609]	CR
Estimated duration moving (H3 - Zone 2)	795 [629, 1.01E+03]	
Estimated duration moving (H4 - Zone 1)	339 [203, 567]	
Estimated duration moving (H4 - Zone 2)	825 [545, 1.25E+03]	CR
Estimated duration moving (H5 - Zone 1)	230 [127, 420]	CR
Estimated duration moving (H5 - Zone 2)	784 [567, 1.08E+03]	
Estimated duration moving (H6 - Zone 1)	415 [223, 771]	CR
Estimated duration moving (H6 - Zone 2)	668 [506, 883]	CR
Estimated duration moving (H7 - Zone 1)	267 [132, 541]	CR
Estimated duration moving (H7 - Zone 2)	688 [507, 932]	

CR = Check residuals

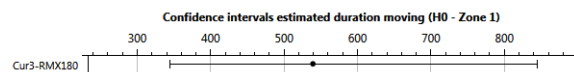
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean H0 - Zone 1	StdErr H0 - Zone 1	Mean H0 - Zone 2	StdErr H0 - Zone 2	Mean H1 - Zone 1	StdErr H1 - Zone 1	Mean H1 - Zone 2	StdErr H1 - Zone 2	Mean H2 - Zone 1	StdErr H2 - Zone 1	Mean H2 - Zone 2	StdErr H2 - Zone 2	Mean H3 - Zone 1	StdErr H3 - Zone 1	Mean H3 - Zone 2	StdErr H3 - Zone 2	Mean H4 - Zone 1	StdErr H4 - Zone 1	Mean H4 - Zone 2	StdErr H4 - Zone 2	Mean H5 - Zone 1	StdErr H5 - Zone 1	Mean H5 - Zone 2	StdErr H5 - Zone 2	Mean H6 - Zone 1	StdErr H6 - Zone 1	Mean H6 - Zone 2	StdErr H6 - Zone 2
Cur3	RMX180	Neutral	672.24	87.67	1081.73	83.73	652.88	61.4	939.9	81.45	461.8	58.06	930.55	77.86	478.53	57.52	917.12	74.22	374.93	57.89	930.18	84.68	330.74	50.61	940.23	84.42	374.87	60.4	794.43	71.4

Analysis estimated duration moving (H0 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_H0_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals estimated duration moving (H0 - Zone 1)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	539.2	344.1	845.2	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_H0_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 109.5

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.8311	-0.1308	0.2311	0.4814	0.9806

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	4.556e-20	2.135e-10
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000e+00	0.000e+00
Residual		1.606e+00	1.267e+00

Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

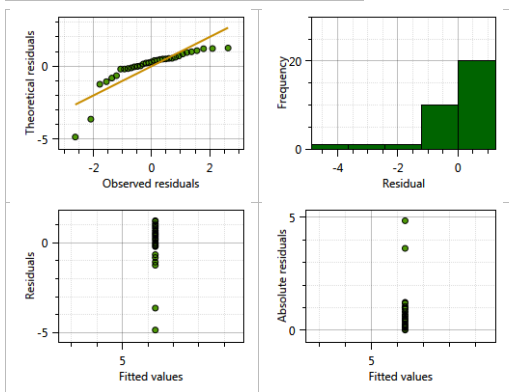
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	6.2902	0.2206	32.0000	28.51	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

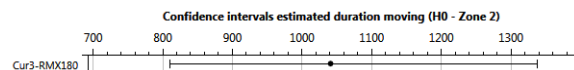
Model residuals

Statistic	Value
Sample skewness	-2.549
Sample excess kurtosis	7.58
Passed Shapiro Wilk normality test	No (p-value = 1.629E-06 < 0.05)



Analysis estimated duration moving (H0 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_H0_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals estimated duration moving (H0 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	1041	809.8	1338	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_H0_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 65.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.7717	-0.2284	0.2504	0.5697	1.1864

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.01979	0.1407
Residual		0.32348	0.5688

Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

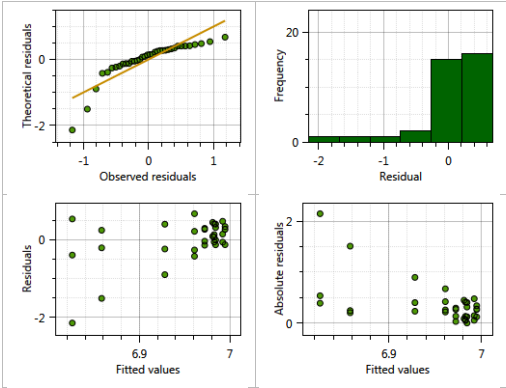
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	6.948	0.105	6.623	66.18	1.36e-10 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

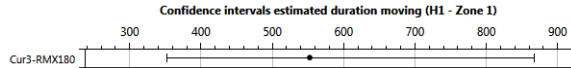
Model residuals

Statistic	Value
Sample skewness	-2.31
Sample excess kurtosis	6.57
Passed Shapiro Wilk normality test	No (p-value = 5.238E-06 < 0.05)



Analysis estimated duration moving (H1 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_H1_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	552.4	351.7	867.6	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_H1_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 110.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-5.2367	-0.1481	0.1698	0.4410	0.8769

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.007191	0.0848
Residual		1.224830	1.1067

Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

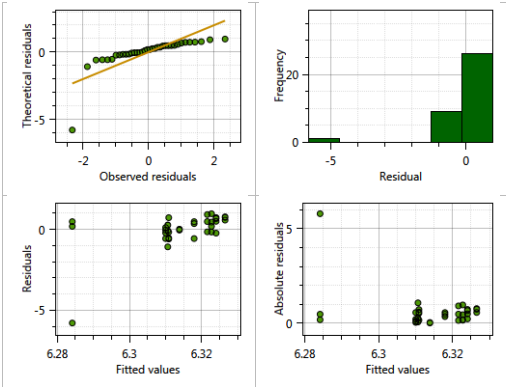
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	6.3142	0.1864	6.2664	33.87	2.46e-08 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

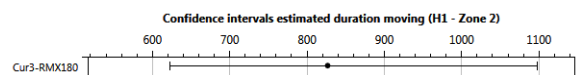
Model residuals

Statistic	Value
Sample skewness	-4.323
Sample excess kurtosis	22.62
Passed Shapiro Wilk normality test	No (p-value = 3.192E-09 < 0.05)



Analysis estimated duration moving (H1 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_H1_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	826.6	622.1	1098	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method [`lmerModLmerTest`]
Formula: `Estimated_duration_moving_H1_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)`
Data: data

REML criterion at convergence: 81.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.0629	-0.3097	0.3666	0.6545	1.1656

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.01707	0.1307
Residual		0.49055	0.7004

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

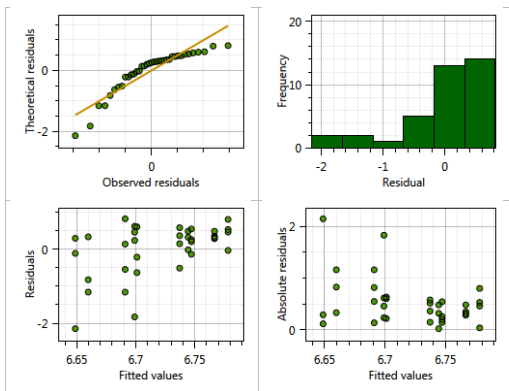
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	6.7173	0.1224	7.7210	54.87	2.74e-11 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

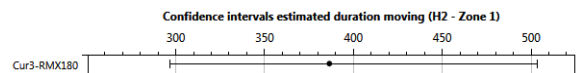
Model residuals

Statistic	Value
Sample skewness	-1.566
Sample excess kurtosis	2.285
Passed Shapiro Wilk normality test	No (p-value = 9.811E-05 < 0.05)



Analysis estimated duration moving (H2 - Zone 1)

Analysis model	Linear mixed model fit by REML: <code>Estimated_duration_moving_H2_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)</code>
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	386.4	296.5	503.6	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method [`lmerModLmerTest`]
Formula: `Estimated_duration_moving_H2_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)`
Data: data

REML criterion at convergence: 85.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.69890	-0.55542	0.09798	0.69664	1.85849

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000	0.0000
Residual		0.613	0.7829

Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

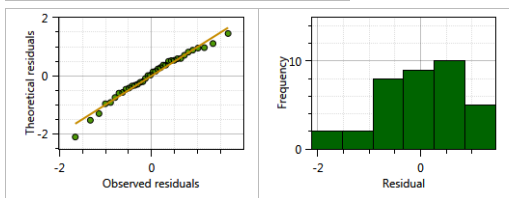
Fixed effects:

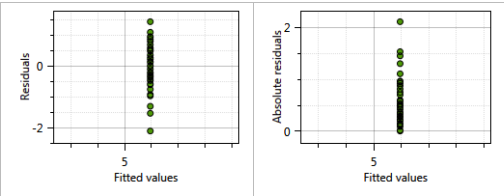
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	5.9570	0.1305	35.0000	45.65	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

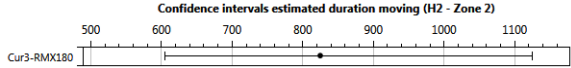
Statistic	Value
Sample skewness	-0.5891
Sample excess kurtosis	0.3496
Passed Shapiro Wilk normality test	Yes (p-value = 0.6406 > 0.05)





Analysis estimated duration moving (H2 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_H2_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	824.7	604.4	1125	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_H2_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 77.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.4025	-0.0777	0.2117	0.5198	1.4051

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.06992	0.2644
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.00000	0.0000
Residual		0.40132	0.6335

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

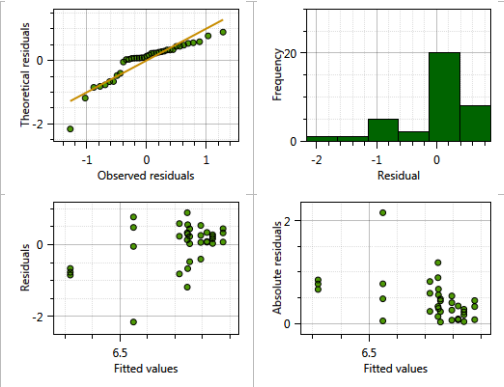
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	6.7150	0.1338	7.6958	50.18	5.8e-11 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

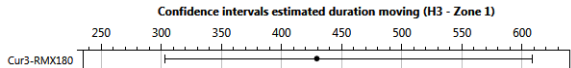
Model residuals

Statistic	Value
Sample skewness	-1.596
Sample excess kurtosis	3.435
Passed Shapiro Wilk normality test	No (p-value = 0.0002749 < 0.05)



Analysis estimated duration moving (H3 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_H3_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	429.2	302.7	608.6	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_H3_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 93.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.9937	-0.0793	0.2235	0.5723	1.1327

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		0.9696	0.9847

Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

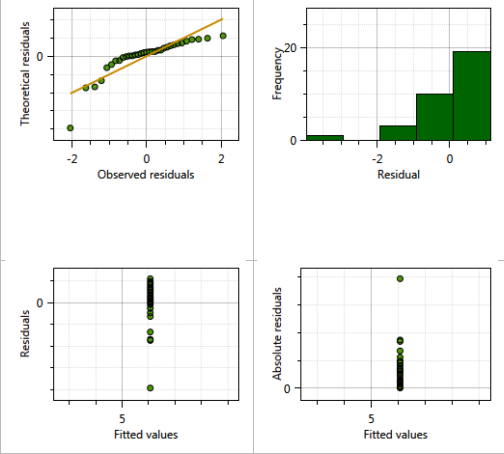
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	6.0620	0.1714	32.0000	35.37	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

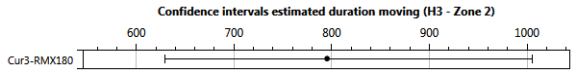
Model residuals

Statistic	Value
Sample skewness	-2.361
Sample excess kurtosis	7.32
Passed Shapiro Wilk normality test	No (p-value = 1.009E-05 < 0.05)



Analysis estimated duration moving (H3 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_H3_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	795.3	628.9	1006	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_H3_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 67.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.6058	-0.3872	0.1659	0.5740	1.4811

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.03026	0.1740
Residual		0.28930	0.5379

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

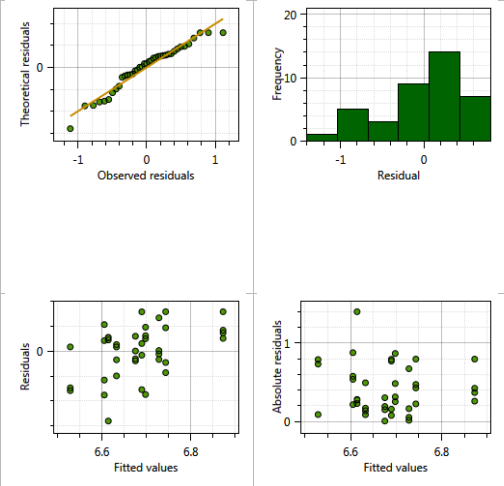
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	6.6787	0.1023	8.2299	65.31	1.81e-12 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

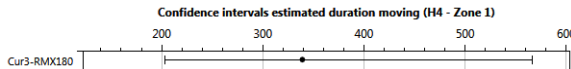
Model residuals

Statistic	Value
Sample skewness	-0.6682
Sample excess kurtosis	0.1274
Passed Shapiro Wilk normality test	Yes (p-value = 0.1016 > 0.05)



Analysis estimated duration moving (H4 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_H4_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	339.1	202.9	566.7	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_H4_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 75.5

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.13875	-0.58884	0.09216	0.50197	1.54447

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.3169	0.5630
Residual		0.5101	0.7142

Number of obs: 30, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

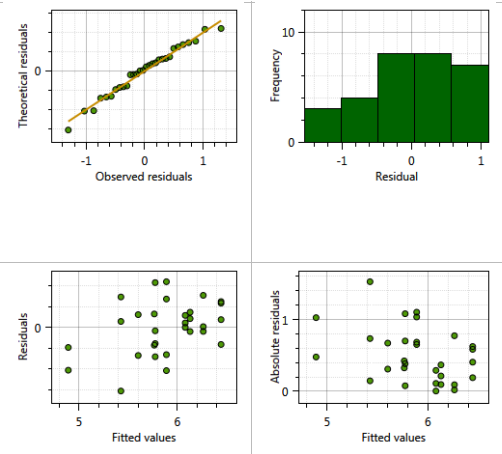
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	5.8262	0.2225	7.9488	26.19	5.32e-09 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

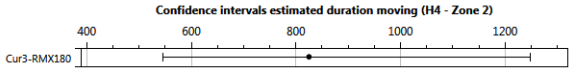
Model residuals

Statistic	Value
Sample skewness	-0.3674
Sample excess kurtosis	-0.1597
Passed Shapiro Wilk normality test	Yes (p-value = 0.79 > 0.05)



Analysis estimated duration moving (H4 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_H4_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	824.9	545	1249	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_H4_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 71.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.4442	-0.4414	0.1686	0.6439	1.3418

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.04075	0.2019
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.06681	0.2585
Residual		0.30959	0.5564

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

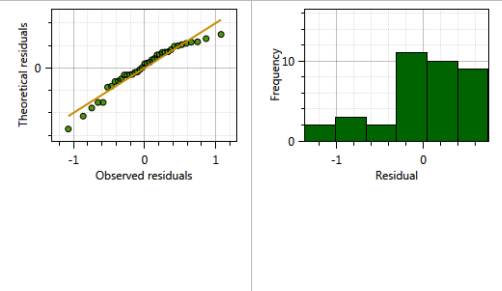
Fixed effects:

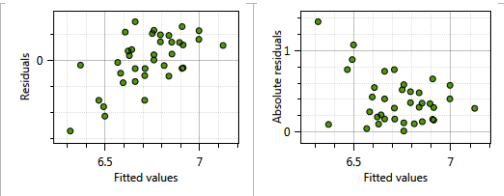
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	6.7153	0.1389	3.3942	48.33	6.14e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

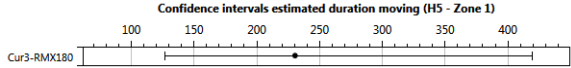
Statistic	Value
Sample skewness	-0.8454
Sample excess kurtosis	0.3786
Passed Shapiro Wilk normality test	No (p-value = 0.04813 < 0.05)





Analysis estimated duration moving (H5 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_H5_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals estimated duration moving (H5 - Zone 1)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	230.4	126.5	419.7	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_H5_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 118

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.6409	-0.2410	0.3382	0.5687	0.9498

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000	0.000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000	0.000
Residual		2.671	1.634

Number of obs: 31, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

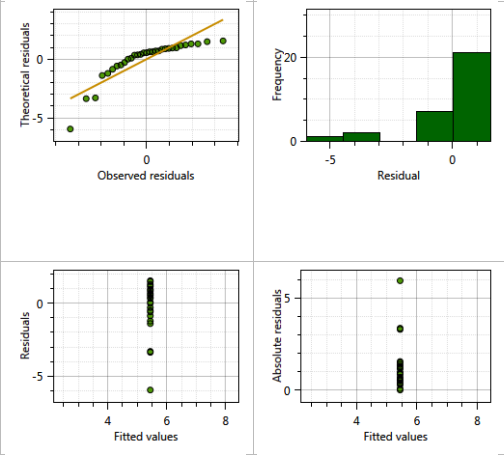
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	5.4399	0.2935	30.0000	18.53	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

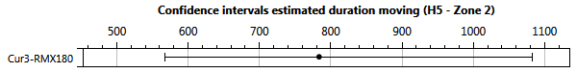
Model residuals

Statistic	Value
Sample skewness	-2.205
Sample excess kurtosis	5.419
Passed Shapiro Wilk normality test	No (p-value = 8.417E-06 < 0.05)



Analysis estimated duration moving (H5 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_H5_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals estimated duration moving (H5 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	783.6	566.9	1083	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_H5_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 71.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.1665	-0.7662	0.1534	0.7225	1.4448

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	2.573e-15	5.072e-08
Genotype_Zone_2:Plant_Zone_2	(Intercept)	1.308e-01	3.617e-01
Residual		2.744e-01	5.239e-01

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

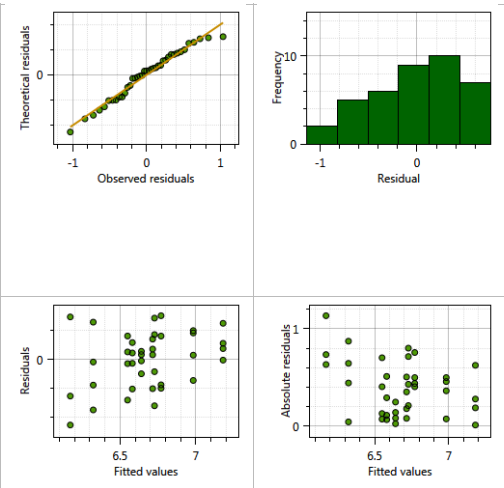
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	6.664	0.142	8.556	46.95	1.27e-11 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

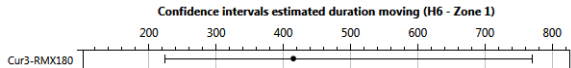
Model residuals

Statistic	Value
Sample skewness	-0.402
Sample excess kurtosis	-0.5149
Passed Shapiro Wilk normality test	Yes (p-value = 0.3341 > 0.05)



Analysis estimated duration moving (H6 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_H6_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype_Zone_1	Genotype_Zone_2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	414.9	223.3	770.8	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_H6_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 71.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.0821	-0.7107	0.2912	0.7461	1.1857

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.08502	0.2916
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.07435	0.2727
Residual		0.66837	0.8175

Number of obs: 27, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

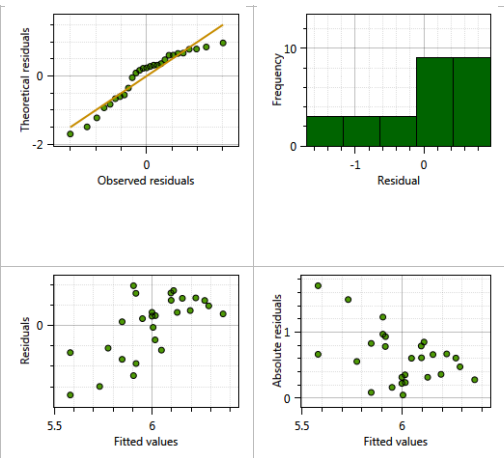
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	6.0280	0.2055	3.3221	29.33	3.96e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

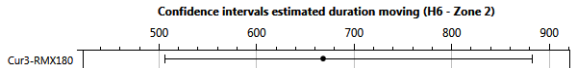
Model residuals

Statistic	Value
Sample skewness	-0.8171
Sample excess kurtosis	-0.3317
Passed Shapiro Wilk normality test	No (p-value = 0.02286 < 0.05)



Analysis estimated duration moving (H6 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_H6_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals estimated duration moving (H6 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	668.2	505.7	882.9	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_H6_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 84.5

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.8620	-0.3899	0.1680	0.4969	1.4608

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.01911	0.1382
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.00000	0.0000
Residual		0.50400	0.7099

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

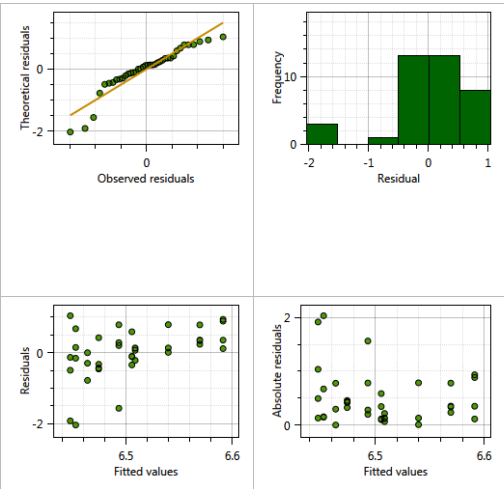
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	6.5045	0.1233	9.0434	52.77	1.43e-12 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

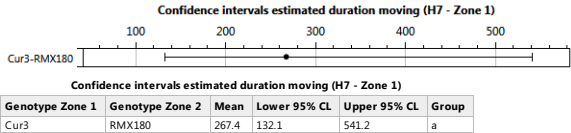
Model residuals

Statistic	Value
Sample skewness	-1.277
Sample excess kurtosis	2.209
Passed Shapiro Wilk normality test	No (p-value = 0.001406 < 0.05)



Analysis estimated duration moving (H7 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_H7_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_H7_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 112.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.2022	-0.0309	0.2724	0.5915	0.9168

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000	0.000
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000	0.000
Residual		3.308	1.819

Number of obs: 28, groups: Genotype_Zone_2:Plant_Zone_2, 10; Genotype_Zone_1:Plant_Zone_1, 9

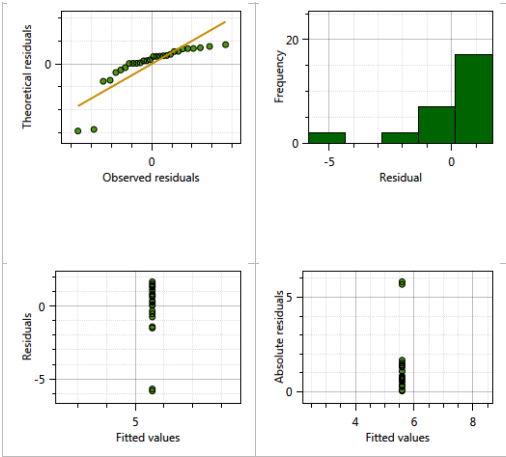
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	5.5886	0.3437	27.0000	16.26	1.8e-15 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

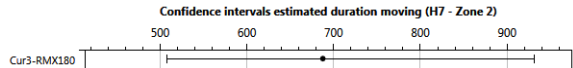
Model residuals

Statistic	Value
Sample skewness	-2.423
Sample excess kurtosis	6.078
Passed Shapiro Wilk normality test	No (p-value = 2.839E-06 < 0.05)



Analysis estimated duration moving (H7 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_H7_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	687.6	507.4	931.7	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_H7_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 78.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.71276	-0.69823	0.06712	0.72765	1.50267

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.05502	0.2346
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.01863	0.1365
Residual		0.36443	0.6037

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

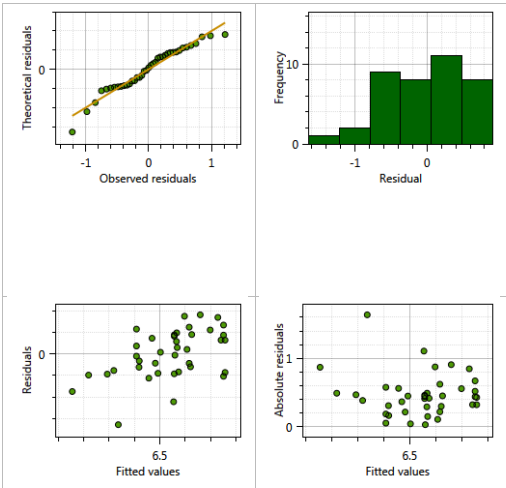
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	6.5332	0.1294	7.2549	50.49	1.65e-10 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

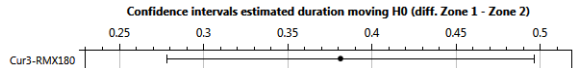
Model residuals

Statistic	Value
Sample skewness	-0.594
Sample excess kurtosis	0.4378
Passed Shapiro Wilk normality test	Yes (p-value = 0.1514 > 0.05)



Analysis estimated duration moving H0 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_moving_H0_Zone_1,Estimated_duration_moving_H0_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.3813	0.278	0.4967	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data

Weights: wi

REML criterion at convergence: 114.5

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.5988	-0.7117	-0.1117	0.5502	1.9715

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.1602	0.4003
Residual		416.9781	20.4200

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

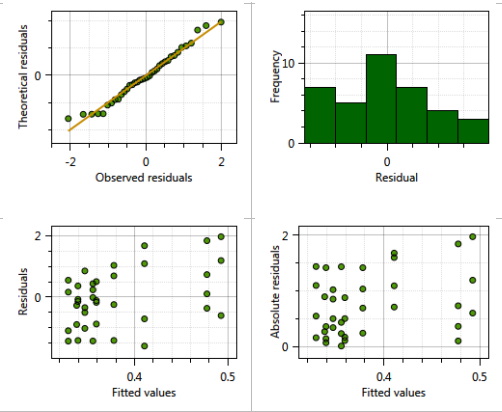
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.4839	0.2062	8.5097	-2.347	0.0451 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 20.42

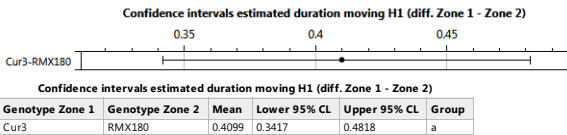
Model residuals

Statistic	Value
Sample skewness	0.2618
Sample excess kurtosis	-0.5147
Passed Shapiro Wilk normality test	Yes (p-value = 0.4709 > 0.05)



Analysis estimated duration moving H1 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_moving_H1_Zone_1,Estimated_duration_moving_H1_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: ziFormula

Data: data

Weights: wi

REML criterion at convergence: 98.1

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.01985	-0.70455	-0.03301	0.73535	2.35570

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0	0.00
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0	0.00
Residual		310.1	17.61

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

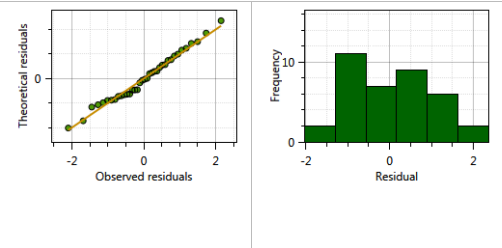
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.3644	0.1437	36.0000	-2.536	0.0157 *

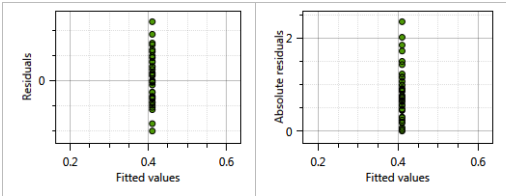
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 17.61

Model residuals

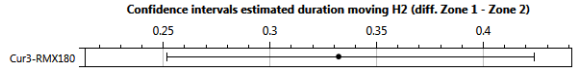
Statistic	Value
Sample skewness	0.2559
Sample excess kurtosis	-0.3053
Passed Shapiro Wilk normality test	Yes (p-value = 0.8644 > 0.05)





Analysis estimated duration moving H2 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_moving_H2_Zone_1,Estimated_duration_moving_H2_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals estimated duration moving H2 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.3322	0.2515	0.424	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 117.4

Scaled residuals:
Min 1Q Median 3Q Max
-1.4223 -0.7000 -0.3715 0.6439 3.2448

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.01426 0.1194
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.00000 0.0000
Residual 304.91028 17.4617
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

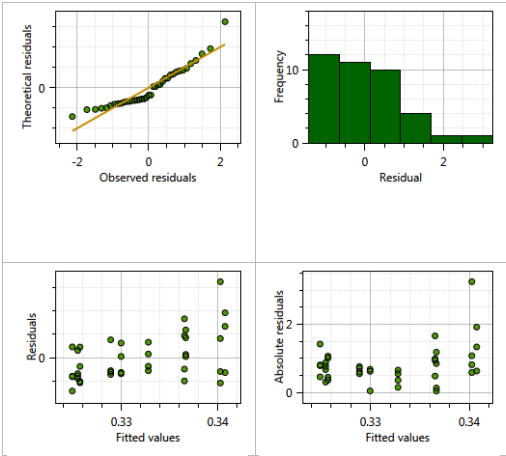
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -0.6985 0.1638 6.5995 -4.265 0.00426 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 17.46

Model residuals

Statistic	Value
Sample skewness	1.166
Sample excess kurtosis	1.558
Passed Shapiro Wilk normality test	No (p-value = 0.002728 < 0.05)

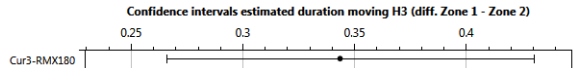


Data points with high residuals

Trial	Arena
Trial 3	7

Analysis estimated duration moving H3 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_moving_H3_Zone_1,Estimated_duration_moving_H3_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals estimated duration moving H3 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.3435	0.2658	0.4305	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 112.6

Scaled residuals:
Min 1Q Median 3Q Max
-1.7248 -0.8401 -0.0809 0.6312 1.8493

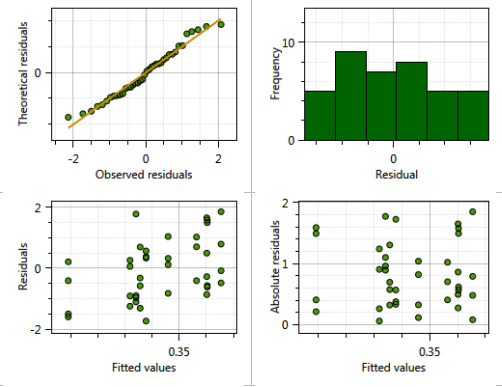
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.00000 0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.04056 0.2014

Residual 281.08054 16.7655
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -0.6478 0.1650 9.9218 -3.925 0.00289 **

Signif. codes: 0 '****' 0.001 '***' 0.01 '**' 0.05 '.' 0.1 ' ' 1
Dispersion: 16.77

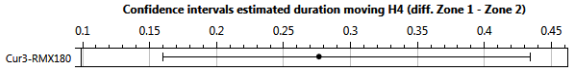
Model residuals

Statistic	Value
Sample skewness	0.2549
Sample excess kurtosis	-0.7679
Passed Shapiro Wilk normality test	Yes (p-value = 0.3462 > 0.05)



Analysis estimated duration moving H4 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_moving_H4_Zone_1,Estimated_duration_moving_H4_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2764	0.1596	0.4344	a

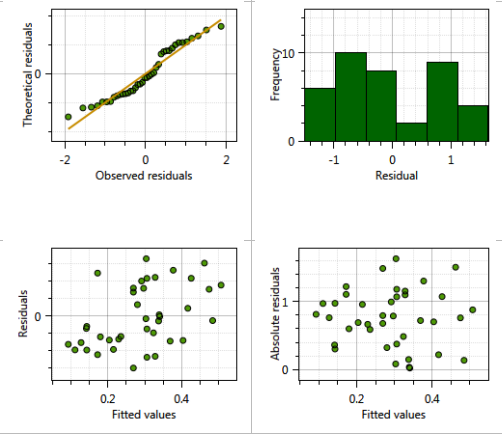
Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi
REML criterion at convergence: 131.7
Scaled residuals:
Min 1Q Median 3Q Max
-1.4930 -0.7129 -0.1462 0.7927 1.6369
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.2548 0.5047
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.3871 0.6222
Residual 254.3667 15.9489
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -0.9624 0.3063 8.5424 -3.142 0.0127 *

Signif. codes: 0 '****' 0.001 '***' 0.01 '**' 0.05 '.' 0.1 ' ' 1
Dispersion: 15.95

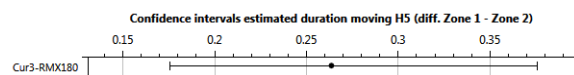
Model residuals

Statistic	Value
Sample skewness	0.3085
Sample excess kurtosis	-1.189
Passed Shapiro Wilk normality test	No (p-value = 0.03202 < 0.05)



Analysis estimated duration moving H5 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_moving_H5_Zone_1,Estimated_duration_moving_H5_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2636	0.1754	0.3759	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 128.4

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.3429 -0.8668 -0.1809  0.9336  1.9980

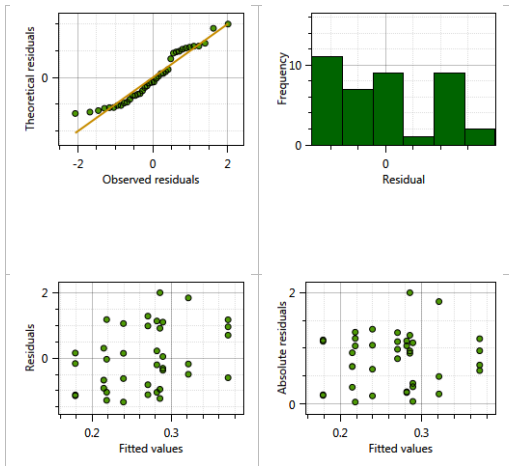
Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.0000  0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.2149  0.4635
Residual                                298.1035 17.2657
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -1.0273     0.2328   9.765  -4.412  0.00138 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 17.27
```

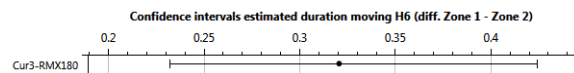
Model residuals

Statistic	Value
Sample skewness	0.4216
Sample excess kurtosis	-0.9675
Passed Shapiro Wilk normality test	No (p-value = 0.02295 < 0.05)



Analysis estimated duration moving H6 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_moving_H6_Zone_1,Estimated_duration_moving_H6_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.3206	0.2319	0.4243	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 132.3

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.5254 -0.7821 -0.0025  0.8627  2.0517

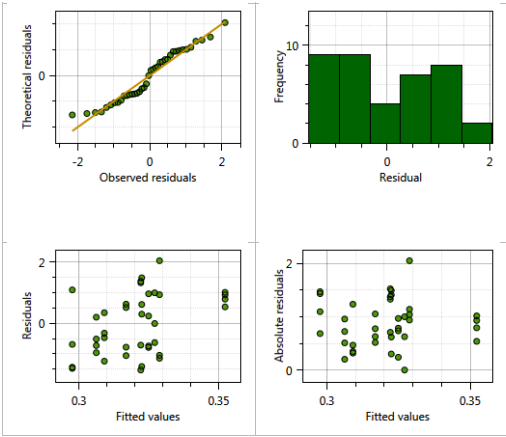
Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.04419  0.2102
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.00000  0.0000
Residual                                363.56810 19.0675
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -0.7512     0.2034  11.2918  -3.694  0.00339 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 19.07
```

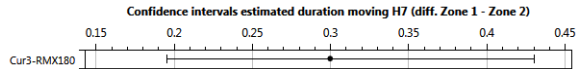
Model residuals

Statistic	Value
Sample skewness	0.1649
Sample excess kurtosis	-1.16
Passed Shapiro Wilk normality test	Yes (p-value = 0.05542 > 0.05)



Analysis estimated duration moving H7 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_moving_H7_Zone_1,Estimated_duration_moving_H7_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2997	0.195	0.4304	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 133.8

Scaled residuals:
  Min       1Q   Median       3Q      Max
-1.3894 -0.8097 -0.1488  0.5466  1.7670

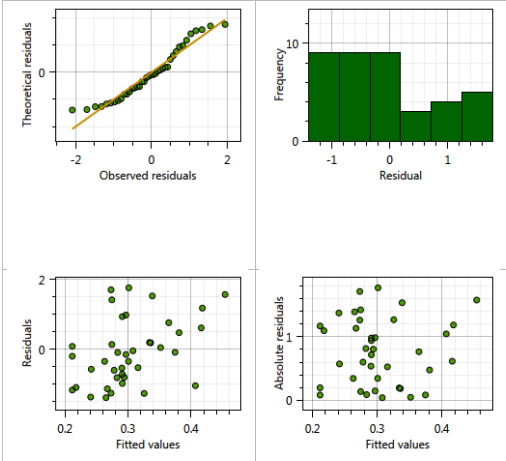
Random effects:
Groups              Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.18141  0.4259
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.06732  0.2595
Residual                                     328.31874 18.1196
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -0.8488      0.2459   7.8554  -3.452  0.00891 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 18.12
```

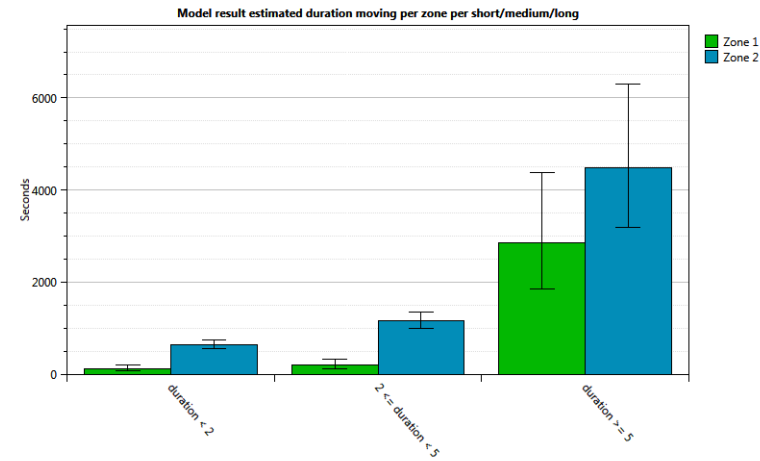
Model residuals

Statistic	Value
Sample skewness	0.4923
Sample excess kurtosis	-0.777
Passed Shapiro Wilk normality test	No (p-value = 0.03432 < 0.05)



Estimated duration moving per zone per short/medium/long

Selected zones	Zone 1, Zone 2
Event duration categories	duration < 2, 2 <= duration < 5, duration >= 5
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

Behaviour statistic	Cur3-RMX180	Remark
Estimated duration moving duration < 2 (diff. Zone 1 - Zone 2)	p=0.000274*** [-1.89, -0.938]	
Estimated duration moving 2 <= duration < 5 (diff. Zone 1 - Zone 2)	p=2.58E-05*** [-2.01, -1.11]	CR
Estimated duration moving duration >= 5 (diff. Zone 1 - Zone 2)	p=0.00275** [-0.79, -0.227]	

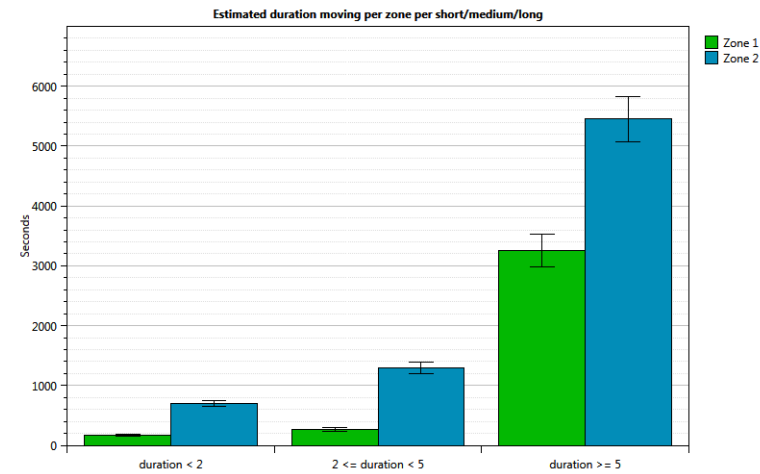
CR = Check residuals

The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Estimated duration moving (duration < 2 - Zone 1)	125 [80.1, 196]	CR
Estimated duration moving (2 <= duration < 5 - Zone 1)	204 [124, 334]	CR
Estimated duration moving (duration >= 5 - Zone 1)	2.85E+03 [1.85E+03, 4.38E+03]	CR
Estimated duration moving (duration < 2 - Zone 2)	641 [556, 739]	
Estimated duration moving (2 <= duration < 5 - Zone 2)	1.16E+03 [989, 1.35E+03]	
Estimated duration moving (duration >= 5 - Zone 2)	4.48E+03 [3.19E+03, 6.31E+03]	CR

CR = Check residuals

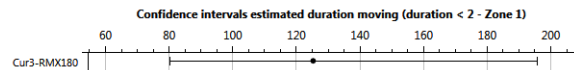
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean duration < 2 - Zone 1	StdErr duration < 2 - Zone 1	Mean 2 <= duration < 5 - Zone 1	StdErr 2 <= duration < 5 - Zone 1	Mean duration >= 5 - Zone 1	StdErr duration >= 5 - Zone 1	Mean duration < 2 - Zone 2	StdErr duration < 2 - Zone 2	Mean 2 <= duration < 5 - Zone 2	StdErr 2 <= duration < 5 - Zone 2	Mean duration >= 5 - Zone 2	StdErr duration >= 5 - Zone 2
Cur3	RMX180	Neutral	170.64	19.31	272.33	32.92	3258.74	275.88	697.43	43.71	1287.53	97.01	5452.5	375.31

Analysis estimated duration moving (duration < 2 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_duration_2_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	125.3	80.13	195.8	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_duration_2_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 115.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.2841	-0.2283	0.2514	0.4731	1.1324

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.1029	0.3207
Residual		1.1131	1.0550

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

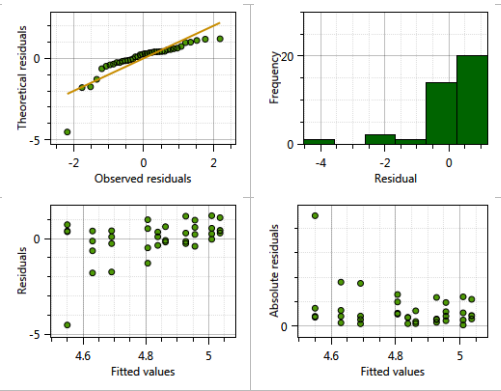
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	4.8305	0.1992	9.5218	24.25	7e-10 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

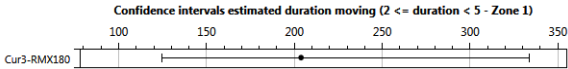
Model residuals

Statistic	Value
Sample skewness	-2.627
Sample excess kurtosis	9.838
Passed Shapiro Wilk normality test	No (p-value = 1.897E-06 < 0.05)



Analysis estimated duration moving (2 <= duration < 5 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_2_duration_5_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	203.8	124.4	333.8	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method [`lmerModLmerTest`]

Formula: Estimated_duration_moving_2_duration_5_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)

Data: data

REML criterion at convergence: 107.7

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.0944	-0.1895	0.2030	0.5169	1.3479

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.15549	0.3943
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.04729	0.2175
Residual		0.81978	0.9054

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

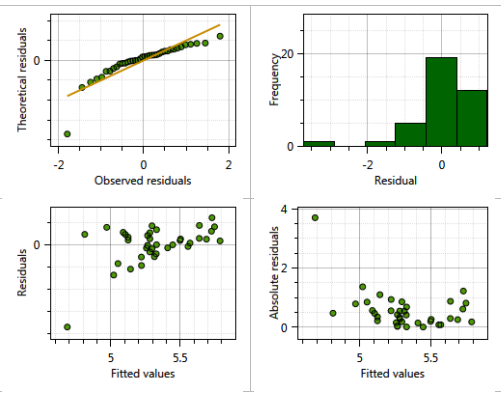
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	5.317	0.205	6.428	25.94	9.48e-08 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

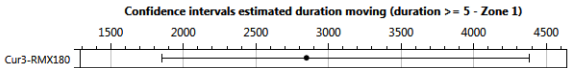
Model residuals

Statistic	Value
Sample skewness	-2.456
Sample excess kurtosis	9.445
Passed Shapiro Wilk normality test	No (p-value = 1.161E-05 < 0.05)



Analysis estimated duration moving (duration >= 5 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_duration_5_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	2848	1850	4385	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_duration_5_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 92.5

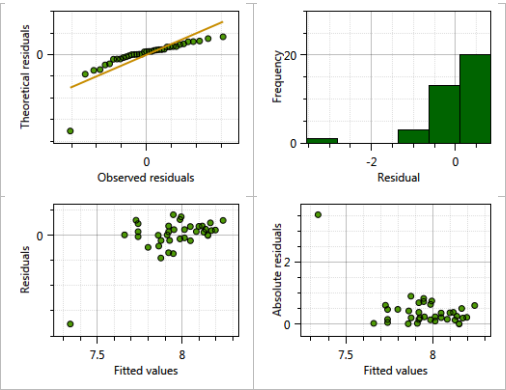
Scaled residuals:
    Min       1Q   Median       3Q      Max
-4.5892 -0.1771  0.1908  0.4718  1.0752

Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.05846  0.2418
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.06561  0.2561
Residual                        0.59186  0.7693
Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   7.9544     0.1692 5.1397  47.01 5.7e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

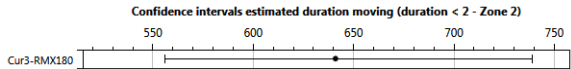
Model residuals

Statistic	Value
Sample skewness	-3.451
Sample excess kurtosis	16.26
Passed Shapiro Wilk normality test	No (p-value = 1.132E-07 < 0.05)



Analysis estimated duration moving (duration < 2 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_duration_2_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	641	555.8	739.2	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_duration_2_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 49.1

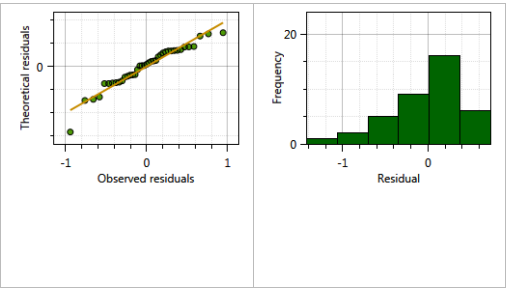
Scaled residuals:
    Min       1Q   Median       3Q      Max
-3.2193 -0.6166  0.1056  0.7587  1.6559

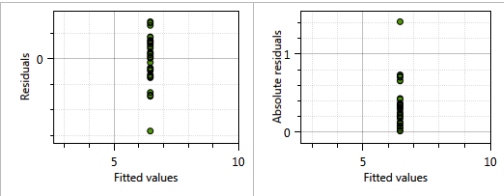
Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0000  0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.0000  0.0000
Residual                        0.1933  0.4397
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   6.46297     0.07041 38.00000  91.79 <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model residuals

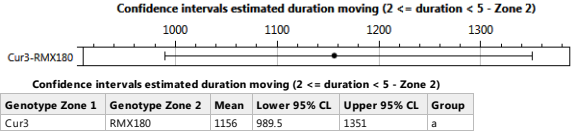
Statistic	Value
Sample skewness	-0.862
Sample excess kurtosis	1.488
Passed Shapiro Wilk normality test	Yes (p-value = 0.06851 > 0.05)





Analysis estimated duration moving (2 <= duration < 5 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_2_duration_5_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_2_duration_5_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 55.7

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-2.69428	-0.58265	-0.06474	0.76099	2.02507

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000e+00	0.000e+00
Genotype_Zone_2:Plant_Zone_2	(Intercept)	3.643e-19	6.036e-10
Residual		2.306e-01	4.802e-01

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

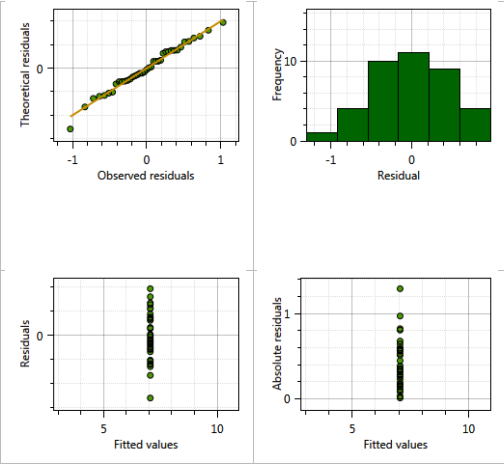
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	7.05281	0.07689	38.00000	91.73	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

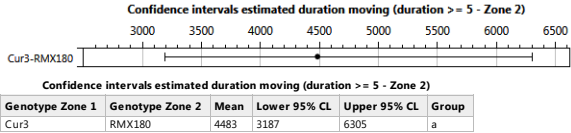
Model residuals

Statistic	Value
Sample skewness	-0.2688
Sample excess kurtosis	0.1722
Passed Shapiro Wilk normality test	Yes (p-value = 0.9146 > 0.05)



Analysis estimated duration moving (duration >= 5 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_duration_5_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_duration_5_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 96.6

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-3.4206	-0.0870	0.2667	0.4905	1.0480

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.05754	0.2399
Residual		0.62777	0.7923

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

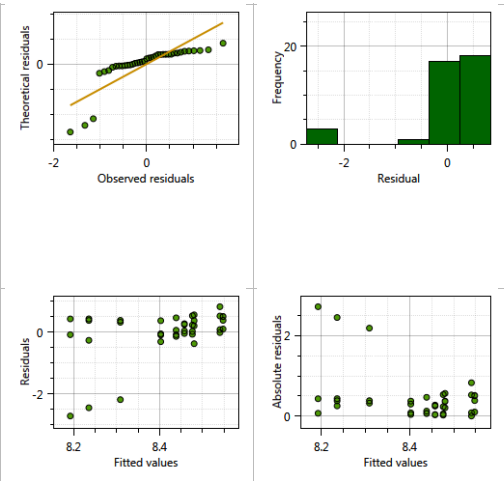
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	8.4080	0.1479	7.9886	56.84	1.05e-11 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

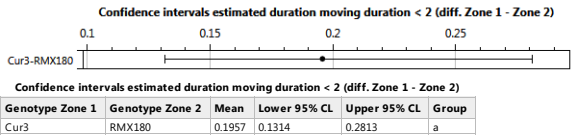
Model residuals

Statistic	Value
Sample skewness	-2.636
Sample excess kurtosis	6.83
Passed Shapiro Wilk normality test	No (p-value = 1.853E-08 < 0.05)



Analysis estimated duration moving duration < 2 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_moving_duration_2_Zone_1,Estimated_duration_moving_duration_2_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 112.9

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.50375 -0.54535  0.02918  0.48328  2.38217

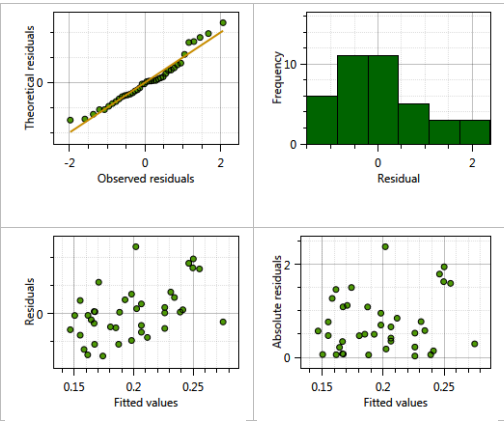
Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.04129  0.2032
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.11966  0.3459
Residual                                119.61625 10.9369
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -1.4133      0.1972   6.4182  -7.166 0.000274 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 10.94
```

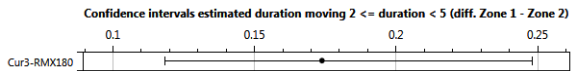
Model residuals

Statistic	Value
Sample skewness	0.651
Sample excess kurtosis	0.1442
Passed Shapiro Wilk normality test	Yes (p-value = 0.1375 > 0.05)



Analysis estimated duration moving 2 <= duration < 5 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_moving_2_duration_5_Zone_1,Estimated_duration_moving_2_duration_5_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals estimated duration moving 2 <= duration < 5 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1738	0.1182	0.2482	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 108.9

Scaled residuals:
  Min       1Q   Median       3Q      Max
-1.3420 -0.7072 -0.1197  0.5343  1.8556

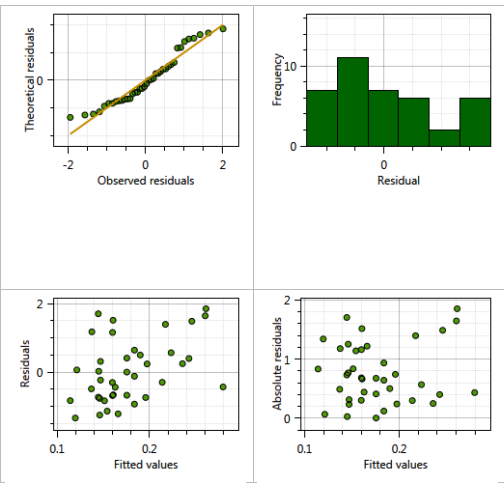
Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.07523  0.2743
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.13218  0.3636
Residual                                158.71001 12.5980
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error      df t value Pr(>|t|)
(Intercept)  -1.5588      0.1993    9.0460  -7.82 2.58e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 12.6
```

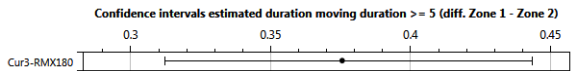
Model residuals

Statistic	Value
Sample skewness	0.5034
Sample excess kurtosis	-0.7932
Passed Shapiro Wilk normality test	No (p-value = 0.03286 < 0.05)



Analysis estimated duration moving duration >= 5 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_moving_duration_5_Zone_1,Estimated_duration_moving_duration_5_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals estimated duration moving duration >= 5 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.3755	0.3121	0.4436	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 79.8

Scaled residuals:
  Min       1Q   Median       3Q      Max
-1.70654 -0.73715 -0.08766  0.68778  1.68656

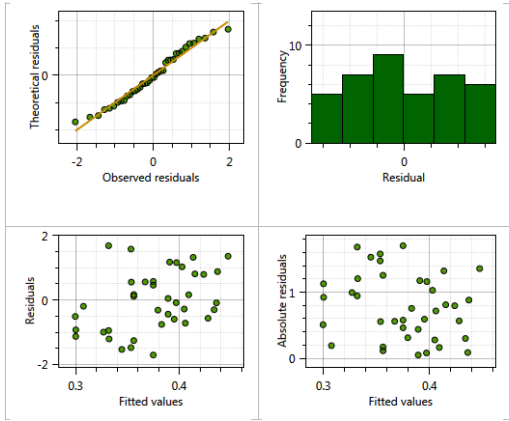
Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.01082  0.1040
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.06497  0.2549
Residual                                608.48639 24.6675
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error      df t value Pr(>|t|)
(Intercept)  -0.5085      0.1247    9.0155  -4.079 0.00275 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 24.67
```

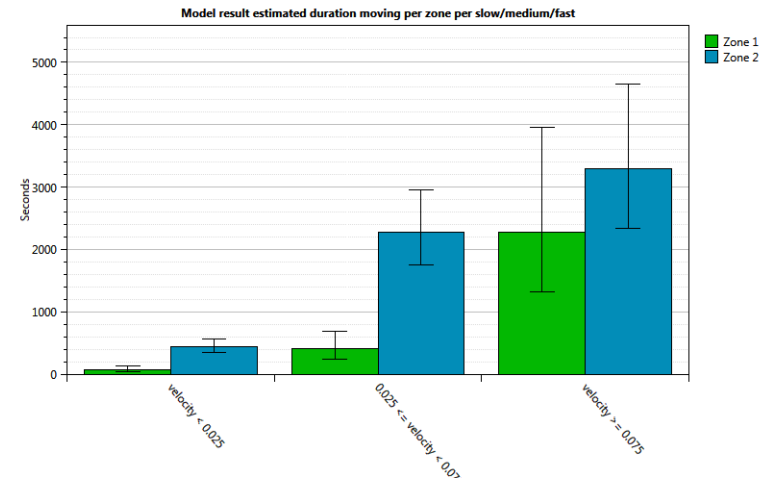
Model residuals

Statistic	Value
Sample skewness	0.1055
Sample excess kurtosis	-0.9616
Passed Shapiro Wilk normality test	Yes (p-value = 0.4312 > 0.05)



Estimated duration moving per zone per slow/medium/fast

Selected zones	Zone 1, Zone 2
Velocity categories	velocity < 0.025, 0.025 <= velocity < 0.075, velocity >= 0.075
Data transformation	Natural logarithm
Analysis	Zone difference analysis



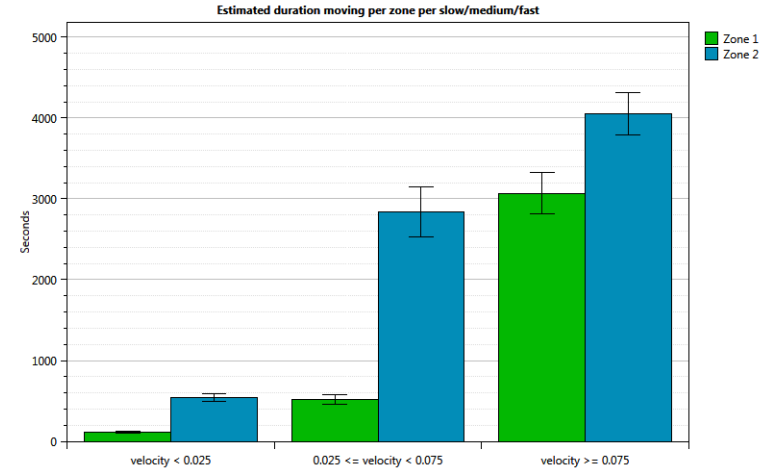
Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

Behaviour statistic	Cur3-RMX180
Estimated duration moving velocity < 0.025 (diff. Zone 1 - Zone 2)	p=0.000244*** [-2.09, -1.05]
Estimated duration moving 0.025 <= velocity < 0.075 (diff. Zone 1 - Zone 2)	p=5.86E-05*** [-2.26, -1.1]
Estimated duration moving velocity >= 0.075 (diff. Zone 1 - Zone 2)	p=0.0102* [-0.477, -0.0892]

The model predictions and 95% confidence intervals for each statistic.		
Statistic	Cur3-RMX180	Remark
Estimated duration moving (velocity < 0.025 - Zone 1)	74.8 [43.7, 128]	CR
Estimated duration moving (0.025 <= velocity < 0.075 - Zone 1)	407 [241, 686]	
Estimated duration moving (velocity >= 0.075 - Zone 1)	2.28E+03 [1.32E+03, 3.95E+03]	CR
Estimated duration moving (velocity < 0.025 - Zone 2)	444 [354, 557]	CR
Estimated duration moving (0.025 <= velocity < 0.075 - Zone 2)	2.27E+03 [1.75E+03, 2.95E+03]	
Estimated duration moving (velocity >= 0.075 - Zone 2)	3.3E+03 [2.33E+03, 4.65E+03]	CR

CR = Check residuals

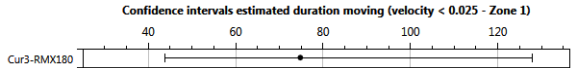
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean velocity < 0.025 - Zone 1	StdErr velocity < 0.025 - Zone 1	Mean 0.025 <= velocity < 0.075 - Zone 1	StdErr 0.025 <= velocity < 0.075 - Zone 1	Mean velocity >= 0.075 - Zone 1	StdErr velocity >= 0.075 - Zone 1	Mean velocity < 0.025 - Zone 2	StdErr velocity < 0.025 - Zone 2	Mean 0.025 <= velocity < 0.075 - Zone 2	StdErr 0.025 <= velocity < 0.075 - Zone 2	Mean velocity >= 0.075 - Zone 2	StdErr velocity >= 0.075 - Zone 2
Cur3	RMX180	Neutral	111.73	13.97	519.81	62.68	3070.18	254.23	542.24	51.5	2840.68	310.85	4054.54	260.17

Analysis estimated duration moving (velocity < 0.025 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_velocity_0_025_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals estimated duration moving (velocity < 0.025 - Zone 1)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	74.78	43.71	128	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_velocity_0_025_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 121.5

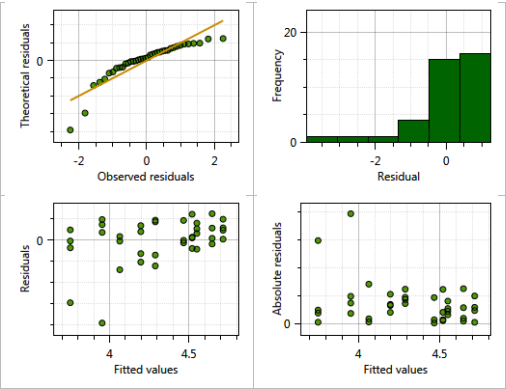
Scaled residuals:
    Min       1Q   Median       3Q      Max
-3.5276 -0.2905  0.1350  0.5887  1.1183

Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0000   0.000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.2401   0.490
Residual                      1.2369   1.112
Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    4.3146     0.2382 9.1960  18.11 1.66e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

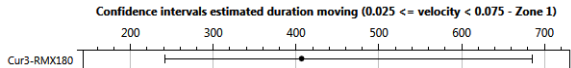
Model residuals

Statistic	Value
Sample skewness	-2.027
Sample excess kurtosis	5.304
Passed Shapiro Wilk normality test	No (p-value = 2.591E-05 < 0.05)



Analysis estimated duration moving (0.025 <= velocity < 0.075 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_0_025_velocity_0_075_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals estimated duration moving (0.025 <= velocity < 0.075 - Zone 1)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	406.6	241.2	685.6	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_0_025_velocity_0_075_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 96.6

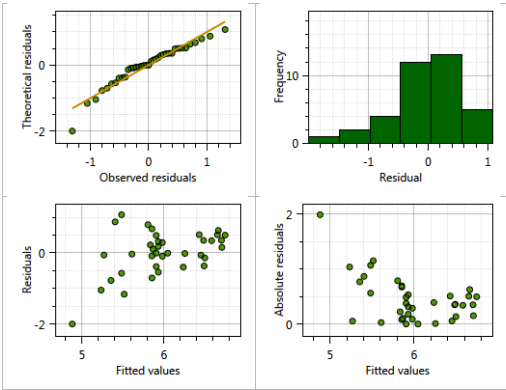
Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.7788 -0.5073 -0.0066  0.4950  1.4961

Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.1780   0.4219
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.2175   0.4664
Residual                      0.5149   0.7176
Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    6.0079     0.2324 9.3841  25.86 4.85e-10 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

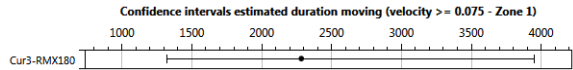
Model residuals

Statistic	Value
Sample skewness	-1.033
Sample excess kurtosis	1.881
Passed Shapiro Wilk normality test	Yes (p-value = 0.06232 > 0.05)



Analysis estimated duration moving (velocity >= 0.075 - Zone 1)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_velocity_0_075_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals estimated duration moving (velocity >= 0.075 - Zone 1)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	2283	1319	3952	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_velocity_0_075_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 130.5

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.9451	0.0222	0.2202	0.4102	0.7360

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.06902	0.2627
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.00000	0.0000
Residual		1.74364	1.3205

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

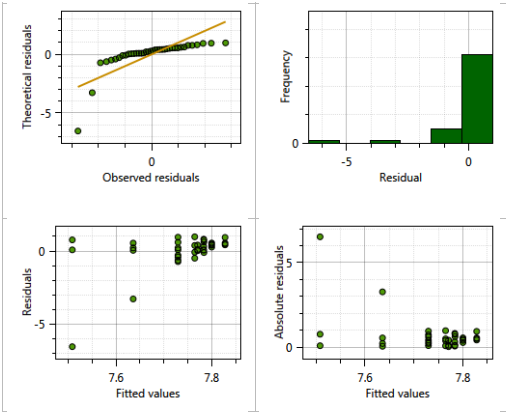
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	7.7332	0.2299	6.6858	33.64	1.04e-08 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

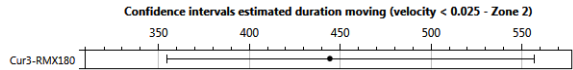
Model residuals

Statistic	Value
Sample skewness	-4.014
Sample excess kurtosis	18.34
Passed Shapiro Wilk normality test	No (p-value = 8.218E-10 < 0.05)



Analysis estimated duration moving (velocity < 0.025 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_velocity_0_025_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals estimated duration moving (velocity < 0.025 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	444.3	354.4	557	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_velocity_0_025_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 84.1

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.6699	-0.6155	0.2229	0.6672	1.8572

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000	0.0000

Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.000 0.0000
Residual 0.486 0.6972
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

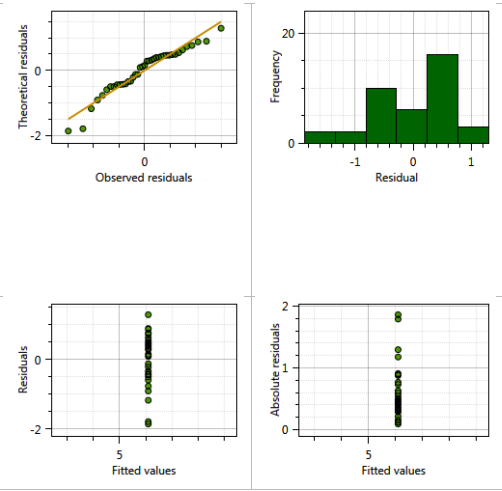
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	6.0965	0.1116	38.0000	54.61	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

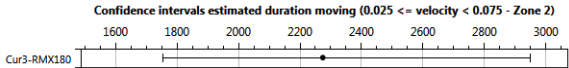
Model residuals

Statistic	Value
Sample skewness	-0.835
Sample excess kurtosis	0.7831
Passed Shapiro Wilk normality test	No (p-value = 0.03979 < 0.05)



Analysis estimated duration moving (0.025 <= velocity < 0.075 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_0_025_velocity_0_075_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals estimated duration moving (0.025 <= velocity < 0.075 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	2274	1753	2950	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated_duration_moving_0_025_velocity_0_075_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 81.8

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-1.8051	-0.7523	-0.2064	0.8612	1.6990

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	6.725e-18	2.593e-09
Genotype_Zone_2:Plant_Zone_2	(Intercept)	1.896e-02	1.377e-01
Residual		4.416e-01	6.645e-01

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

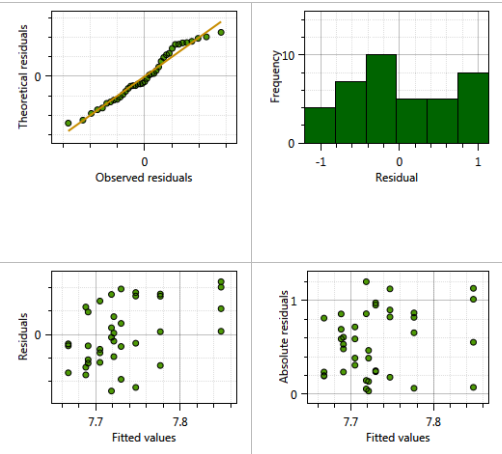
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	7.729	0.115	8.997	67.2	1.82e-13 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

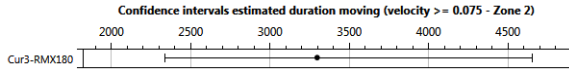
Statistic	Value
Sample skewness	0.08388
Sample excess kurtosis	-1.034
Passed Shapiro Wilk normality test	Yes (p-value = 0.1588 > 0.05)



Analysis estimated duration moving (velocity >= 0.075 - Zone 2)

Analysis model	Linear mixed model fit by REML: Estimated_duration_moving_velocity_0_075_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
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Transformation	Natural logarithm
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Confidence intervals estimated duration moving (velocity >= 0.075 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	3297	2335	4655	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Estimated duration moving_velocity_0_075_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 104

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.7442	-0.0170	0.2774	0.4477	0.9013

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	6.864e-17	8.285e-09
Genotype_Zone_2:Plant_Zone_2	(Intercept)	2.528e-02	1.590e-01
Residual		7.963e-01	8.935e-01

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

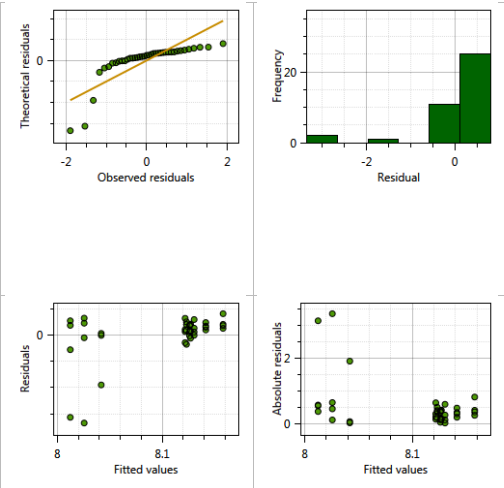
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	8.1007	0.1517	8.6943	53.4	3e-12 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

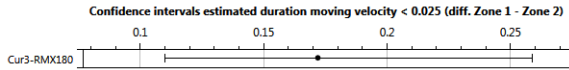
Model residuals

Statistic	Value
Sample skewness	-2.95
Sample excess kurtosis	8.756
Passed Shapiro Wilk normality test	No (p-value = 4.53E-09 < 0.05)



Analysis estimated duration moving velocity < 0.025 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor. formula=cbind(Estimated_duration_moving_velocity_0_025_Zone_1,Estimated_duration_moving_velocity_0_025_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals estimated duration moving velocity < 0.025 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1719	0.1098	0.2589	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziformula
Data: data
Weights: wi

REML criterion at convergence: 125.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.31960	-0.66342	-0.04034	0.56765	2.25676

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	2.608e-03	0.05107
Genotype_Zone_2:Plant_Zone_2	(Intercept)	1.555e-01	0.39434
Residual		1.088e+02	10.42833

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

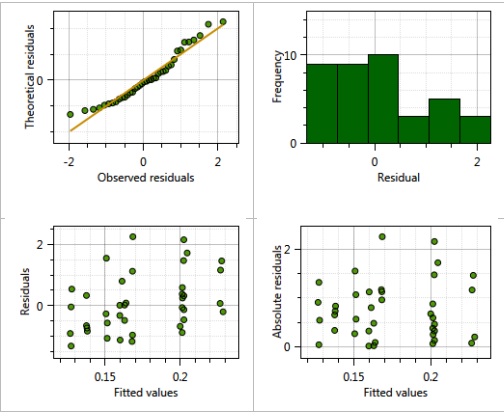
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.5723	0.2165	6.4740	-7.263	0.000244 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 10.43

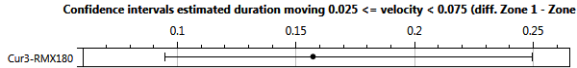
Model residuals

Statistic	Value
Sample skewness	0.6566
Sample excess kurtosis	-0.359
Passed Shapiro Wilk normality test	Yes (p-value = 0.05037 > 0.05)



Analysis estimated duration moving 0.025 <= velocity < 0.075 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_moving_0_025_velocity_0_075_Zone_1,Estimated_duration_moving_0_025_velocity_0_075_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals estimated duration moving 0.025 <= velocity < 0.075 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1572	0.09458	0.2497	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi
REML criterion at convergence: 126.7

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.22685	-0.79728	0.00827	0.95022	1.88724

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)		0.08382	0.2895
	Genotype_Zone_2:Plant_Zone_2 (Intercept)	0.32417	0.5694
	Residual	443.20821	21.0525

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

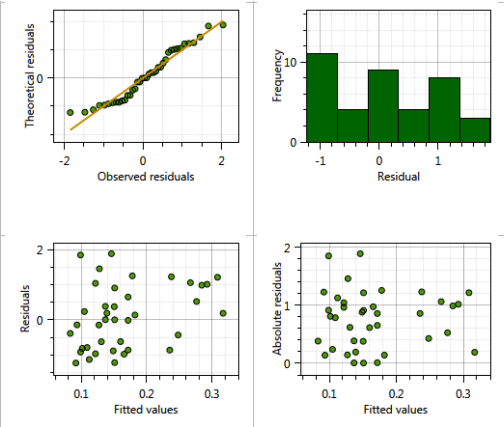
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.6795	0.2622	10.6448	-6.405	5.86e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 21.05

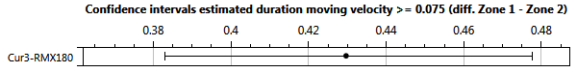
Model residuals

Statistic	Value
Sample skewness	0.2752
Sample excess kurtosis	-1.04
Passed Shapiro Wilk normality test	Yes (p-value = 0.05816 > 0.05)



Analysis estimated duration moving velocity >= 0.075 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Estimated_duration_moving_velocity_0_075_Zone_1,Estimated_duration_moving_velocity_0_075_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals estimated duration moving velocity >= 0.075 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4297	0.3829	0.4777	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi
REML criterion at convergence: 61.4

```
Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.8455 -0.7356 -0.1421  0.7096  2.0087

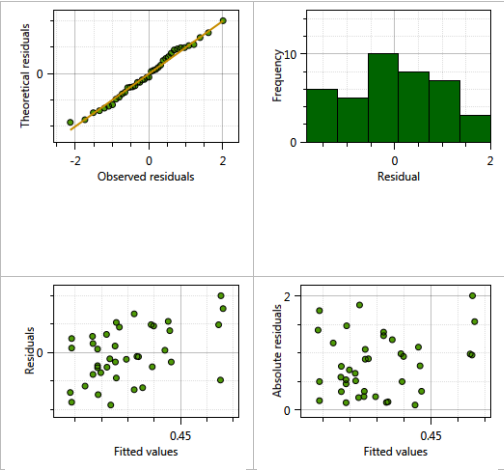
Random effects:
Groups:                               Name      Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 1.721e-02  0.13121
Genotype_Zone_2:Plant_Zone_2 (Intercept) 1.342e-03  0.03663
Residual                                3.405e+02 18.45247
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept) -0.28325    0.08317   7.49360  -3.406  0.0102 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 18.45
```

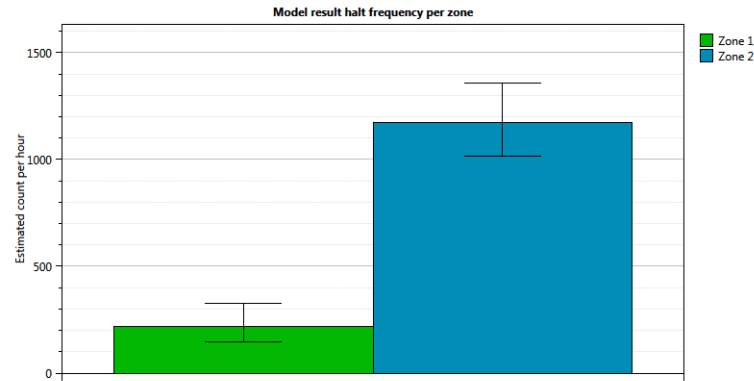
Model residuals

Statistic	Value
Sample skewness	0.06689
Sample excess kurtosis	-0.7175
Passed Shapiro Wilk normality test	Yes (p-value = 0.7951 > 0.05)



Halt frequency per zone

Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

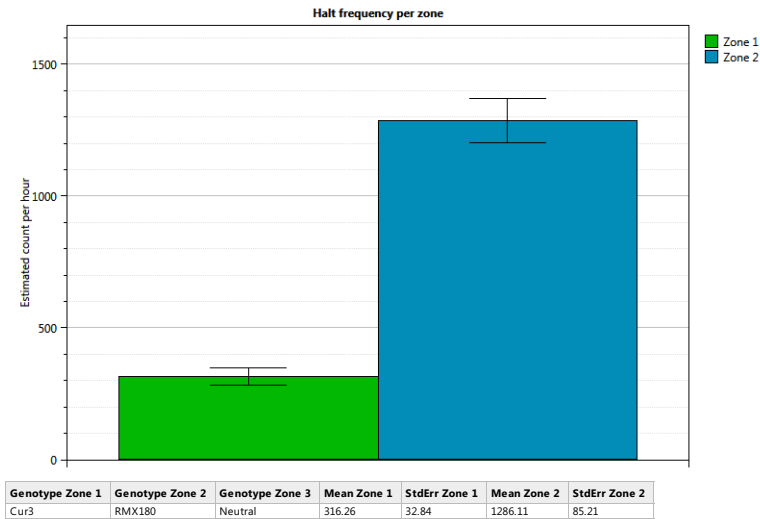
Behaviour statistic	Cur3-RMX180
Halt frequency (diff. Zone 1 - Zone 2)	p=7.73E-05**** [-1.84, -0.967]

The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Halt frequency (Zone 1)	217 [145, 325]	CR
Halt frequency (Zone 2)	1.17E+03 [1.02E+03, 1.36E+03]	

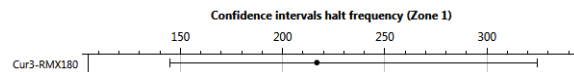
CR = Check residuals

Data summary



Analysis halt frequency (Zone 1)

Analysis model Linear mixed model fit by REML: Halt_frequency_Zone_1 ~ 1 + (1|Genotype_Zone_1:Plant_Zone_1) + (1|Genotype_Zone_2:Plant_Zone_2)
Transformation Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Halt_frequency_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 128.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.1279	-0.0675	0.1788	0.5340	1.0915

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000e+00	0.000e+00
Genotype_Zone_2:Plant_Zone_2	(Intercept)	4.891e-15	6.994e-08
Residual		1.555e+00	1.247e+00

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

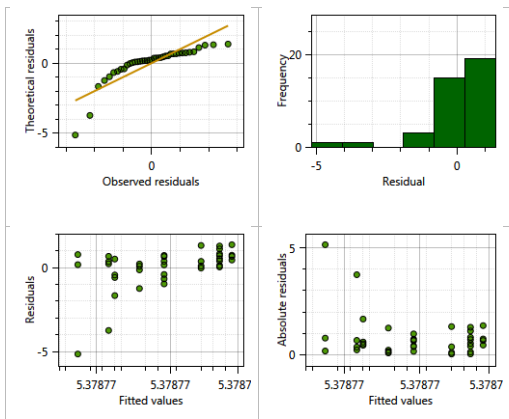
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	5.3788	0.1997	38.0000	26.94	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

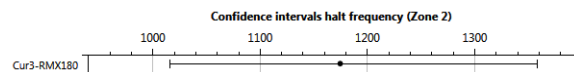
Model residuals

Statistic	Value
Sample skewness	-2.648
Sample excess kurtosis	8.513
Passed Shapiro Wilk normality test	No (p-value = 3.19E-07 < 0.05)



Analysis halt frequency (Zone 2)

Analysis model Linear mixed model fit by REML: Halt_frequency_Zone_2 ~ 1 + (1|Genotype_Zone_1:Plant_Zone_1) + (1|Genotype_Zone_2:Plant_Zone_2)
Transformation Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Halt_frequency_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 50.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.95640	-0.71408	0.06847	0.79717	1.86046

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		0.2014	0.4488

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

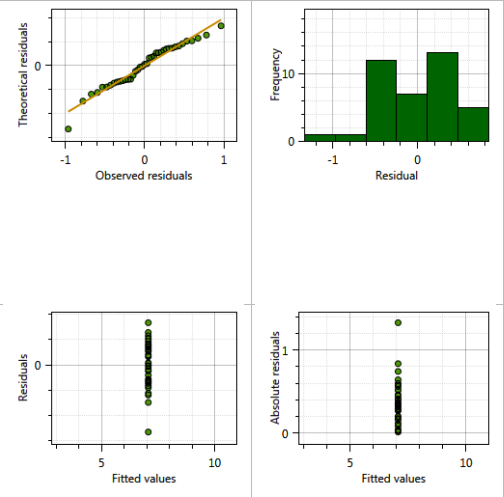
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	7.06865	0.07187	38.00000	98.36	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

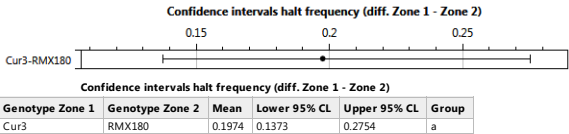
Model residuals

Statistic	Value
Sample skewness	-0.558
Sample excess kurtosis	0.4709
Passed Shapiro Wilk normality test	Yes (p-value = 0.2477 > 0.05)



Analysis halt frequency (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Halt_frequency_Zone_1,Halt_frequency_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 108.7

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.40874	-0.66926	-0.06651	0.64189	1.99740

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.05099	0.2258
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.10237	0.3199
Residual		194.95683	13.9627

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

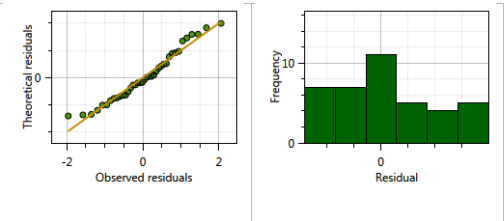
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.4023	0.1884	7.9113	-7.445	7.73e-05 ***

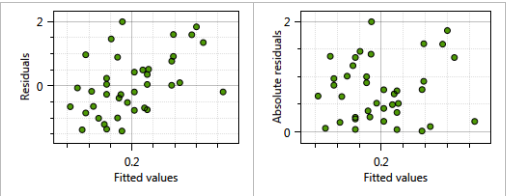
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 13.96

Model residuals

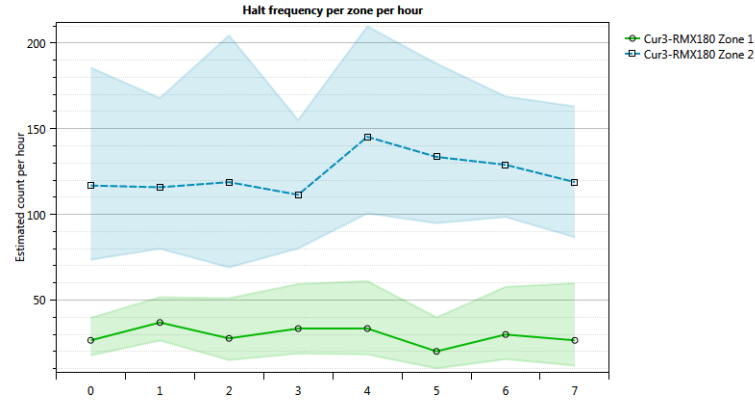
Statistic	Value
Sample skewness	0.4086
Sample excess kurtosis	-0.6569
Passed Shapiro Wilk normality test	Yes (p-value = 0.191 > 0.05)





Halt frequency per zone per hour

Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

Behaviour statistic	Cur3-RMX180	Remark
Halt frequency H0 (diff. Zone 1 - Zone 2)	p=0.000622*** [-1.95, -0.769]	CR
Halt frequency H1 (diff. Zone 1 - Zone 2)	p=0.000185*** [-1.86, -0.761]	
Halt frequency H2 (diff. Zone 1 - Zone 2)	p=0.00314*** [-2.05, -0.58]	CR
Halt frequency H3 (diff. Zone 1 - Zone 2)	p=0.00358*** [-1.81, -0.482]	CR
Halt frequency H4 (diff. Zone 1 - Zone 2)	p=0.00279*** [-2.18, -0.7]	CR
Halt frequency H5 (diff. Zone 1 - Zone 2)	p=0.000343*** [-2.3, -0.97]	CR
Halt frequency H6 (diff. Zone 1 - Zone 2)	p=0.000276*** [-2.23, -0.922]	CR
Halt frequency H7 (diff. Zone 1 - Zone 2)	p=0.00422*** [-2.32, -0.692]	CR

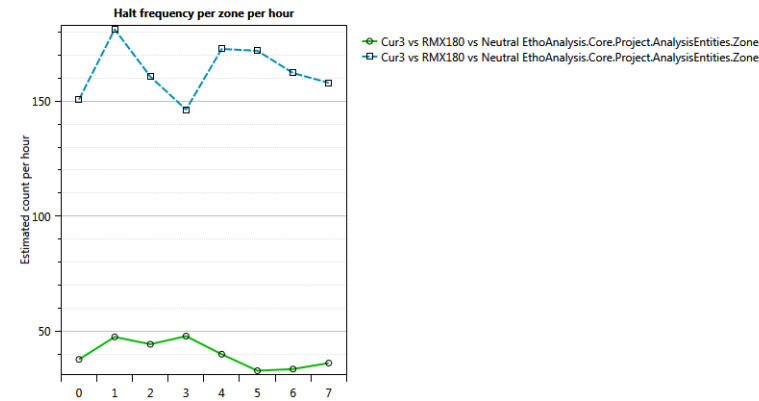
CR = Check residuals

The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Halt frequency (H0 - Zone 1)	26.5 [17.7, 39.7]	
Halt frequency (H0 - Zone 2)	117 [73.5, 186]	CR
Halt frequency (H1 - Zone 1)	37 [26.4, 51.7]	CR
Halt frequency (H1 - Zone 2)	116 [80, 168]	CR
Halt frequency (H2 - Zone 1)	27.7 [15, 51.1]	
Halt frequency (H2 - Zone 2)	119 [69.1, 204]	CR
Halt frequency (H3 - Zone 1)	33.4 [18.8, 59.4]	CR
Halt frequency (H3 - Zone 2)	111 [80.1, 155]	CR
Halt frequency (H4 - Zone 1)	33.4 [18.3, 61.1]	CR
Halt frequency (H4 - Zone 2)	145 [101, 210]	CR
Halt frequency (H5 - Zone 1)	20.1 [10.1, 39.9]	CR
Halt frequency (H5 - Zone 2)	134 [94.8, 188]	CR
Halt frequency (H6 - Zone 1)	29.9 [15.5, 57.8]	
Halt frequency (H6 - Zone 2)	129 [98.5, 169]	CR
Halt frequency (H7 - Zone 1)	26.5 [11.8, 59.8]	
Halt frequency (H7 - Zone 2)	119 [86.6, 163]	CR

CR = Check residuals

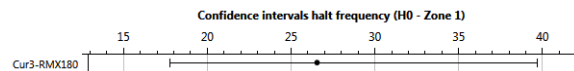
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean H0 - Zone 1	StdErr H0 - Zone 1	Mean H0 - Zone 2	StdErr H0 - Zone 2	Mean H1 - Zone 1	StdErr H1 - Zone 1	Mean H1 - Zone 2	StdErr H1 - Zone 2	Mean H2 - Zone 1	StdErr H2 - Zone 1	Mean H2 - Zone 2	StdErr H2 - Zone 2	Mean H3 - Zone 1	StdErr H3 - Zone 1	Mean H3 - Zone 2	StdErr H3 - Zone 2	Mean H4 - Zone 1	StdErr H4 - Zone 1	Mean H4 - Zone 2	StdErr H4 - Zone 2	Mean H5 - Zone 1	StdErr H5 - Zone 1	Mean H5 - Zone 2	StdErr H5 - Zone 2	Mean H6 - Zone 1	StdErr H6 - Zone 1	Mean H6 - Zone 2	StdErr H6 - Zone 2
Cur3	RMX180	Neutral	37.78	6.47	150.72	13.16	47.56	5.6	181.21	42.45	44.37	8.47	160.67	14.9	47.9	7.82	146.3	14.19	40.04	7.31	172.67	17.16	32.88	5.92	171.89	16.55	33.6	7.52	162.2	17.48

Analysis halt frequency (H0 - Zone 1)

Analysis model	Linear mixed model fit by REML: Halt_frequency_H0_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	26.55	17.75	39.7	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Halt_frequency_H0_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 106.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.8249	-0.7370	0.2439	0.6566	1.7006

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	9.845e-19	9.922e-10
Genotype_Zone_2:Plant_Zone_2	(Intercept)	9.644e-16	3.106e-08
Residual		1.331e+00	1.154e+00

Number of obs: 34, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

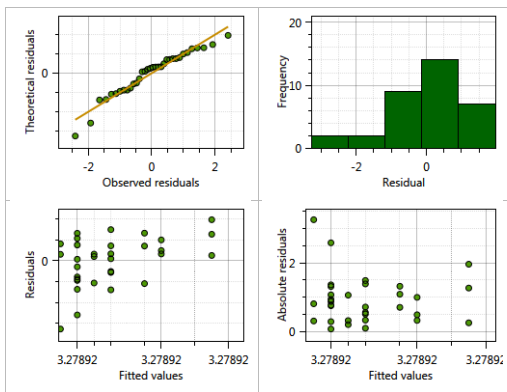
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	3.2789	0.1979	33.0000	16.57	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

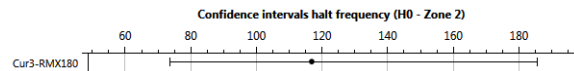
Model residuals

Statistic	Value
Sample skewness	-0.8491
Sample excess kurtosis	0.8543
Passed Shapiro Wilk normality test	Yes (p-value = 0.09851 > 0.05)



Analysis halt frequency (H0 - Zone 2)

Analysis model	Linear mixed model fit by REML: Halt_frequency_H0_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	116.8	73.53	185.7	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Halt_frequency_H0_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 108.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.5893	-0.2300	0.2751	0.5137	1.0619

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	4.061e-18	2.015e-09
Genotype_Zone_2:Plant_Zone_2	(Intercept)	1.842e-01	4.292e-01
Residual		8.582e-01	9.264e-01

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

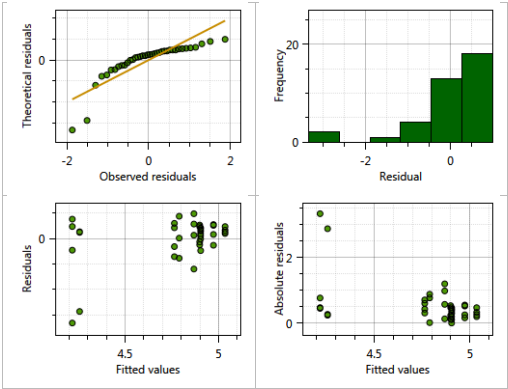
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	4.7609	0.2028	8.4728	23.48	5.23e-09 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

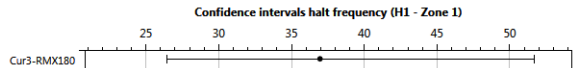
Model residuals

Statistic	Value
Sample skewness	-2.537
Sample excess kurtosis	7.37
Passed Shapiro Wilk normality test	No (p-value = 3.956E-07 < 0.05)



Analysis halt frequency (H1 - Zone 1)

Analysis model	Linear mixed model fit by REML: Halt_frequency_H1_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	36.96	26.42	51.7	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Halt_frequency_H1_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 102.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.8805	-0.3526	0.1873	0.7406	1.1875

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		0.9846	0.9923

Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

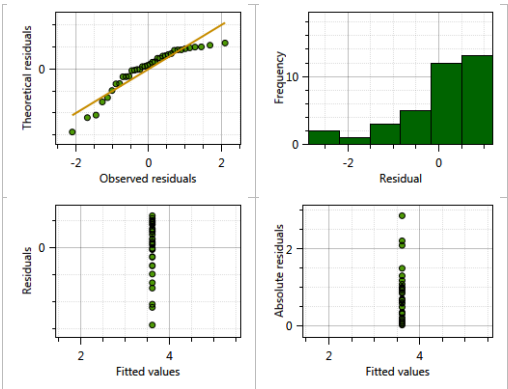
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	3.6097	0.1654	35.0000	21.83	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

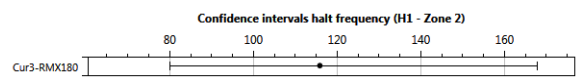
Model residuals

Statistic	Value
Sample skewness	-1.257
Sample excess kurtosis	1.202
Passed Shapiro Wilk normality test	No (p-value = 0.001176 < 0.05)



Analysis halt frequency (H1 - Zone 2)

Analysis model	Linear mixed model fit by REML: Halt_frequency_H1_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals halt frequency (H1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	115.9	79.96	167.9	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Halt_frequency_H1_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 117.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.2028	-0.3595	0.2161	0.5381	2.3877

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000	0.000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000	0.000
Residual		1.273	1.128

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

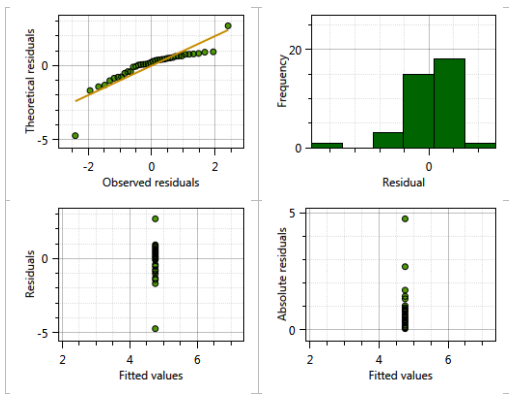
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	4.7525	0.1831	37.0000	25.96	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

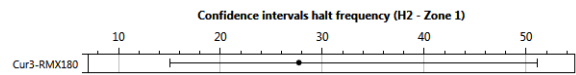
Model residuals

Statistic	Value
Sample skewness	-1.884
Sample excess kurtosis	8.115
Passed Shapiro Wilk normality test	No (p-value = 2.162E-05 < 0.05)



Analysis halt frequency (H2 - Zone 1)

Analysis model	Linear mixed model fit by REML: Halt_frequency_H2_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals halt frequency (H2 - Zone 1)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	27.7	15.01	51.12	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Halt_frequency_H2_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 109.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.18997	-0.52381	-0.00736	0.70586	1.51948

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.4395	0.6630
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		0.9343	0.9666

Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

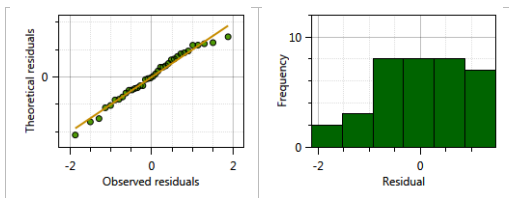
Fixed effects:

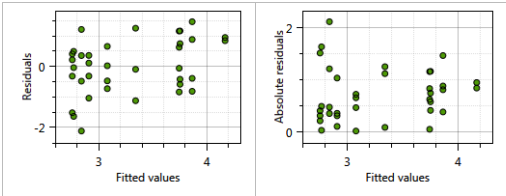
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	3.3214	0.2657	7.9891	12.5	1.59e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

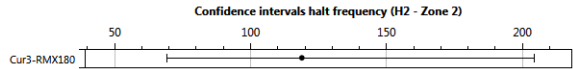
Statistic	Value
Sample skewness	-0.37
Sample excess kurtosis	-0.3845
Passed Shapiro Wilk normality test	Yes (p-value = 0.5993 > 0.05)





Analysis halt frequency (H2 - Zone 2)

Analysis model	Linear mixed model fit by REML: Halt_frequency_H2_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	118.8	69.07	204.5	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Halt_frequency_H2_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 117.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.9703	-0.1487	0.4056	0.5393	1.0067

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.09501	0.3082
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.05383	0.2320
Residual		1.13844	1.0670

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

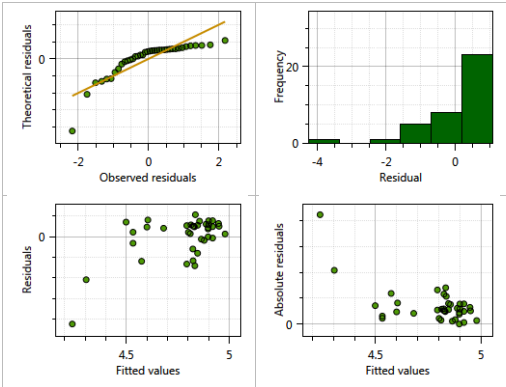
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	4.7778	0.2121	5.0787	22.53	2.76e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

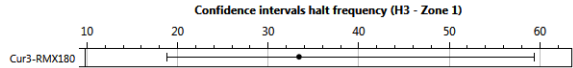
Model residuals

Statistic	Value
Sample skewness	-2.394
Sample excess kurtosis	7.319
Passed Shapiro Wilk normality test	No (p-value = 9.62E-07 < 0.05)



Analysis halt frequency (H3 - Zone 1)

Analysis model	Linear mixed model fit by REML: Halt_frequency_H3_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	33.4	18.78	59.4	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Halt_frequency_H3_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 108

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.71802	-0.35683	0.06245	0.71211	1.23960

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.002235	0.04728
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.109772	0.33132
Residual		1.437781	1.19908

Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

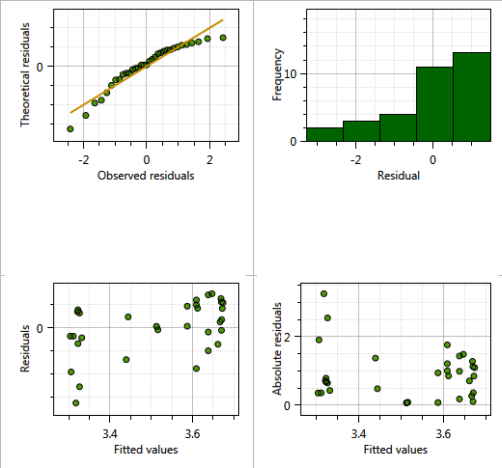
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	3.5086	0.2351	5.9847	14.92	5.83e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

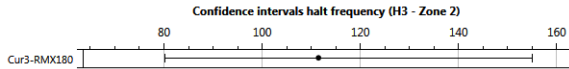
Statistic	Value
Sample skewness	-1.071

Statistic	Value
Sample excess kurtosis	0.8806
Passed Shapiro Wilk normality test	No (p-value = 0.01406 < 0.05)



Analysis halt frequency (H3 - Zone 2)

Analysis model	Linear mixed model fit by REML: Halt_frequency_H3_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals halt frequency (H3 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	111.5	80.12	155.1	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Halt_frequency_H3_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 103.7

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.9391	-0.3770	0.2304	0.6896	1.3376

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	1.117e-69	3.343e-35
Genotype_Zone_2:Plant_Zone_2	(Intercept)	9.663e-05	9.830e-03
Residual		8.132e-01	9.018e-01

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

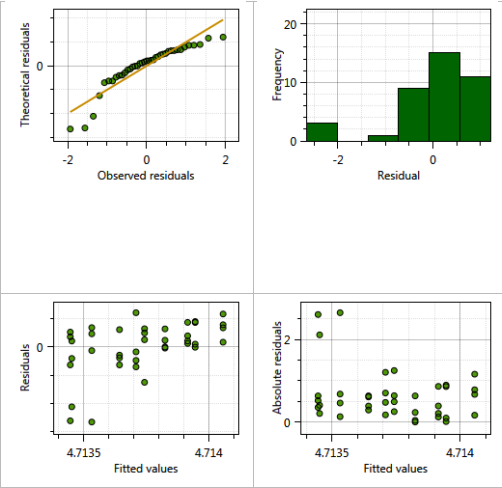
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	4.7137	0.1444	8.4146	32.63	3.7e-10 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

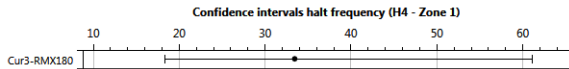
Model residuals

Statistic	Value
Sample skewness	-1.558
Sample excess kurtosis	2.611
Passed Shapiro Wilk normality test	No (p-value = 0.0001429 < 0.05)



Analysis halt frequency (H4 - Zone 1)

Analysis model	Linear mixed model fit by REML: Halt_frequency_H4_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals halt frequency (H4 - Zone 1)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	33.44	18.29	61.13	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

```
Formula: Halt_frequency_H4_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 91.3

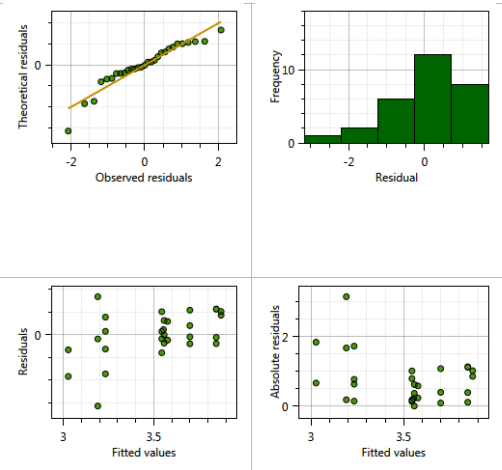
Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.90185 -0.36488 -0.00732  0.71373  1.54451

Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.2266   0.4761
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.0000   0.0000
Residual                        1.1792   1.0859
Number of obs: 29, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    3.5098     0.2558  7.0903   13.72  2.3e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

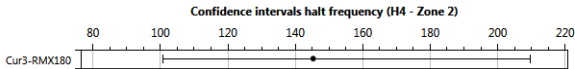
Model residuals

Statistic	Value
Sample skewness	-1.12
Sample excess kurtosis	2.116
Passed Shapiro Wilk normality test	No (p-value = 0.03542 < 0.05)



Analysis halt frequency (H4 - Zone 2)

Analysis model	Linear mixed model fit by REML: Halt_frequency_H4_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals halt frequency (H4 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	145.3	100.6	209.7	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Halt_frequency_H4_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 87.9

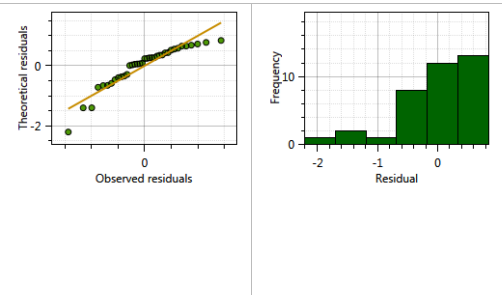
Scaled residuals:
    Min       1Q   Median       3Q      Max
-3.0567 -0.5098  0.3280  0.6061  1.1673

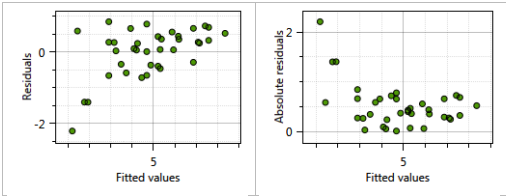
Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.03978   0.1995
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.06790   0.2606
Residual                        0.52178   0.7223
Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    4.9787     0.1584  7.7589   31.44 1.84e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model residuals

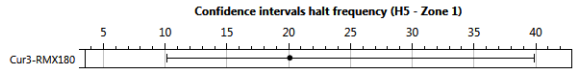
Statistic	Value
Sample skewness	-1.381
Sample excess kurtosis	2.185
Passed Shapiro Wilk normality test	No (p-value = 0.001132 < 0.05)





Analysis halt frequency (H5 - Zone 1)

Analysis model	Linear mixed model fit by REML: Halt_frequency_H5_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	20.09	10.11	39.9	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Halt_frequency_H5_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 113.7

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.9857	-0.5769	0.2693	0.7196	1.2692

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.2656	0.5154
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		2.0962	1.4478

Number of obs: 31, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

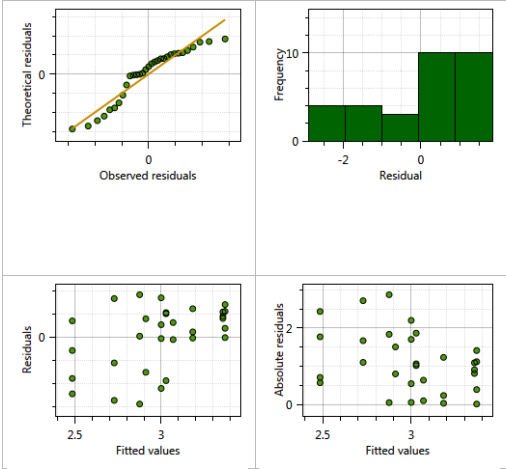
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	3.0001	0.3085	10.1349	9.724	1.85e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

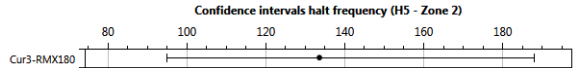
Model residuals

Statistic	Value
Sample skewness	-0.7741
Sample excess kurtosis	-0.5479
Passed Shapiro Wilk normality test	No (p-value = 0.008469 < 0.05)



Analysis halt frequency (H5 - Zone 2)

Analysis model	Linear mixed model fit by REML: Halt_frequency_H5_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	133.6	94.85	188.1	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Halt_frequency_H5_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 95.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.3102	-0.5327	0.1638	0.5980	1.3298

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.07791	0.2791
Residual		0.59014	0.7682

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

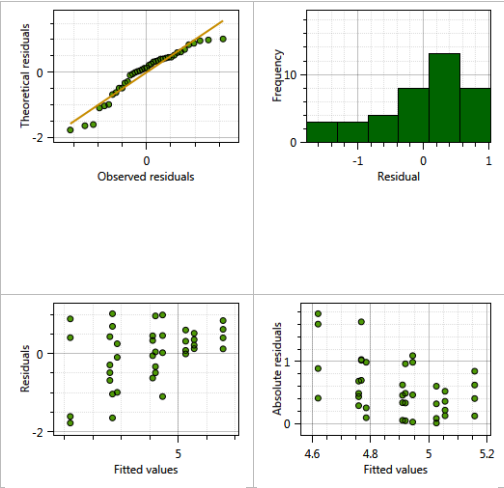
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	4.8946	0.1515	9.0796	32.3	1.1e-10 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

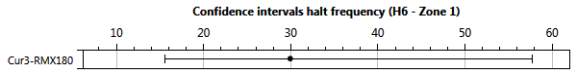
Model residuals

Statistic	Value
Sample skewness	-0.88
Sample excess kurtosis	0.1789
Passed Shapiro Wilk normality test	No (p-value = 0.01112 < 0.05)



Analysis halt frequency (H6 - Zone 1)

Analysis model	Linear mixed model fit by REML: Halt_frequency_H6_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	29.94	15.52	57.75	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Halt_frequency_H6_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 83.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.9041	-0.3843	0.2775	0.5110	1.4848

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.1184	0.3441
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.2090	0.4572
Residual		1.0371	1.0184

Number of obs: 27, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

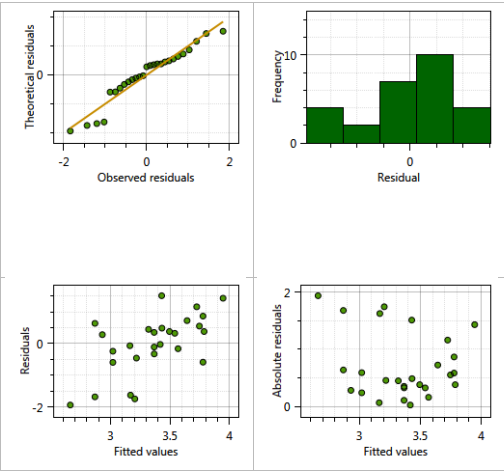
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	3.3991	0.2728	6.4209	12.46	9.77e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

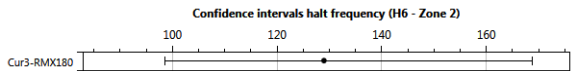
Model residuals

Statistic	Value
Sample skewness	-0.6552
Sample excess kurtosis	0.05336
Passed Shapiro Wilk normality test	Yes (p-value = 0.07888 > 0.05)



Analysis halt frequency (H6 - Zone 2)

Analysis model	Linear mixed model fit by REML: Halt_frequency_H6_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	129	98.5	168.8	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Halt_frequency_H6_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 93.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.2038	-0.3594	-0.0172	0.8064	1.3676

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000	0.0000
Residual		0.672	0.8197

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

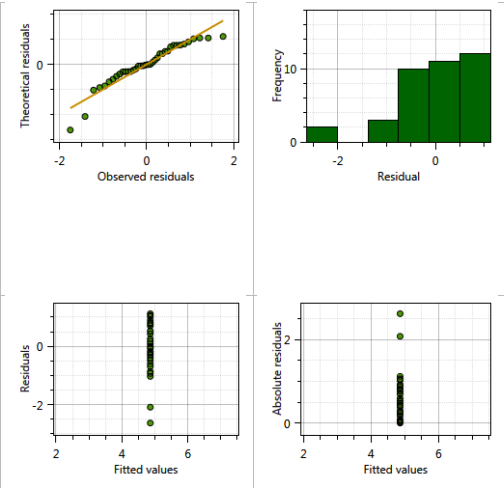
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	4.859	0.133	37.000	36.54	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

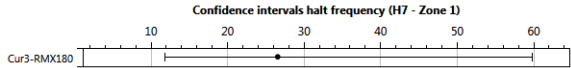
Model residuals

Statistic	Value
Sample skewness	-1.147
Sample excess kurtosis	2.169
Passed Shapiro Wilk normality test	No (p-value = 0.006195 < 0.05)



Analysis halt frequency (H7 - Zone 1)

Analysis model	Linear mixed model fit by REML: Halt_frequency_H7_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype_Zone_1	Genotype_Zone_2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	26.54	11.77	59.83	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Halt_frequency_H7_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 92.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.9434	-0.5607	0.1414	0.5312	1.9558

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.02285	0.1512
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.27690	0.5262
Residual		1.57011	1.2530

Number of obs: 27, groups: Genotype_Zone_2:Plant_Zone_2, 10; Genotype_Zone_1:Plant_Zone_1, 9

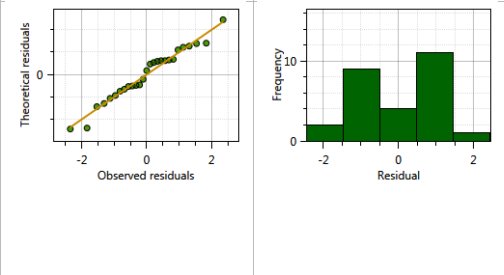
Fixed effects:

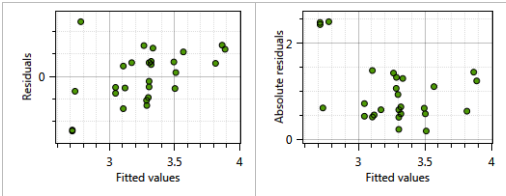
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	3.2785	0.3052	4.4763	10.74	0.000231 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

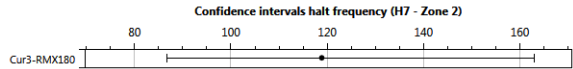
Statistic	Value
Sample skewness	-0.2435
Sample excess kurtosis	-0.1607
Passed Shapiro Wilk normality test	Yes (p-value = 0.5984 > 0.05)





Analysis halt frequency (H7 - Zone 2)

Analysis model	Linear mixed model fit by REML: Halt_frequency_H7_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	118.9	86.65	163	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Halt_frequency_H7_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 97.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.0358	-0.8320	0.2636	0.7630	1.4173

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.02265	0.1505
Residual		0.67721	0.8229

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

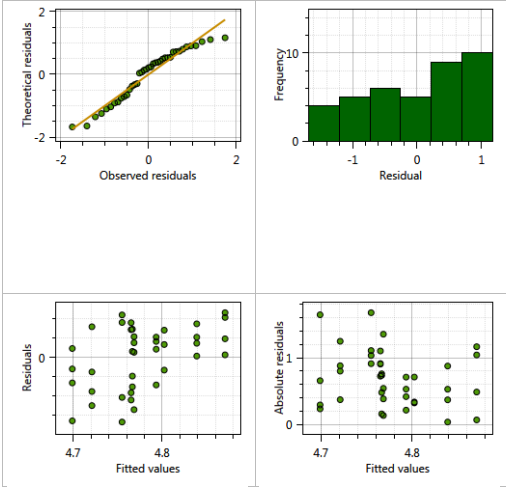
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	4.7779	0.1401	9.1786	34.09	5.56e-11 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

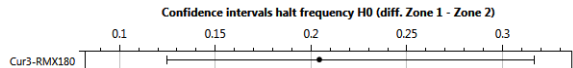
Model residuals

Statistic	Value
Sample skewness	-0.5205
Sample excess kurtosis	-0.8435
Passed Shapiro Wilk normality test	No (p-value = 0.03017 < 0.05)



Analysis halt frequency H0 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Halt_frequency_H0_Zone_1,Halt_frequency_H0_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2043	0.1246	0.3166	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 139.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.27002	-0.72518	-0.05042	0.52532	2.83511

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.2348	0.4846
Residual		50.0923	7.0776

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

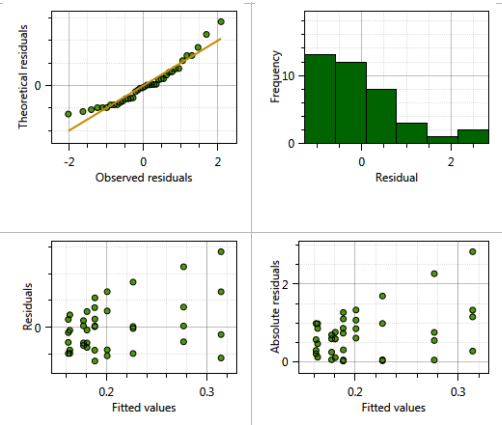
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.3595	0.2589	8.5544	-5.252	0.000622 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 7.078

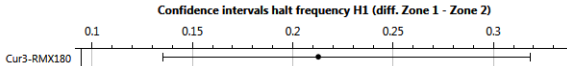
Model residuals

Statistic	Value
Sample skewness	1.025
Sample excess kurtosis	0.9694
Passed Shapiro Wilk normality test	No (p-value = 0.01179 < 0.05)



Analysis halt frequency H1 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Halt_frequency_H1_Zone_1,Halt_frequency_H1_Zone_2) ~ 1 + (1 Genotype_Zone_1 Plant_Zone_1) + (1 Genotype_Zone_2 Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2127	0.1351	0.3185	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 149.3

Scaled residuals:
Min IQ Median 3Q Max
-2.13745 -0.49998 -0.01474 1.02042 1.98771

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 6.121e-02 2.474e-01
Genotype_Zone_2:Plant_Zone_2 (Intercept) 1.833e-16 1.354e-08
Residual 8.416e+01 9.174e+00
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

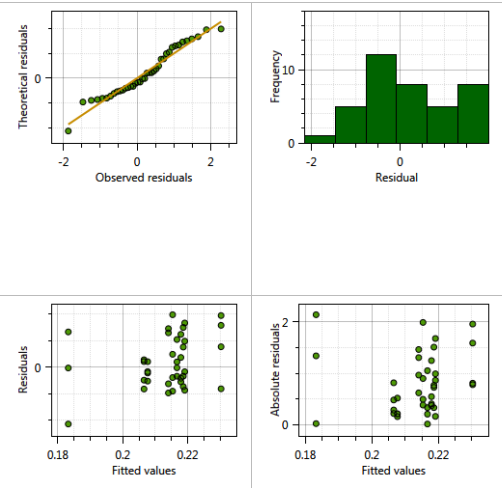
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -1.3088 0.2535 12.9413 -5.162 0.000185 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 9.174

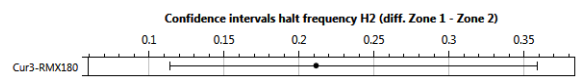
Model residuals

Statistic	Value
Sample skewness	0.1158
Sample excess kurtosis	-0.4971
Passed Shapiro Wilk normality test	Yes (p-value = 0.1552 > 0.05)



Analysis halt frequency H2 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Halt_frequency_H2_Zone_1,Halt_frequency_H2_Zone_2) ~ 1 + (1 Genotype_Zone_1 Plant_Zone_1) + (1 Genotype_Zone_2 Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2113	0.1136	0.359	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 147.4

Scaled residuals:
  Min       1Q   Median       3Q      Max
-1.2856 -0.6482 -0.3098  0.5937  2.6035

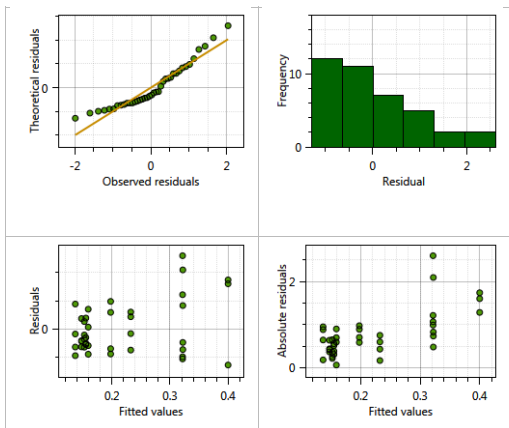
Random effects:
Groups              Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.5276  0.7263
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.0000  0.0000
Residual                                64.3852  8.0240
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -1.3170     0.3228  8.4640  -4.079  0.00314 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 8.024
```

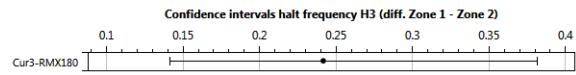
Model residuals

Statistic	Value
Sample skewness	0.9917
Sample excess kurtosis	0.4151
Passed Shapiro Wilk normality test	No (p-value = 0.005248 < 0.05)



Analysis halt frequency H3 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Halt_frequency_H3_Zone_1,Halt_frequency_H3_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2416	0.1412	0.3817	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 141.6

Scaled residuals:
  Min       1Q   Median       3Q      Max
-1.2755 -0.7261 -0.1318  0.8153  2.1030

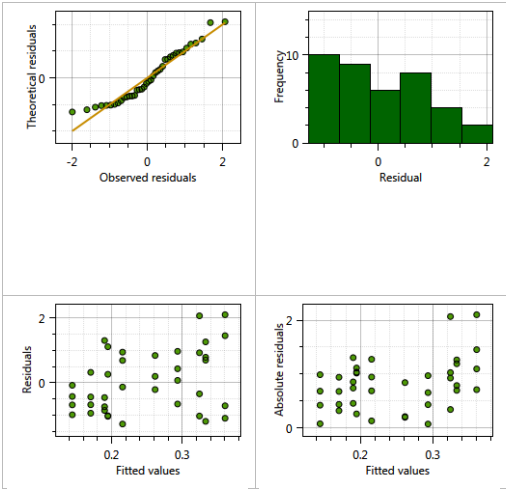
Random effects:
Groups              Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.0000  0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.3856  0.6209
Residual                                61.4165  7.8369
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -1.1440     0.2923  8.9520  -3.914  0.00358 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 7.837
```

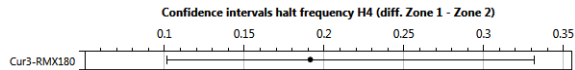
Model residuals

Statistic	Value
Sample skewness	0.4843
Sample excess kurtosis	-0.7841
Passed Shapiro Wilk normality test	No (p-value = 0.03065 < 0.05)



Analysis halt frequency H4 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Halt_frequency_H4_Zone_1,Halt_frequency_H4_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1914	0.1013	0.3319	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 153.6

Scaled residuals:
Min 1Q Median 3Q Max
-0.9677 -0.6909 -0.3162 0.6960 2.4941

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.2155 0.4642
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.0603 0.2456
Residual 84.0930 9.1702
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

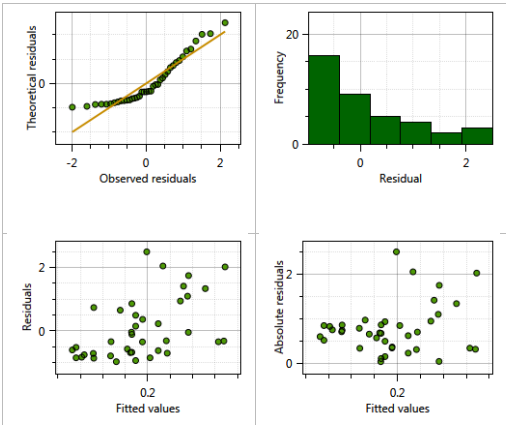
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -1.4411 0.3087 6.4940 -4.669 0.00279 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 9.17

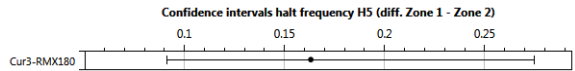
Model residuals

Statistic	Value
Sample skewness	0.9875
Sample excess kurtosis	-0.05196
Passed Shapiro Wilk normality test	No (p-value = 0.0004254 < 0.05)



Analysis halt frequency H5 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Halt_frequency_H5_Zone_1,Halt_frequency_H5_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1631	0.09108	0.2749	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

```
REML criterion at convergence: 155

Scaled residuals:
    Min       1Q   Median       3Q      Max
-0.9713 -0.6835 -0.2139  0.6619  2.3546

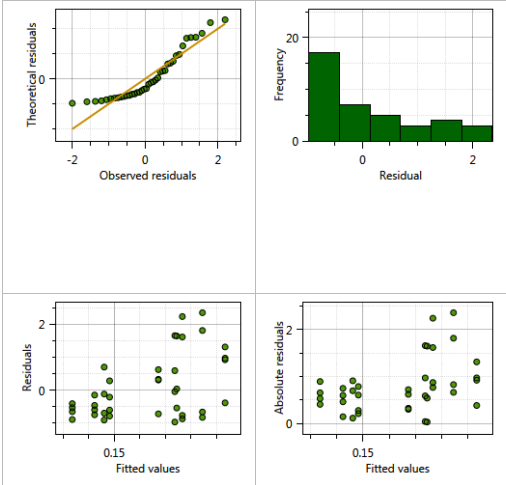
Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.0000  0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.1388  0.3725
Residual                                     77.8072  8.8208
Number of obs: 39, groups:  Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error      df t value Pr(>|t|)
(Intercept)  -1.6352     0.2946    9.0936  -5.551 0.000343 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 8.821
```

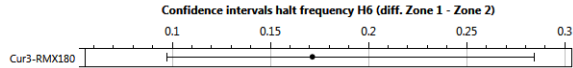
Model residuals

Statistic	Value
Sample skewness	0.9078
Sample excess kurtosis	-0.3529
Passed Shapiro Wilk normality test	No (p-value = 0.0003709 < 0.05)



Analysis halt frequency H6 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Halt_frequency_H6_Zone_1,Halt_frequency_H6_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1714	0.0971	0.2845	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
  Data: data
Weights: wi

REML criterion at convergence: 159.2

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.0286 -0.6773 -0.0583  0.4813  3.2221

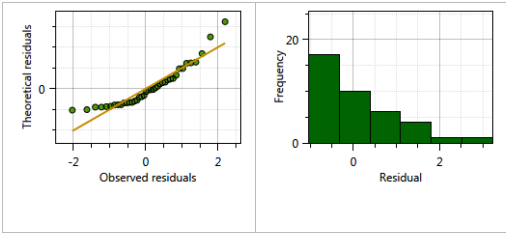
Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.000000  0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.09222  0.3037
Residual                                     84.27056  9.1799
Number of obs: 39, groups:  Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

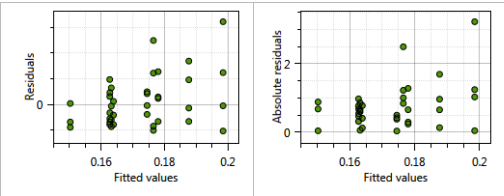
Fixed effects:
              Estimate Std. Error      df t value Pr(>|t|)
(Intercept)  -1.5759     0.2956  10.5643  -5.331 0.000276 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 9.18
```

Model residuals

Statistic	Value
Sample skewness	1.32
Sample excess kurtosis	1.82
Passed Shapiro Wilk normality test	No (p-value = 0.000616 < 0.05)



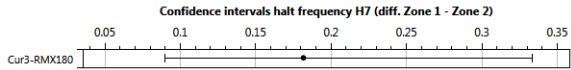


Data points with high residuals

Trial	Arena
Trial 3	11

Analysis halt frequency H7 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Halt_frequency_H7_Zone_1,Halt_frequency_H7_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1816	0.08959	0.3336	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 159.7

Scaled residuals:
Min 1Q Median 3Q Max
-1.1553 -0.6093 -0.3529 0.8142 2.4040

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.33280 0.5769
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.01618 0.1272
Residual 80.45962 8.9699
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

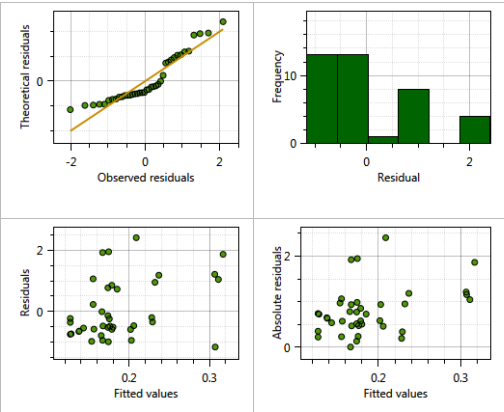
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -1.5054 0.3288 5.7449 -4.578 0.00422 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 8.97

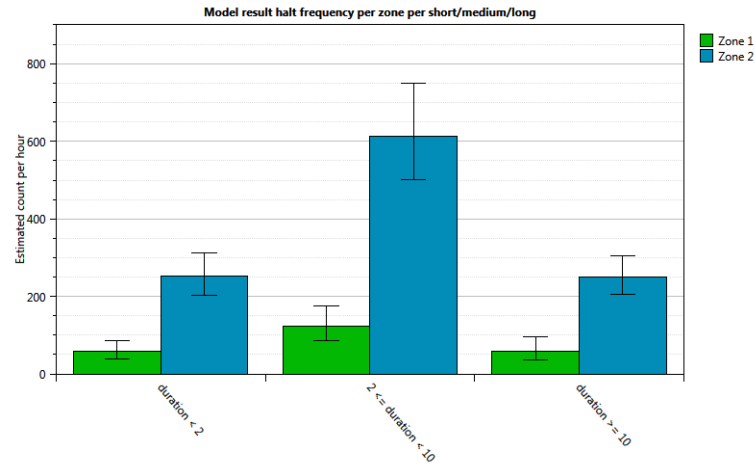
Model residuals

Statistic	Value
Sample skewness	0.9646
Sample excess kurtosis	-0.1876
Passed Shapiro Wilk normality test	No (p-value = 0.000314 < 0.05)



Halt frequency per zone per short/medium/long

Selected zones	Zone 1, Zone 2
Event duration categories	duration < 2, 2 <= duration < 10, duration >= 10
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

Behaviour statistic	Cur3-RMX180	Remark
Halt frequency duration < 2 (diff. Zone 1 - Zone 2)	p=8.17E-06**** [-1.88, -1.06]	CR
Halt frequency 2 <= duration < 10 (diff. Zone 1 - Zone 2)	p=2.39E-05**** [-1.91, -1.06]	
Halt frequency duration >= 10 (diff. Zone 1 - Zone 2)	p=0.00413*** [-1.79, -0.544]	

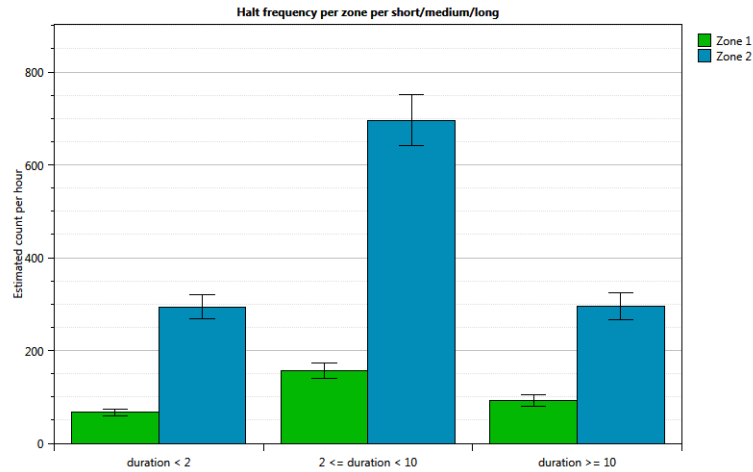
CR = Check residuals

The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Halt frequency (duration < 2 - Zone 1)	57.4 [38.7, 85.4]	
Halt frequency (2 <= duration < 10 - Zone 1)	123 [85.5, 176]	CR
Halt frequency (duration >= 10 - Zone 1)	58.2 [35.1, 96.5]	CR
Halt frequency (duration < 2 - Zone 2)	252 [202, 313]	
Halt frequency (2 <= duration < 10 - Zone 2)	614 [501, 751]	
Halt frequency (duration >= 10 - Zone 2)	250 [205, 305]	CR

CR = Check residuals

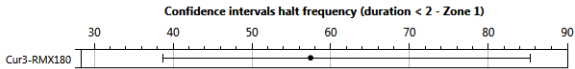
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean duration < 2 - Zone 1	StdErr duration < 2 - Zone 1	Mean 2 <= duration < 10 - Zone 1	StdErr 2 <= duration < 10 - Zone 1	Mean duration >= 10 - Zone 1	StdErr duration >= 10 - Zone 1	Mean duration < 2 - Zone 2	StdErr duration < 2 - Zone 2	Mean 2 <= duration < 10 - Zone 2	StdErr 2 <= duration < 10 - Zone 2	Mean duration >= 10 - Zone 2	StdErr duration >= 10 - Zone 2
Cur3	RMX180	Neutral	66.64	7.22	156.78	16.48	92.85	11.99	294.09	25.55	696.3	55.25	295.72	29.32

Analysis halt frequency (duration < 2 - Zone 1)

Analysis model	Linear mixed model fit by REML: Halt_frequency_duration_2_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	57.45	38.66	85.36	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Halt_frequency_duration_2_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 77.6

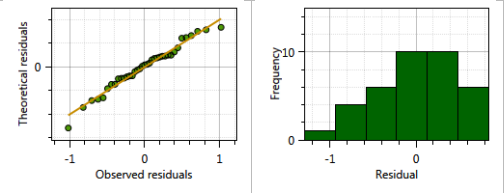
Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.31843 -0.42933  0.08153  0.44836  1.50659

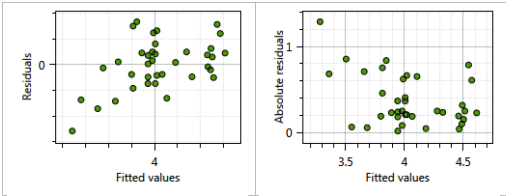
Random effects:
Groups             Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.1196   0.3458
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.1029   0.3207
Residual              0.3093   0.5562
Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    4.0508     0.1758 9.2694   23.04 1.69e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model residuals

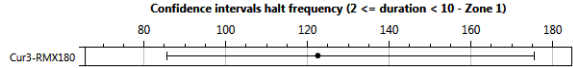
Statistic	Value
Sample skewness	-0.4089
Sample excess kurtosis	0.3046
Passed Shapiro Wilk normality test	Yes (p-value = 0.5546 > 0.05)





Analysis halt frequency (2 <= duration < 10 - Zone 1)

Analysis model	Linear mixed model fit by REML: Halt_frequency_2_duration_10_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals halt frequency (2 <= duration < 10 - Zone 1)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	122.6	85.55	175.6	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Halt_frequency_2_duration_10_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 105.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.4368	-0.2463	0.1444	0.4963	1.3135

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	1.198e-16	1.095e-08
Genotype_Zone_2:Plant_Zone_2	(Intercept)	1.943e-02	1.394e-01
Residual		8.985e-01	9.479e-01

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

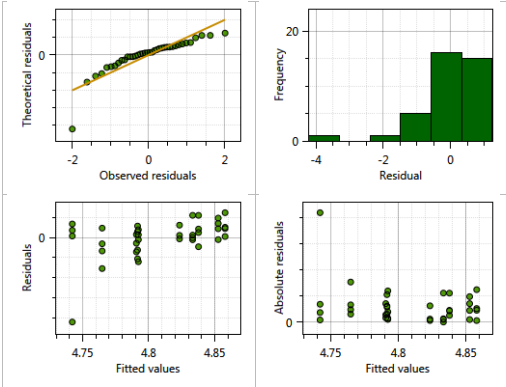
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	4.809	0.160	9.431	30.05	1.1e-10 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

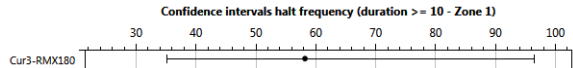
Model residuals

Statistic	Value
Sample skewness	-2.567
Sample excess kurtosis	10.22
Passed Shapiro Wilk normality test	No (p-value = 5.752E-06 < 0.05)



Analysis halt frequency (duration >= 10 - Zone 1)

Analysis model	Linear mixed model fit by REML: Halt_frequency_duration_10_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals halt frequency (duration >= 10 - Zone 1)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	58.18	35.08	96.51	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Halt_frequency_duration_10_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 126.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.1151	-0.3522	0.2182	0.5227	1.3186

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	4.889e-15	6.992e-08
Genotype_Zone_2:Plant_Zone_2	(Intercept)	1.567e-01	3.958e-01
Residual		1.352e+00	1.163e+00

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

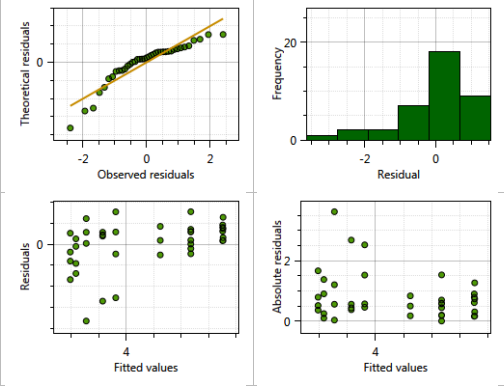
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	4.0636	0.2245	9.2234	18.1	1.61e-08 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

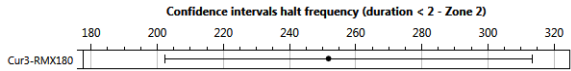
Model residuals

Statistic	Value
Sample skewness	-1.519
Sample excess kurtosis	2.563
Passed Shapiro Wilk normality test	No (p-value = 0.000259 < 0.05)



Analysis halt frequency (duration < 2 - Zone 2)

Analysis model	Linear mixed model fit by REML: Halt_frequency_duration_2_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	251.8	202.2	313.5	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Halt_frequency_duration_2_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 71.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.81733	-0.64063	-0.00936	0.76242	1.64038

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000000	0.00000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.002417	0.04917
Residual		0.344596	0.58702

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

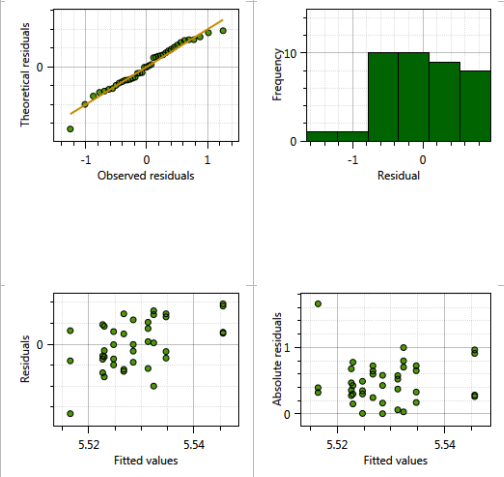
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	5.52856	0.09528	8.11758	58.02	6.38e-12 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

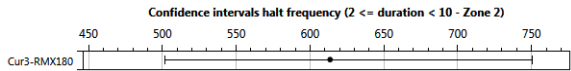
Model residuals

Statistic	Value
Sample skewness	-0.4416
Sample excess kurtosis	0.1336
Passed Shapiro Wilk normality test	Yes (p-value = 0.3447 > 0.05)



Analysis halt frequency (2 <= duration < 10 - Zone 2)

Analysis model	Linear mixed model fit by REML: Halt_frequency_2_duration_10_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	613.6	501.5	750.7	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Halt_frequency_2_duration_10_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

```
REML criterion at convergence: 63

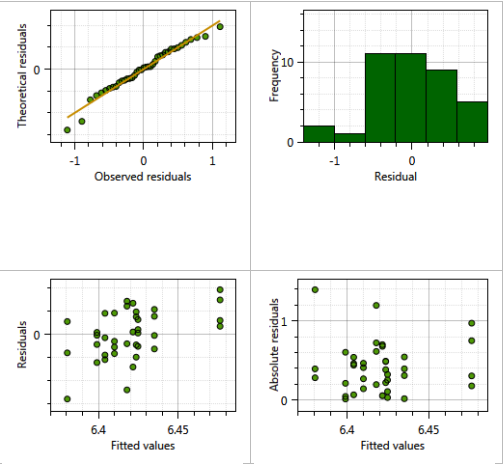
Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.66734 -0.55529  0.06335  0.74756  1.85903

Random effects:
Groups:                               Name      Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 1.661e-18 1.289e-09
Genotype_Zone_2:Plant_Zone_2 (Intercept) 7.040e-03 8.391e-02
Residual                                2.725e-01 5.221e-01
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   6.41929    0.08773  8.13895   73.17 9.18e-13 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

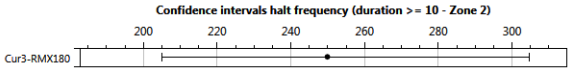
Model residuals

Statistic	Value
Sample skewness	-0.5252
Sample excess kurtosis	0.4633
Passed Shapiro Wilk normality test	Yes (p-value = 0.5002 > 0.05)



Analysis halt frequency (duration >= 10 - Zone 2)

Analysis model	Linear mixed model fit by REML: Halt_frequency_duration_10_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	249.9	204.9	304.8	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Halt_frequency_duration_10_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 74.2

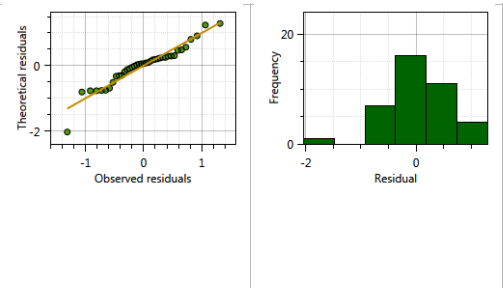
Scaled residuals:
    Min       1Q   Median       3Q      Max
-3.3178 -0.4918  0.0974  0.4433  2.1087

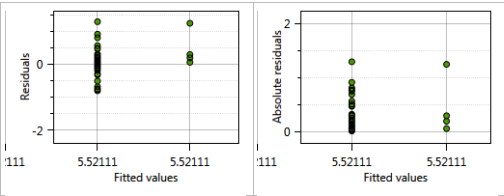
Random effects:
Groups:                               Name      Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.000e+00 0.000e+00
Genotype_Zone_2:Plant_Zone_2 (Intercept) 9.727e-17 9.863e-09
Residual                                3.746e-01 6.121e-01
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   5.52111    0.09801 38.00000   56.33 <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model residuals

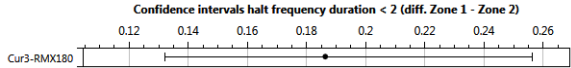
Statistic	Value
Sample skewness	-0.646
Sample excess kurtosis	2.372
Passed Shapiro Wilk normality test	No (p-value = 0.03196 < 0.05)





Analysis halt frequency duration < 2 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Halt_frequency_duration_2_Zone_1,Halt_frequency_duration_2_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals halt frequency duration < 2 (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1863	0.132	0.2564	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 106.1

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.44923 -0.83993 -0.04734  0.80258  1.81012

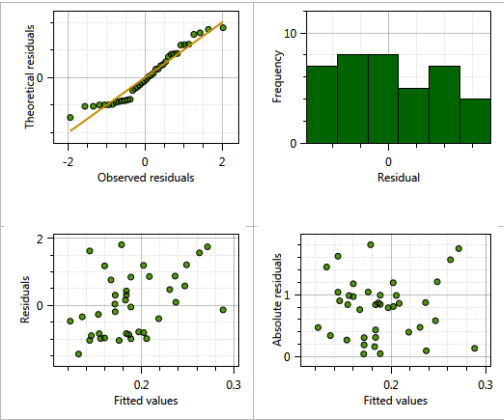
Random effects:
Groups:                               Name      Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.06534 0.2556
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.10567 0.3251
Residual                                34.83674 5.9023
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   -1.4742      0.1854 10.7130   -7.95 8.17e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 5.902
```

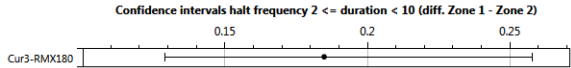
Model residuals

Statistic	Value
Sample skewness	0.355
Sample excess kurtosis	-1.014
Passed Shapiro Wilk normality test	No (p-value = 0.03409 < 0.05)



Analysis halt frequency 2 <= duration < 10 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Halt_frequency_2_duration_10_Zone_1,Halt_frequency_2_duration_10_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals halt frequency 2 <= duration < 10 (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1848	0.1288	0.258	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 109.1

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.49883 -0.67540  0.00213  0.83586  1.64206

Random effects:
Groups:                               Name      Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.07457 0.2731
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.08763 0.2960
Residual                                94.94699 9.7441
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   -1.4841      0.1894  9.1429   -7.835 2.39e-05 ***
---

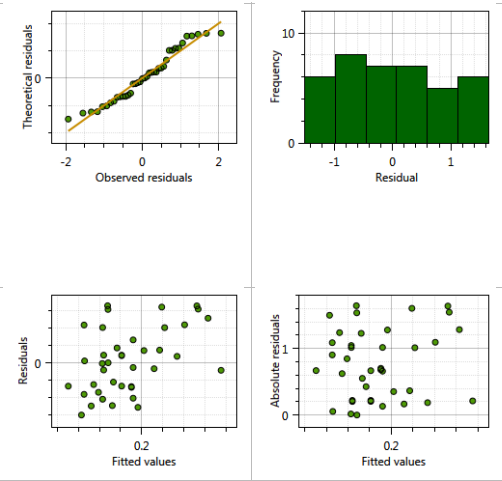
```

Signif. codes: 0 '****' 0.001 '***' 0.01 '**' 0.05 '.' 0.1 ' ' 1

Dispersion: 9.744

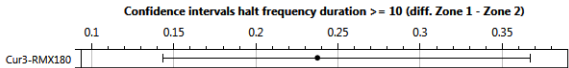
Model residuals

Statistic	Value
Sample skewness	0.2347
Sample excess kurtosis	-1.012
Passed Shapiro Wilk normality test	Yes (p-value = 0.07345 > 0.05)



Analysis halt frequency duration >= 10 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Halt_frequency_duration_10_Zone_1,Halt_frequency_duration_10_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2374	0.1431	0.3672	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 123.9

Scaled residuals:
Min 1Q Median 3Q Max
-1.61160 -0.52792 0.00661 0.53848 2.50898

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.1349 0.3673
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.2169 0.4657
Residual 71.6324 8.4636
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

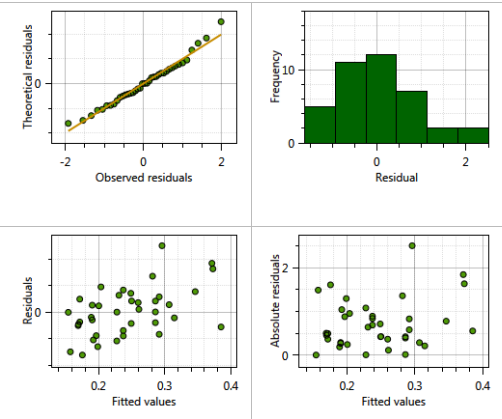
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -1.167 0.250 5.592 -4.668 0.00413 **

Signif. codes: 0 '****' 0.001 '***' 0.01 '**' 0.05 '.' 0.1 ' ' 1

Dispersion: 8.464

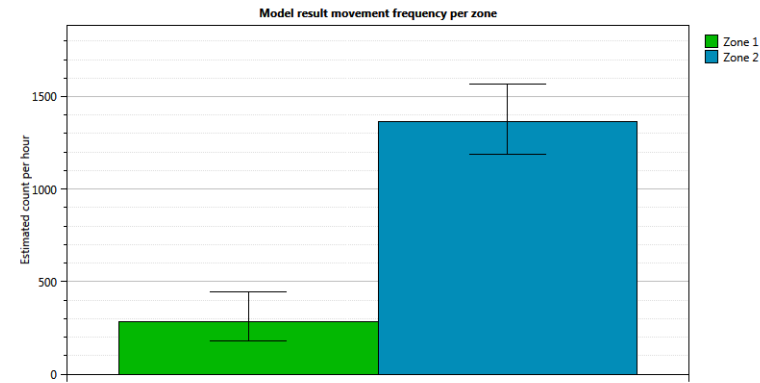
Model residuals

Statistic	Value
Sample skewness	0.5131
Sample excess kurtosis	0.3951
Passed Shapiro Wilk normality test	Yes (p-value = 0.6645 > 0.05)



Movement frequency per zone

Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

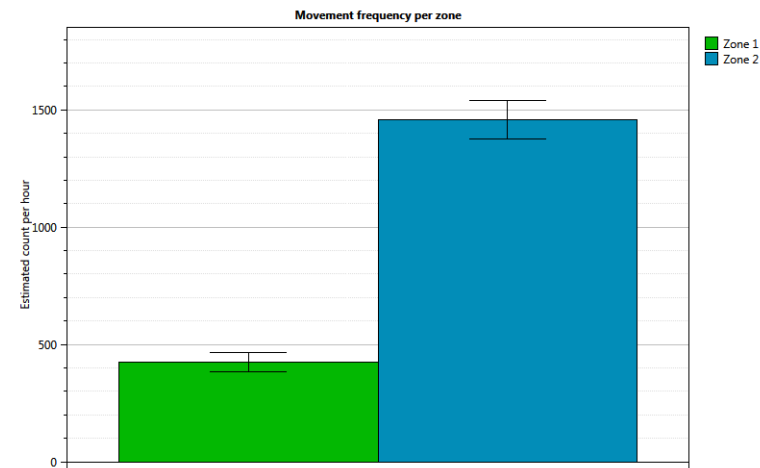
Behaviour statistic	Cur3-RMX180
Movement frequency (diff. Zone 1 - Zone 2)	p=6E-05**** [-1.62, -0.854]

The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Movement frequency (Zone 1)	285 [182, 446]	CR
Movement frequency (Zone 2)	1.36E+03 [1.19E+03, 1.57E+03]	

CR = Check residuals

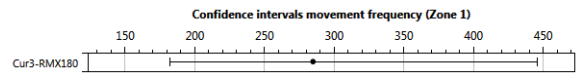
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean Zone 1	StdErr Zone 1	Mean Zone 2	StdErr Zone 2
Cur3	RMX180	Neutral	424.97	42.26	1457.98	83.57

Analysis movement frequency (Zone 1)

Analysis model	Linear mixed model fit by REML: Movement_frequency_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	284.7	181.8	445.9	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 136.2

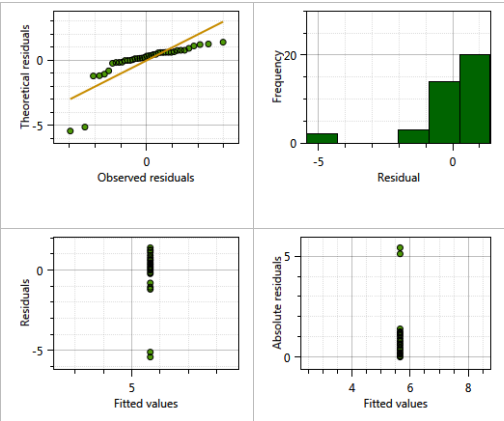
Scaled residuals:
    Min       1Q   Median       3Q      Max
-3.9177 -0.0530  0.2426  0.4475  1.0106

Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.000    0.000
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.000    0.000
Residual                                1.914    1.384
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   5.6516     0.2216 38.0000   25.51  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

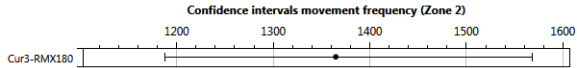
Model residuals

Statistic	Value
Sample skewness	-2.996
Sample excess kurtosis	9.921
Passed Shapiro Wilk normality test	No (p-value = 1.753E-08 < 0.05)



Analysis movement frequency (Zone 2)

Analysis model	Linear mixed model fit by REML: Movement_frequency_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	1365	1187	1569	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 37.7

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.9445	-0.5495	0.2641	0.7086	1.8936

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	1.013e-17	3.183e-09
Genotype_Zone_2:Plant_Zone_2	(Intercept)	9.706e-04	3.115e-02
Residual		1.425e-01	3.775e-01

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

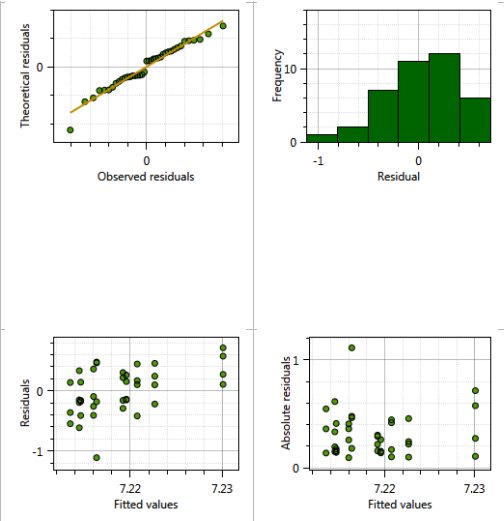
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	7.21871	0.06125	8.73890	117.9	2.69e-15 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

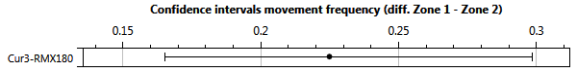
Model residuals

Statistic	Value
Sample skewness	-0.5062
Sample excess kurtosis	0.576
Passed Shapiro Wilk normality test	Yes (p-value = 0.3482 > 0.05)



Analysis movement frequency (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Movement_frequency_Zone_1,Movement_frequency_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2249	0.1651	0.2985	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

```
REML criterion at convergence: 99.4

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.4889 -0.7263 -0.1373  0.6020  1.7427

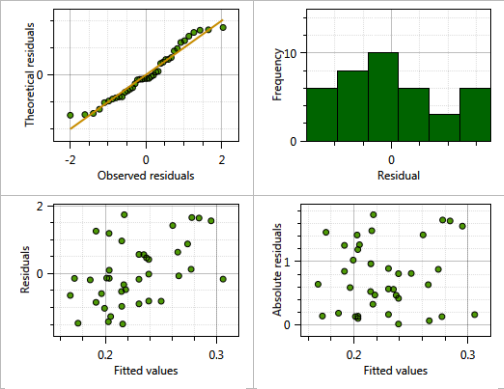
Random effects:
Groups:                               Name      Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.03525  0.1878
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.08651  0.2941
Residual                                199.17749 14.1130
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -1.2375     0.1676   8.3984  -7.386   6e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 14.11
```

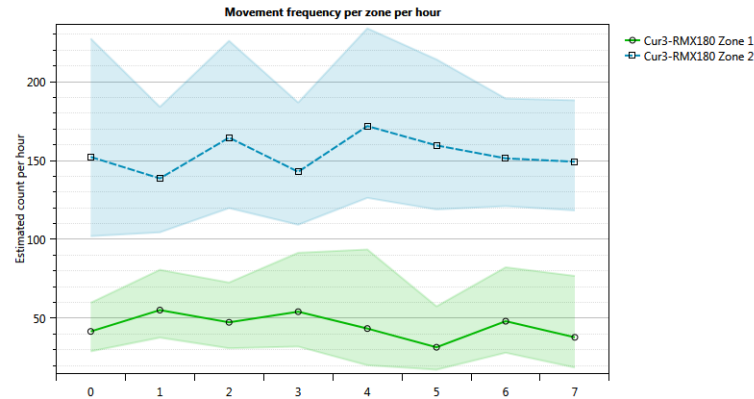
Model residuals

Statistic	Value
Sample skewness	0.2979
Sample excess kurtosis	-0.843
Passed Shapiro Wilk normality test	Yes (p-value = 0.1244 > 0.05)



Movement frequency per zone per hour

Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

Behaviour statistic	Cur3-RMX180	Remark
Movement frequency H0 (diff. Zone 1 - Zone 2)	p=0.00131** [-1.79, -0.634]	
Movement frequency H1 (diff. Zone 1 - Zone 2)	p=7.34E-06**** [-1.29, -0.569]	
Movement frequency H2 (diff. Zone 1 - Zone 2)	p=0.00204** [-1.73, -0.559]	CR
Movement frequency H3 (diff. Zone 1 - Zone 2)	p=0.00195** [-1.51, -0.468]	
Movement frequency H4 (diff. Zone 1 - Zone 2)	p=0.00322** [-2.01, -0.601]	CR
Movement frequency H5 (diff. Zone 1 - Zone 2)	p=0.000302*** [-2.05, -0.871]	CR
Movement frequency H6 (diff. Zone 1 - Zone 2)	p=2.16E-06**** [-1.89, -0.885]	CR
Movement frequency H7 (diff. Zone 1 - Zone 2)	p=0.00281** [-2.12, -0.629]	CR

CR = Check residuals

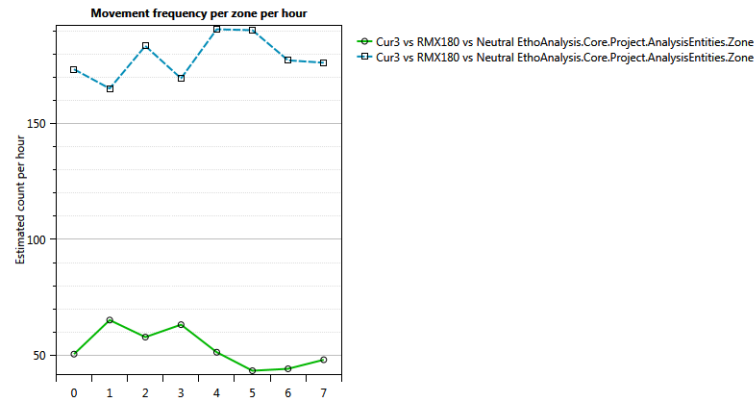
The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Movement frequency (H0 - Zone 1)	41.6 [29, 59.8]	CR
Movement frequency (H0 - Zone 2)	152 [102, 227]	CR
Movement frequency (H1 - Zone 1)	55.2 [37.7, 80.7]	CR
Movement frequency (H1 - Zone 2)	139 [104, 184]	CR
Movement frequency (H2 - Zone 1)	47.4 [30.9, 72.7]	
Movement frequency (H2 - Zone 2)	165 [120, 226]	CR
Movement frequency (H3 - Zone 1)	54.1 [32, 91.6]	CR
Movement frequency (H3 - Zone 2)	143 [109, 187]	CR
Movement frequency (H4 - Zone 1)	43.5	

Statistic	Cur3-RMX180	Remark
	[20.2, 93.6]	
Movement frequency (H4 - Zone 2)	172	CR
	[126, 234]	
Movement frequency (H5 - Zone 1)	31.6	CR
	[17.3, 57.5]	
Movement frequency (H5 - Zone 2)	160	
	[119, 214]	
Movement frequency (H6 - Zone 1)	48.1	
	[28.1, 82.3]	
Movement frequency (H6 - Zone 2)	151	CR
	[121, 189]	
Movement frequency (H7 - Zone 1)	37.9	CR
	[18.7, 76.8]	
Movement frequency (H7 - Zone 2)	149	
	[118, 188]	

CR = Check residuals

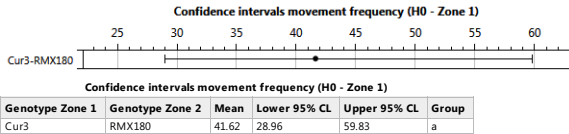
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean H0 - Zone 1	StdErr H0 - Zone 1	Mean H0 - Zone 2	StdErr H0 - Zone 2	Mean H1 - Zone 1	StdErr H1 - Zone 1	Mean H1 - Zone 2	StdErr H1 - Zone 2	Mean H2 - Zone 1	StdErr H2 - Zone 1	Mean H2 - Zone 2	StdErr H2 - Zone 2	Mean H3 - Zone 1	StdErr H3 - Zone 1	Mean H3 - Zone 2	StdErr H3 - Zone 2	Mean H4 - Zone 1	StdErr H4 - Zone 1	Mean H4 - Zone 2	StdErr H4 - Zone 2	Mean H5 - Zone 1	StdErr H5 - Zone 1	Mean H5 - Zone 2	StdErr H5 - Zone 2	Mean H6 - Zone 1	StdErr H6 - Zone 1	Mean H6 - Zone 2	StdErr H6 - Zone 2
Cur3	RMX180	Neutral	50.54	7.65	173.42	15.49	65.23	6.55	165.11	15.17	57.88	8.64	183.47	14.81	63.24	8.37	169.49	13.64	51.36	8.27	190.66	16.91	43.38	7.17	190.29	15.95	44.21	8.27	177.26	16.77

Analysis movement frequency (H0 - Zone 1)

Analysis model	Linear mixed model fit by REML: Movement_frequency_H0_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_H0_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 95.8

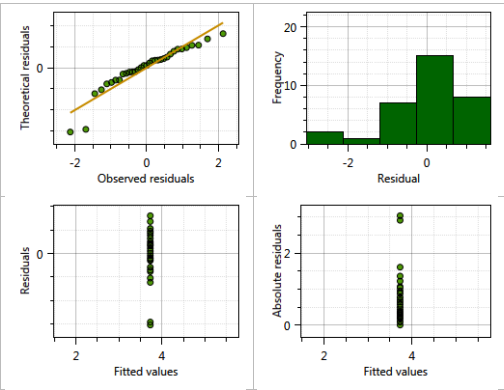
Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.9667 -0.2899  0.1068  0.6292  1.5740

Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.000    0.000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.000    0.000
Residual              1.047    1.023
Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   3.7287    0.1781 32.0000  20.93  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

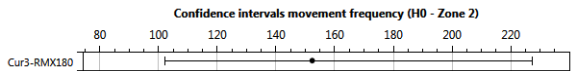
Model residuals

Statistic	Value
Sample skewness	-1.375
Sample excess kurtosis	2.758
Passed Shapiro Wilk normality test	No (p-value = 0.003536 < 0.05)



Analysis movement frequency (H0 - Zone 2)

Analysis model	Linear mixed model fit by REML: Movement_frequency_H0_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	152.3	102	227.4	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_H0_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 87

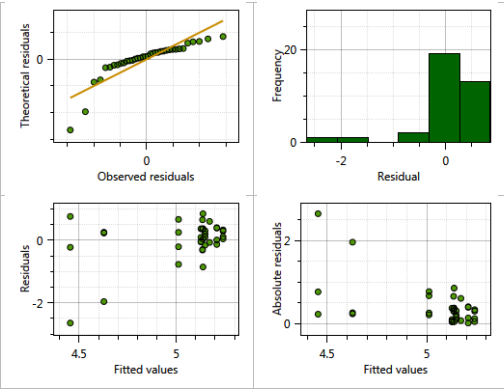
Scaled residuals:
    Min       1Q   Median       3Q      Max
-3.6254 -0.1890  0.1479  0.4897  1.1653

Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  4.519e-14  2.126e-07
Genotype_Zone_2:Plant_Zone_2 (Intercept)  1.447e-01  3.804e-01
Residual                                5.333e-01  7.303e-01
Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    5.026      0.172 7.551  29.23 4.81e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

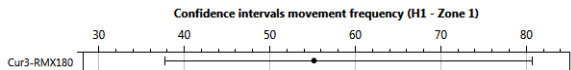
Model residuals

Statistic	Value
Sample skewness	-2.373
Sample excess kurtosis	7.074
Passed Shapiro Wilk normality test	No (p-value = 3.525E-06 < 0.05)



Analysis movement frequency (H1 - Zone 1)

Analysis model	Linear mixed model fit by REML: Movement_frequency_H1_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	55.16	37.7	80.73	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_H1_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 96.6

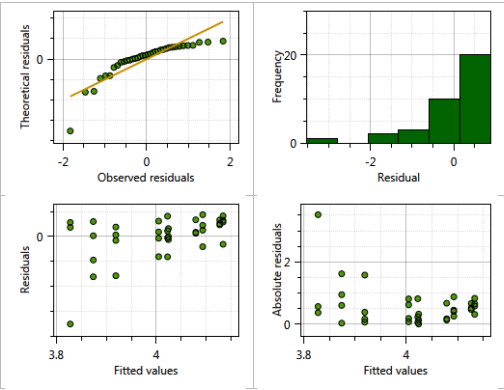
Scaled residuals:
    Min       1Q   Median       3Q      Max
-3.9662 -0.1505  0.2289  0.6409  0.9874

Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.00000  0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.05552  0.2356
Residual                                0.78785  0.8876
Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    4.0103      0.1659 8.2262  24.17 6.21e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

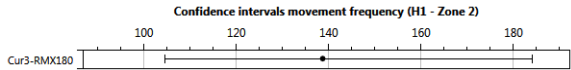
Model residuals

Statistic	Value
Sample skewness	-2.335
Sample excess kurtosis	7.13
Passed Shapiro Wilk normality test	No (p-value = 5.307E-06 < 0.05)



Analysis movement frequency (H1 - Zone 2)

Analysis model	Linear mixed model fit by REML: Movement_frequency_H1_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	138.7	104.5	184.1	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_H1_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 94.1

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.4977	-0.2975	0.3630	0.6762	1.0349

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	1.724e-17	4.152e-09
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000e+00	0.000e+00
Residual		7.221e-01	8.497e-01

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

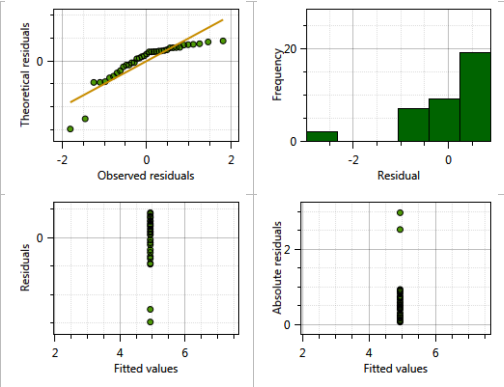
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	4.9323	0.1397	36.0000	35.31	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

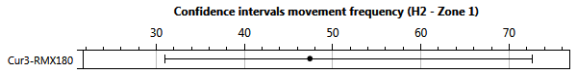
Model residuals

Statistic	Value
Sample skewness	-1.979
Sample excess kurtosis	4.566
Passed Shapiro Wilk normality test	No (p-value = 1.084E-05 < 0.05)



Analysis movement frequency (H2 - Zone 1)

Analysis model	Linear mixed model fit by REML: Movement_frequency_H2_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	47.41	30.94	72.66	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_H2_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 84.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.7796	-0.6102	-0.0905	0.7285	1.9394

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.2053	0.4531
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000

Residual 0.4679 0.6840
Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

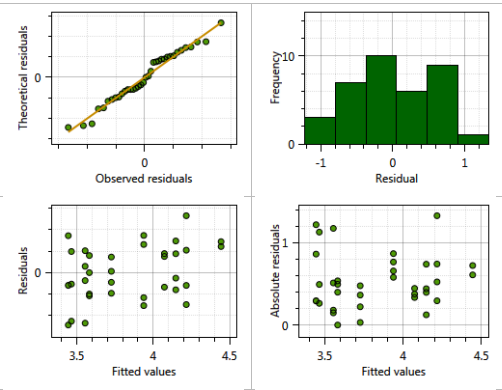
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	3.859	0.184	7.735	20.97	4.27e-08 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

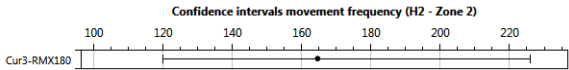
Model residuals

Statistic	Value
Sample skewness	-0.1025
Sample excess kurtosis	-0.6266
Passed Shapiro Wilk normality test	Yes (p-value = 0.4444 > 0.05)



Analysis movement frequency (H2 - Zone 2)

Analysis model	Linear mixed model fit by REML: Movement_frequency_H2_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	164.6	119.8	226	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_H2_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 72.1

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.0816	-0.5016	0.3670	0.5775	1.2583

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.09494	0.3081
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.00000	0.0000
Residual		0.32719	0.5720

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

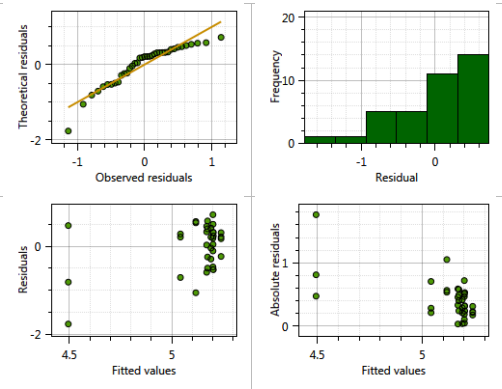
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	5.1034	0.1357	7.4026	37.61	1e-09 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

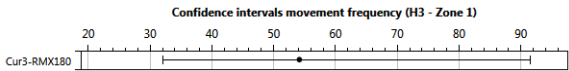
Model residuals

Statistic	Value
Sample skewness	-1.292
Sample excess kurtosis	1.905
Passed Shapiro Wilk normality test	No (p-value = 0.001727 < 0.05)



Analysis movement frequency (H3 - Zone 1)

Analysis model	Linear mixed model fit by REML: Movement_frequency_H3_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	54.14	32.01	91.56	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_H3_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 94.7

Scaled residuals:
Min 1Q Median 3Q Max
-3.6761 -0.4504 0.1936 0.6224 1.0698

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.06913 0.2629
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.07745 0.2783
Residual 0.88832 0.9425

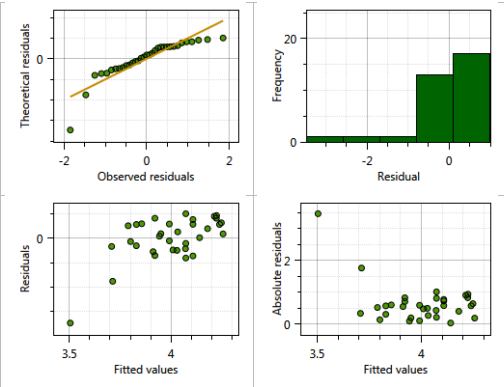
Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 3.9916 0.2053 5.0774 19.44 5.8e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

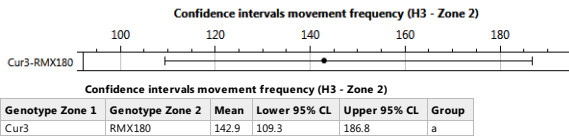
Model residuals

Statistic	Value
Sample skewness	-2.047
Sample excess kurtosis	6.328
Passed Shapiro Wilk normality test	No (p-value = 9.294E-05 < 0.05)



Analysis movement frequency (H3 - Zone 2)

Analysis model	Linear mixed model fit by REML: Movement_frequency_H3_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_H3_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 81.6

Scaled residuals:
Min 1Q Median 3Q Max
-3.5254 -0.3473 0.0500 0.6880 1.4767

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.00000 0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.02836 0.1684
Residual 0.43146 0.6569

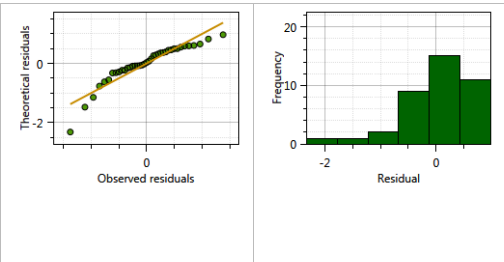
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

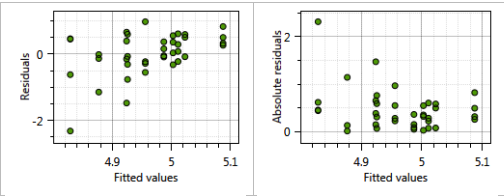
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 4.962 0.118 8.727 42.07 2.21e-11 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

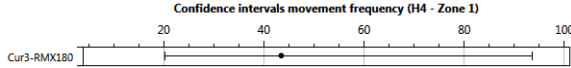
Statistic	Value
Sample skewness	-1.568
Sample excess kurtosis	3.712
Passed Shapiro Wilk normality test	No (p-value = 0.0008123 < 0.05)





Analysis movement frequency (H4 - Zone 1)

Analysis model	Linear mixed model fit by REML: Movement_frequency_H4_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	43.46	20.17	93.62	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_H4_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 84

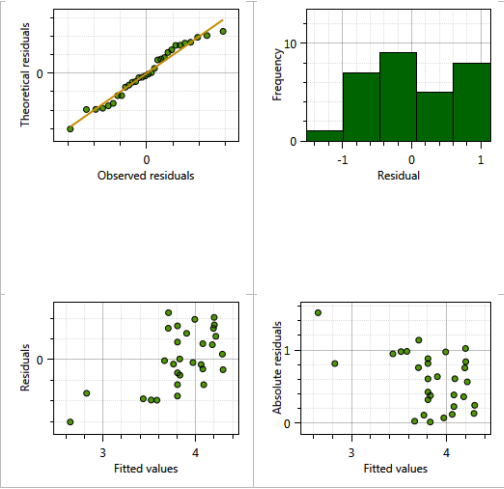
Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.85283 -0.67229 -0.05976  0.75749  1.39241

Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0863  0.2938
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.3070  0.5541
Residual              0.6666  0.8165
Number of obs: 30, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   3.7718      0.2511  3.2334  15.02 0.000422 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

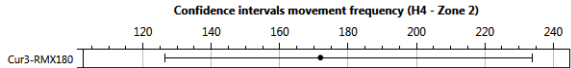
Model residuals

Statistic	Value
Sample skewness	-0.1942
Sample excess kurtosis	-0.8818
Passed Shapiro Wilk normality test	Yes (p-value = 0.3768 > 0.05)



Analysis movement frequency (H4 - Zone 2)

Analysis model	Linear mixed model fit by REML: Movement_frequency_H4_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	171.9	126.3	233.9	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_H4_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 71.2

Scaled residuals:
    Min       1Q   Median       3Q      Max
-3.0285 -0.4900  0.1517  0.6561  1.1644

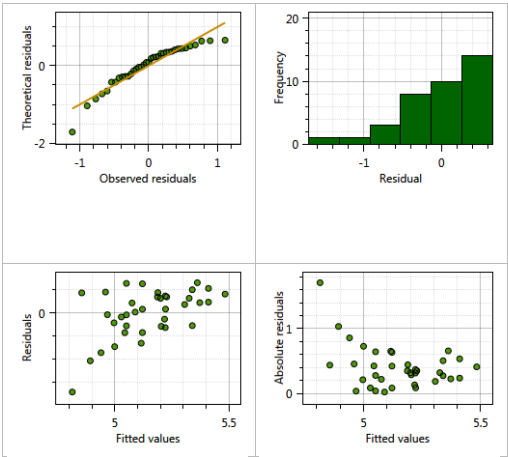
Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.04563  0.2136
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.03586  0.1894
Residual              0.31882  0.5646
Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    5.147      0.130  6.928  39.59 2.01e-09 ***
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

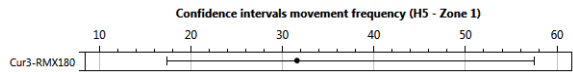
Model residuals

Statistic	Value
Sample skewness	-1.242
Sample excess kurtosis	1.919
Passed Shapiro Wilk normality test	No (p-value = 0.004964 < 0.05)



Analysis movement frequency (H5 - Zone 1)

Analysis model	Linear mixed model fit by REML: Movement_frequency_H5_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	31.59	17.34	57.54	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_H5_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 107.1

Scaled residuals:
Min IQ Median 3Q Max
-2.5055 -0.3202 0.2338 0.7579 1.0646

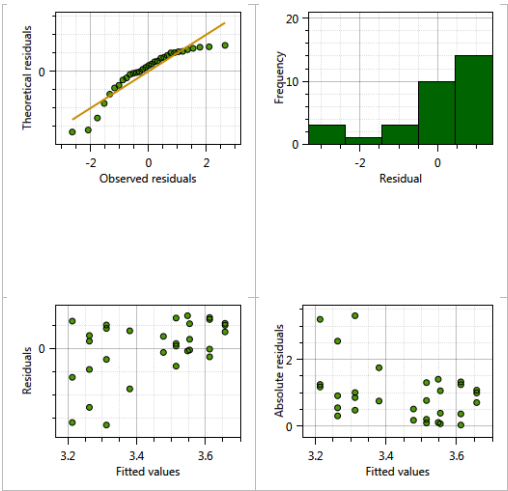
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.128 0.3578
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.000 0.0000
Residual 1.747 1.3219
Number of obs: 31, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 3.4529 0.2644 8.8620 13.06 4.34e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

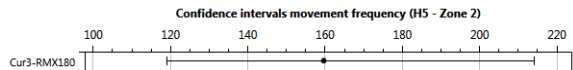
Model residuals

Statistic	Value
Sample skewness	-1.297
Sample excess kurtosis	1.166
Passed Shapiro Wilk normality test	No (p-value = 0.0009972 < 0.05)



Analysis movement frequency (H5 - Zone 2)

Analysis model	Linear mixed model fit by REML: Movement_frequency_H5_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals movement frequency (H5 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	159.6	119	214.2	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_H5_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 77.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.2698	-0.4637	0.1441	0.5292	1.4058

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.07788	0.2791
Residual		0.35419	0.5951

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

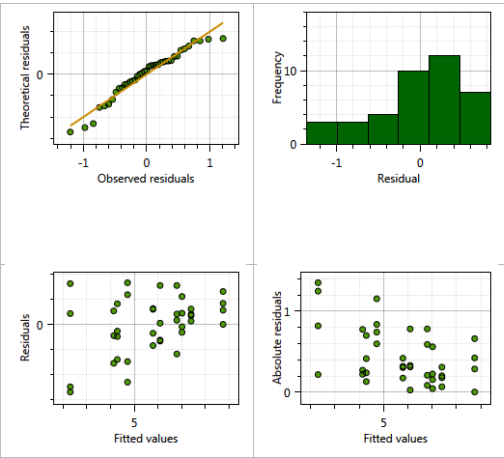
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	5.073	0.130	9.000	39.03	2.37e-11 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

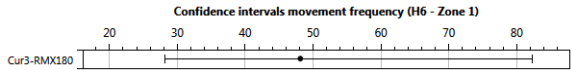
Model residuals

Statistic	Value
Sample skewness	-0.6952
Sample excess kurtosis	0.09543
Passed Shapiro Wilk normality test	Yes (p-value = 0.07206 > 0.05)



Analysis movement frequency (H6 - Zone 1)

Analysis model	Linear mixed model fit by REML: Movement_frequency_H6_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals movement frequency (H6 - Zone 1)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	48.11	28.12	82.34	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_H6_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 69.7

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.2745	-0.6573	0.1301	0.5425	1.6557

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.1418	0.3766
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.1463	0.3825
Residual		0.5347	0.7312

Number of obs: 27, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

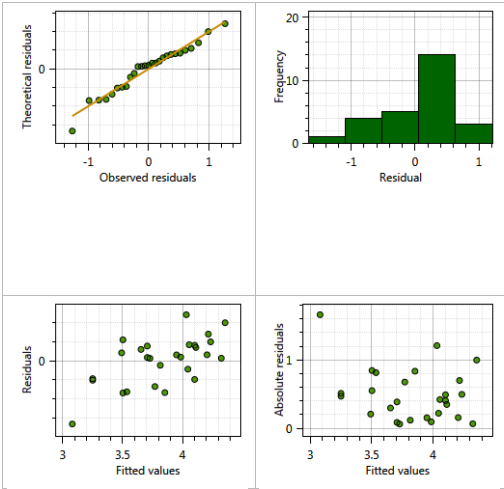
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	3.8736	0.2257	6.7739	17.17	7.79e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

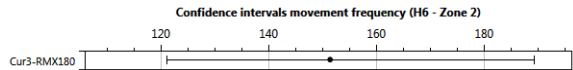
Model residuals

Statistic	Value
Sample skewness	-0.5437
Sample excess kurtosis	0.5821
Passed Shapiro Wilk normality test	Yes (p-value = 0.4612 > 0.05)



Analysis movement frequency (H6 - Zone 2)

Analysis model	Linear mixed model fit by REML: Movement_frequency_H6_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	151.4	121.1	189.4	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_H6_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 80.1

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.97006	-0.38419	-0.03494	0.75310	1.45397

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		0.4629	0.6804

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

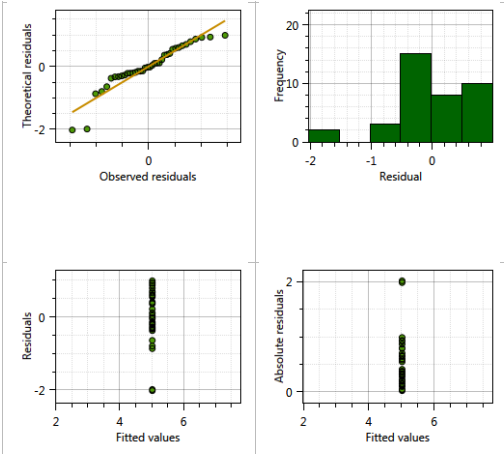
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	5.0201	0.1104	37.0000	45.48	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

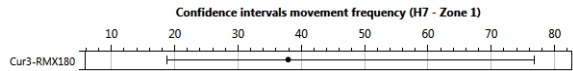
Model residuals

Statistic	Value
Sample skewness	-1.146
Sample excess kurtosis	2.34
Passed Shapiro Wilk normality test	No (p-value = 0.002569 < 0.05)



Analysis movement frequency (H7 - Zone 1)

Analysis model	Linear mixed model fit by REML: Movement_frequency_H7_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	37.9	18.7	76.82	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_H7_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 94.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.65520	-0.42229	-0.02987	0.77728	1.33975

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.10745	0.3278
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.03373	0.1837
Residual		1.57040	1.2532

Number of obs: 28, groups: Genotype_Zone_2:Plant_Zone_2, 10; Genotype_Zone_1:Plant_Zone_1, 9

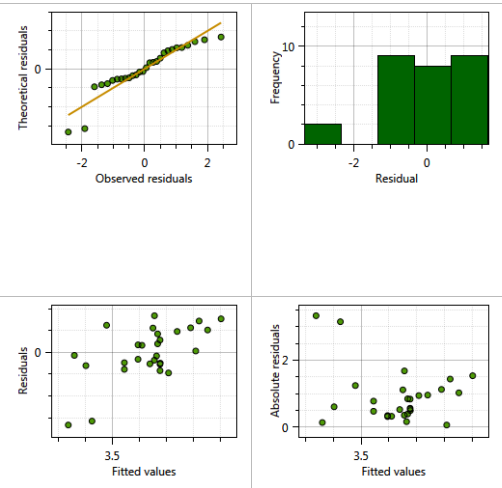
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	3.6350	0.2687	4.6535	13.53	6.5e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

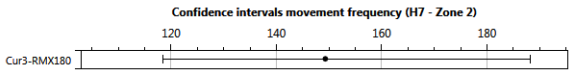
Model residuals

Statistic	Value
Sample skewness	-1.168
Sample excess kurtosis	2.006
Passed Shapiro Wilk normality test	No (p-value = 0.006614 < 0.05)



Analysis movement frequency (H7 - Zone 2)

Analysis model	Linear mixed model fit by REML: Movement_frequency_H7_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	149.3	118.4	188.3	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_H7_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 74.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.74382	-0.75013	-0.01363	0.74837	1.61592

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.01267	0.1126
Residual		0.36412	0.6034

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

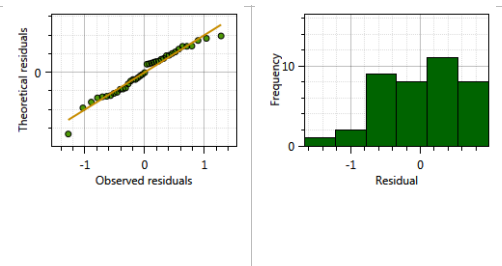
Fixed effects:

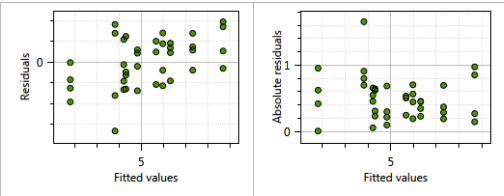
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	5.006	0.103	9.265	48.6	1.79e-12 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

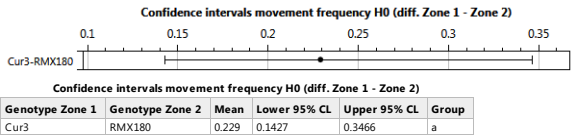
Statistic	Value
Sample skewness	-0.4542
Sample excess kurtosis	-0.02928
Passed Shapiro Wilk normality test	Yes (p-value = 0.2733 > 0.05)





Analysis movement frequency H0 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Movement_frequency_H0_Zone_1,Movement_frequency_H0_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
  Data: data
Weights: wi

REML criterion at convergence: 123.5

Scaled residuals:
   Min       1Q   Median       3Q      Max
-1.4233 -0.7970 -0.0802  0.5153  2.5229

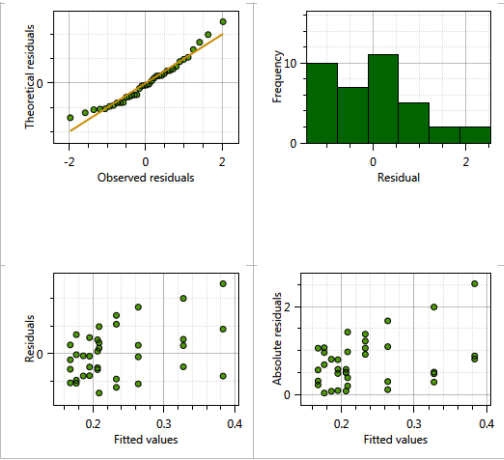
Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.0000  0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.2933  0.5416
Residual                                49.3229  7.0230
Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -1.2137     0.2512   7.9709  -4.832  0.00131 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 7.023
```

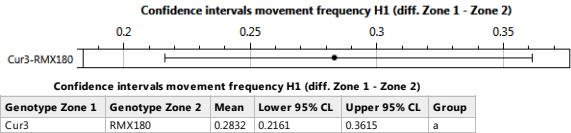
Model residuals

Statistic	Value
Sample skewness	0.709
Sample excess kurtosis	0.1934
Passed Shapiro Wilk normality test	Yes (p-value = 0.1506 > 0.05)



Analysis movement frequency H1 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Movement_frequency_H1_Zone_1,Movement_frequency_H1_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
  Data: data
Weights: wi

REML criterion at convergence: 112.8

Scaled residuals:
   Min       1Q   Median       3Q      Max
-1.48203 -0.63845 -0.03252  0.94577  2.13787

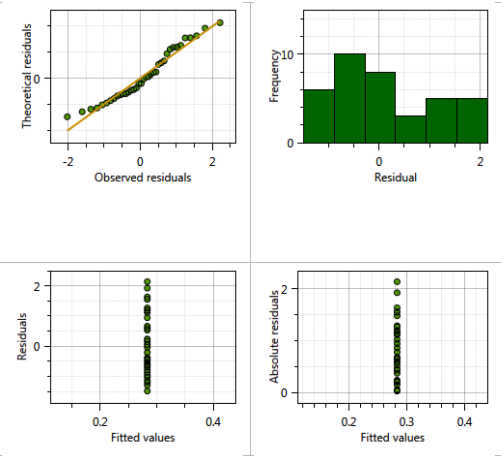
Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.00  0.000
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.00  0.000
Residual                                57.41  7.577
Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -0.9287     0.1774 36.0000  -5.234 7.34e-06 ***
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Dispersion: 7.577

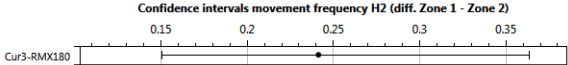
Model residuals

Statistic	Value
Sample skewness	0.4101
Sample excess kurtosis	-0.9063
Passed Shapiro Wilk normality test	Yes (p-value = 0.1155 > 0.05)



Analysis movement frequency H2 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Movement_frequency_H2_Zone_1,Movement_frequency_H2_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2413	0.1503	0.3637	a

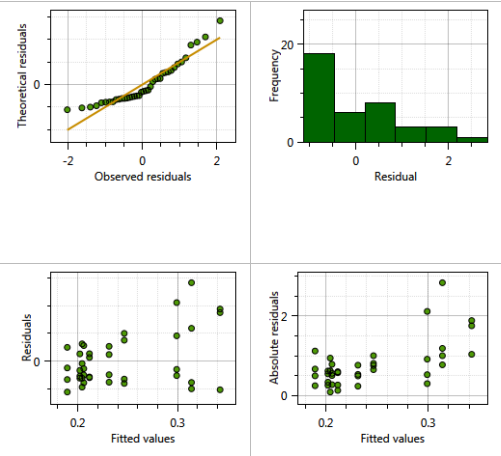
Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi
REML criterion at convergence: 134.9
Scaled residuals:
Min 1Q Median 3Q Max
-1.1195 -0.6358 -0.3006 0.5467 2.8347
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.228 0.4775
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.000 0.0000
Residual 69.492 8.3362
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -1.1456 0.2535 7.8644 -4.52 0.00204 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Dispersion: 8.336

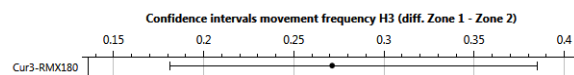
Model residuals

Statistic	Value
Sample skewness	1.177
Sample excess kurtosis	0.9162
Passed Shapiro Wilk normality test	No (p-value = 0.0008287 < 0.05)



Analysis movement frequency H3 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Movement_frequency_H3_Zone_1,Movement_frequency_H3_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2712	0.181	0.3852	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 127.7

Scaled residuals:
  Min       1Q   Median       3Q      Max
-1.44982 -0.80017 -0.04012  0.78323  2.18963

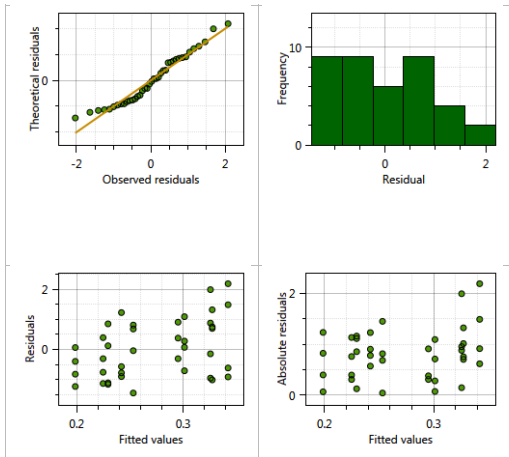
Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.0000  0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.1881  0.4337
Residual                                60.3729  7.7700
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -0.9885     0.2310   9.2096  -4.278  0.00195 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 7.77
```

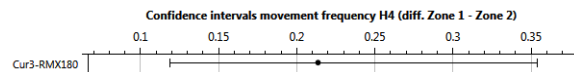
Model residuals

Statistic	Value
Sample skewness	0.4272
Sample excess kurtosis	-0.728
Passed Shapiro Wilk normality test	Yes (p-value = 0.1025 > 0.05)



Analysis movement frequency H4 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Movement_frequency_H4_Zone_1,Movement_frequency_H4_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2135	0.1185	0.3541	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 143.7

Scaled residuals:
  Min       1Q   Median       3Q      Max
-1.0556 -0.7543 -0.1994  0.6292  2.3748

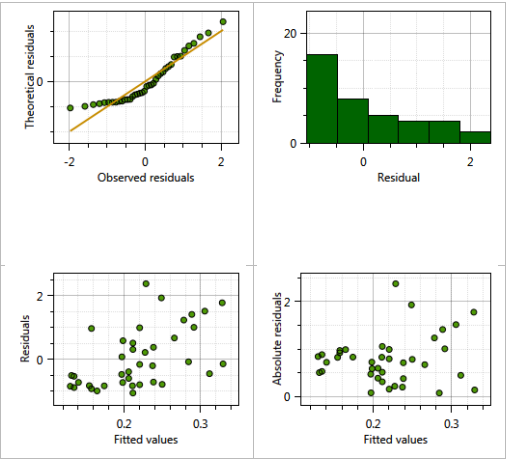
Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.2470  0.4970
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.1315  0.3627
Residual                                76.0190  8.7189
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -1.3037     0.2968   6.9665  -4.392  0.00322 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 8.719
```

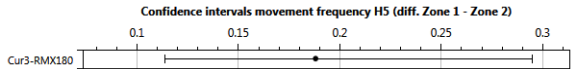
Model residuals

Statistic	Value
Sample skewness	0.8499
Sample excess kurtosis	-0.317
Passed Shapiro Wilk normality test	No (p-value = 0.001467 < 0.05)



Analysis movement frequency H5 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Movement_frequency_H5_Zone_1,Movement_frequency_H5_Zone_2) ~ 1 + (1 Genotype_Zone_1 Plant_Zone_1) + (1 Genotype_Zone_2 Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.188	0.1136	0.295	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 142.1

Scaled residuals:
Min 1Q Median 3Q Max
-1.1534 -0.7190 -0.1474 0.7145 2.1905

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 1.825e-15 4.272e-08
Genotype_Zone_2:Plant_Zone_2 (Intercept) 1.775e-01 4.214e-01
Residual 6.999e+01 8.366e+00
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

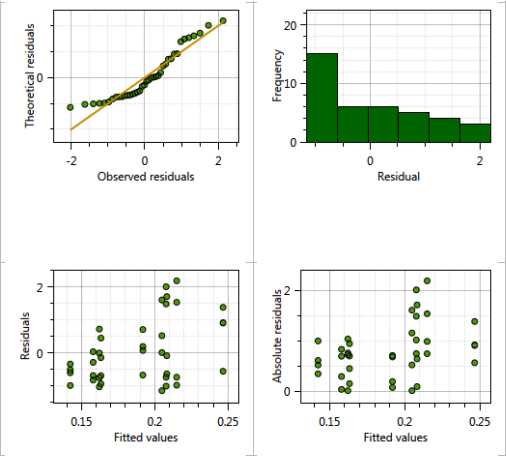
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -1.4629 0.2633 9.4043 -5.556 0.000302 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 8.366

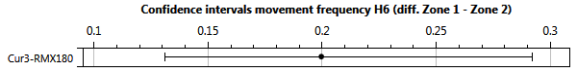
Model residuals

Statistic	Value
Sample skewness	0.7425
Sample excess kurtosis	-0.6345
Passed Shapiro Wilk normality test	No (p-value = 0.002305 < 0.05)



Analysis movement frequency H6 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Movement_frequency_H6_Zone_1,Movement_frequency_H6_Zone_2) ~ 1 + (1 Genotype_Zone_1 Plant_Zone_1) + (1 Genotype_Zone_2 Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1996	0.1309	0.2922	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

```
REML criterion at convergence: 148

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.0895 -0.7448 -0.1537  0.6849  3.1492

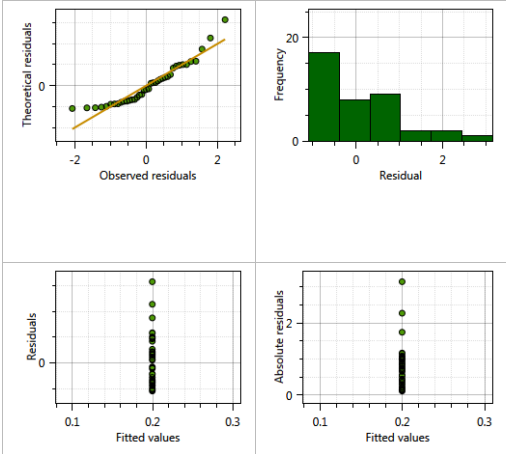
Random effects:
Groups              Name      Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.00    0.00
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.00    0.00
Residual                        85.56    9.25
Number of obs: 39, groups:  Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error   df t value Pr(>|t|)
(Intercept)   -1.389      0.249 38.000  -5.577 2.16e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 9.25
```

Model residuals

Statistic	Value
Sample skewness	1.058
Sample excess kurtosis	1.111
Passed Shapiro Wilk normality test	No (p-value = 0.003135 < 0.05)

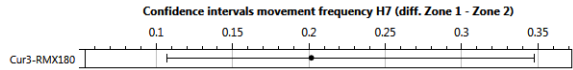


Data points with high residuals

Trial	Arena
Trial 3	11

Analysis movement frequency H7 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Movement_frequency_H7_Zone_1,Movement_frequency_H7_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2015	0.1067	0.3477	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 147.1

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.3494 -0.6825 -0.2940  0.7823  2.0353

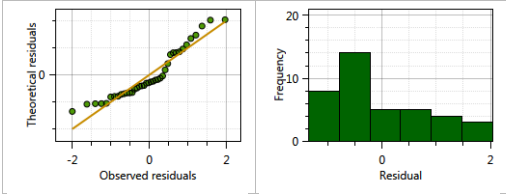
Random effects:
Groups              Name      Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.4005    0.6328
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.1419    0.3767
Residual                        67.8711    8.2384
Number of obs: 39, groups:  Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

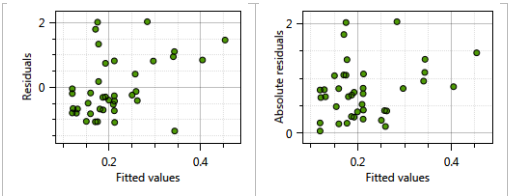
Fixed effects:
              Estimate Std. Error   df t value Pr(>|t|)
(Intercept)   -1.3769      0.3243  8.0078  -4.245 0.00281 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 8.238
```

Model residuals

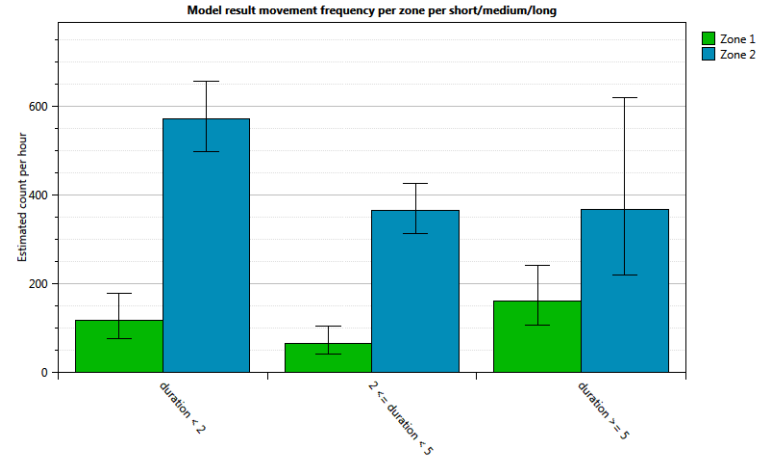
Statistic	Value
Sample skewness	0.8232
Sample excess kurtosis	-0.3231
Passed Shapiro Wilk normality test	No (p-value = 0.003357 < 0.05)





Movement frequency per zone per short/medium/long

Selected zones	Zone 1, Zone 2
Event duration categories	duration < 2, 2 <= duration < 5, duration >= 5
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

Behaviour statistic	Cur3-RMX180	Remark
Movement frequency duration < 2 (diff. Zone 1 - Zone 2)	p=0.000342*** [-1.86, -0.909]	CR
Movement frequency 2 <= duration < 5 (diff. Zone 1 - Zone 2)	p=2.7E-05*** [-2.01, -1.11]	
Movement frequency duration >= 5 (diff. Zone 1 - Zone 2)	p=0.000128*** [-1.18, -0.54]	

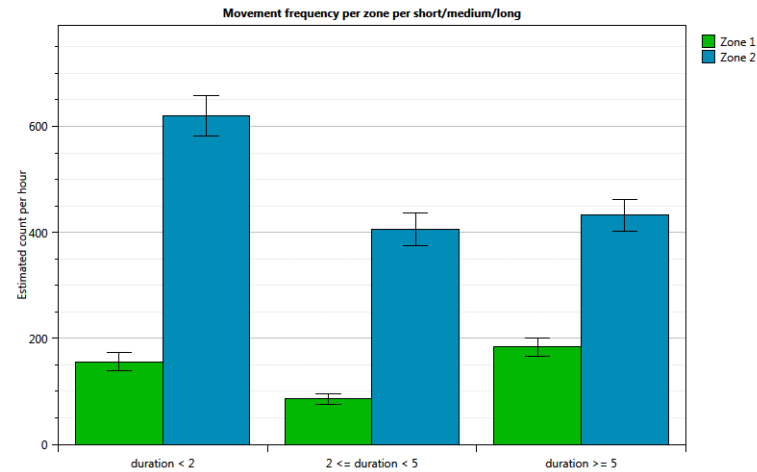
CR = Check residuals

The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Movement frequency (duration < 2 - Zone 1)	116 [75.3, 178]	CR
Movement frequency (2 <= duration < 5 - Zone 1)	64.9 [40.4, 104]	
Movement frequency (duration >= 5 - Zone 1)	160 [107, 241]	CR
Movement frequency (duration < 2 - Zone 2)	572 [498, 657]	
Movement frequency (2 <= duration < 5 - Zone 2)	365 [313, 426]	CR
Movement frequency (duration >= 5 - Zone 2)	368 [219, 619]	

CR = Check residuals

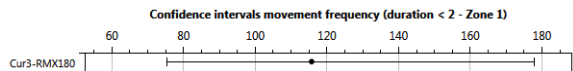
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean duration < 2 - Zone 1	StdErr duration < 2 - Zone 1	Mean 2 <= duration < 5 - Zone 1	StdErr 2 <= duration < 5 - Zone 1	Mean duration >= 5 - Zone 1	StdErr duration >= 5 - Zone 1	Mean duration < 2 - Zone 2	StdErr duration < 2 - Zone 2	Mean 2 <= duration < 5 - Zone 2	StdErr 2 <= duration < 5 - Zone 2	Mean duration >= 5 - Zone 2	StdErr duration >= 5 - Zone 2
Cur3	RMX180	Neutral	155.92	17.86	85.64	10.2	183.41	17.52	619.92	38.16	405.7	30.02	432.36	30.08

Analysis movement frequency (duration < 2 - Zone 1)

Analysis model	Linear mixed model fit by REML: Movement_frequency_duration_2_Zone_1 ~ 1 + (1)Genotype_Zone_1:Plant_Zone_1 + (1)Genotype_Zone_2:Plant_Zone_2
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	115.7	75.25	177.9	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_duration_2_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 110.7

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.9915	-0.2757	0.1980	0.4990	1.2057

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	1.076e-16	1.037e-08
Genotype_Zone_2:Plant_Zone_2	(Intercept)	1.124e-01	3.353e-01
Residual		9.665e-01	9.831e-01

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

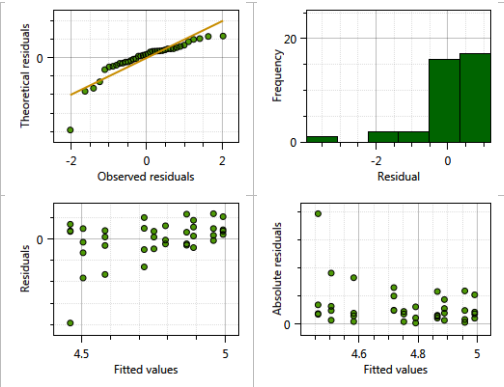
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	4.7511	0.1917	9.5006	24.78	5.93e-10 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

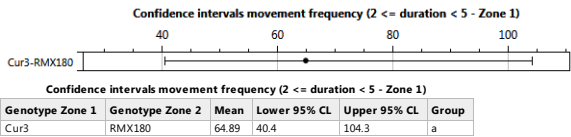
Model residuals

Statistic	Value
Sample skewness	-2.231
Sample excess kurtosis	7.31
Passed Shapiro Wilk normality test	No (p-value = 1.549E-05 < 0.05)



Analysis movement frequency (2 <= duration < 5 - Zone 1)

Analysis model	Linear mixed model fit by REML: Movement_frequency_2_duration_5_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_2_duration_5_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 104.1

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.8906	-0.2335	0.1984	0.5504	1.3423

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.14750	0.3841
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.05295	0.2301
Residual		0.73172	0.8554

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

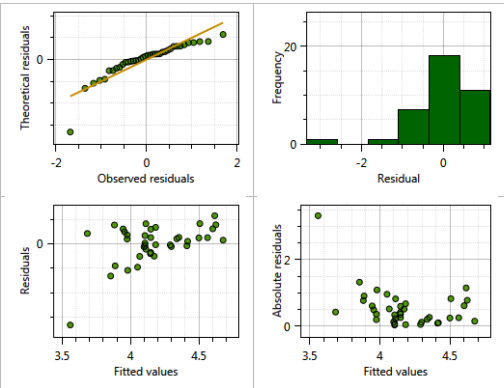
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	4.1728	0.1986	6.6984	21.01	2.3e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

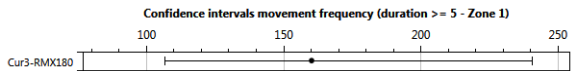
Model residuals

Statistic	Value
Sample skewness	-2.177
Sample excess kurtosis	7.597
Passed Shapiro Wilk normality test	No (p-value = 4.491E-05 < 0.05)



Analysis movement frequency (duration >= 5 - Zone 1)

Analysis model	Linear mixed model fit by REML: Movement_frequency_duration_5_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals movement frequency (duration >= 5 - Zone 1)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	160.2	106.5	240.7	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_duration_5_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 81.9

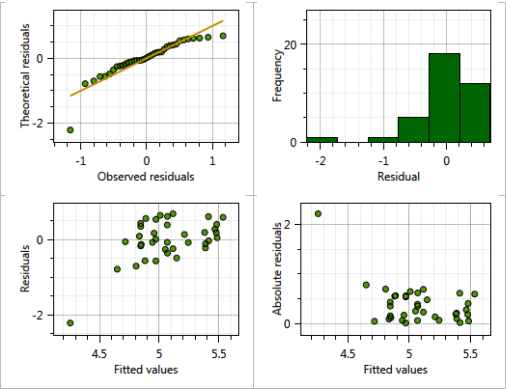
Scaled residuals:
    Min       1Q   Median       3Q      Max
-3.5887 -0.3495  0.0277  0.6395  1.1247

Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.10163  0.3188
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.08903  0.2984
Residual                                0.37968  0.6162
Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    5.0761     0.1721 6.9571  29.49 1.45e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

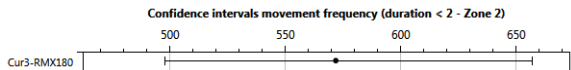
Model residuals

Statistic	Value
Sample skewness	-1.855
Sample excess kurtosis	6.352
Passed Shapiro Wilk normality test	No (p-value = 0.0002255 < 0.05)



Analysis movement frequency (duration < 2 - Zone 2)

Analysis model	Linear mixed model fit by REML: Movement_frequency_duration_2_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals movement frequency (duration < 2 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	571.8	497.6	657.1	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_duration_2_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 47.1

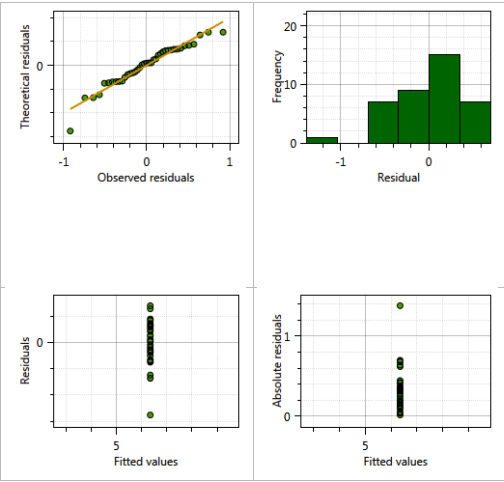
Scaled residuals:
    Min       1Q   Median       3Q      Max
-3.2251 -0.6806  0.1122  0.7484  1.6316

Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.0000  0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.0000  0.0000
Residual                                0.1837  0.4286
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    6.34882     0.06864 38.00000   92.5 <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

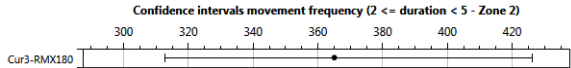
Model residuals

Statistic	Value
Sample skewness	-0.8299
Sample excess kurtosis	1.463
Passed Shapiro Wilk normality test	Yes (p-value = 0.0846 > 0.05)



Analysis movement frequency (2 <= duration < 5 - Zone 2)

Analysis model	Linear mixed model fit by REML: Movement_frequency_2_duration_5_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	365.1	312.7	426.3	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_2_duration_5_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 55.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.8532	-0.5796	-0.1040	0.7626	2.0273

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		0.2287	0.4782

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

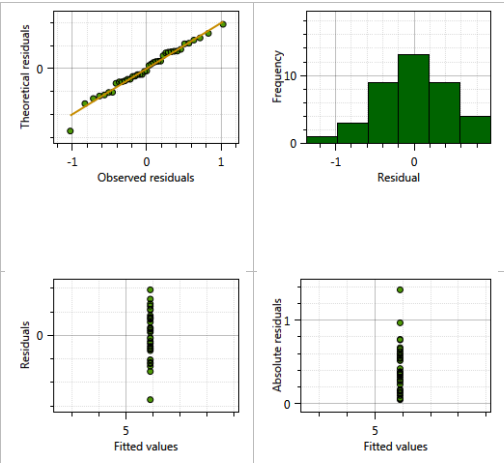
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	5.90012	0.07658	38.00000	77.05	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

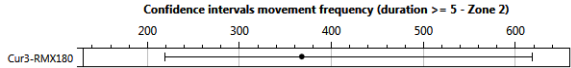
Model residuals

Statistic	Value
Sample skewness	-0.3765
Sample excess kurtosis	0.4729
Passed Shapiro Wilk normality test	Yes (p-value = 0.7817 > 0.05)



Analysis movement frequency (duration >= 5 - Zone 2)

Analysis model	Linear mixed model fit by REML: Movement_frequency_duration_5_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	367.7	218.6	618.6	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_duration_5_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

```
REML criterion at convergence: 81.8

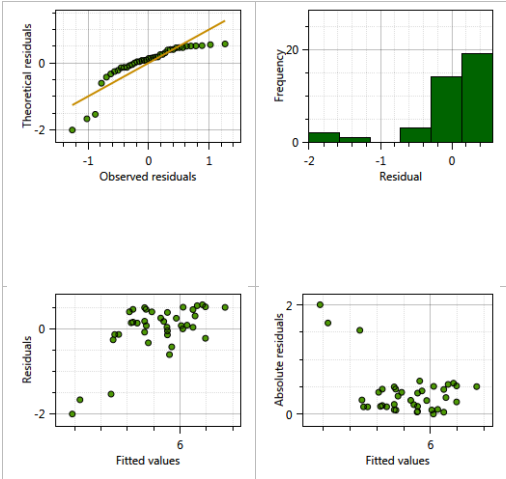
Scaled residuals:
    Min       1Q   Median       3Q      Max
-3.1962 -0.2123  0.2149  0.6371  0.9041

Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.03361  0.1833
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.04472  0.2115
Residual                                0.39390  0.6276
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    5.907      0.134 2.247   44.07  0.00024 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

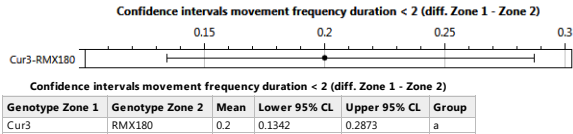
Model residuals

Statistic	Value
Sample skewness	-2.094
Sample excess kurtosis	4.613
Passed Shapiro Wilk normality test	No (p-value = 1.497E-06 < 0.05)



Analysis movement frequency duration < 2 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Movement_frequency_duration_2_Zone_1,Movement_frequency_duration_2_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 112.5

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.49276 -0.57059  0.00217  0.53921  2.39490

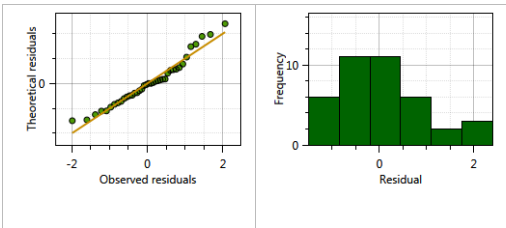
Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.03599  0.1897
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.12768  0.3573
Residual                                107.40165  10.3635
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

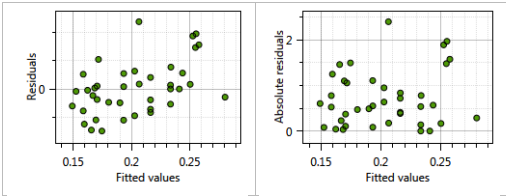
Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   -1.3865      0.1973  6.2677  -7.026  0.000342 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 10.36
```

Model residuals

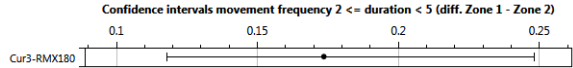
Statistic	Value
Sample skewness	0.6672
Sample excess kurtosis	0.1855
Passed Shapiro Wilk normality test	Yes (p-value = 0.1459 > 0.05)





Analysis movement frequency 2 <= duration < 5 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Movement_frequency_2_duration_5_Zone_1,Movement_frequency_2_duration_5_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals movement frequency 2 <= duration < 5 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1735	0.1178	0.2483	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 109.1

Scaled residuals:
Min 1Q Median 3Q Max
-1.36119 -0.71427 -0.07216 0.55318 1.82377

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.07562 0.2750
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.13474 0.3671
Residual 50.22089 7.0867
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

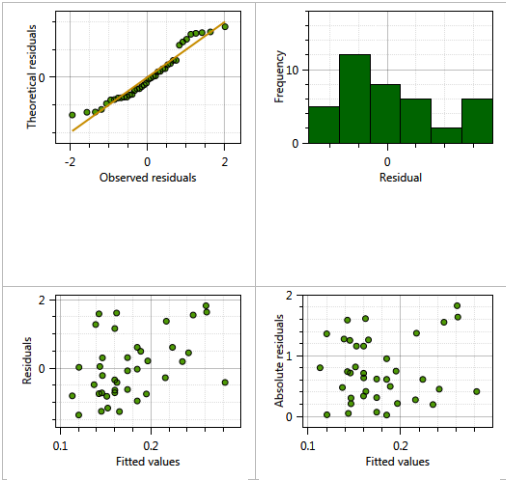
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -1.5608 0.2003 9.0150 -7.793 2.7e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 7.087

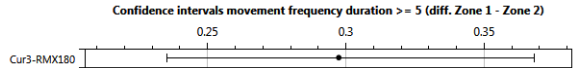
Model residuals

Statistic	Value
Sample skewness	0.4924
Sample excess kurtosis	-0.7928
Passed Shapiro Wilk normality test	No (p-value = 0.02897 < 0.05)



Analysis movement frequency duration >= 5 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Movement_frequency_duration_5_Zone_1,Movement_frequency_duration_5_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals movement frequency duration >= 5 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2974	0.2352	0.3682	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 86.2

Scaled residuals:
Min 1Q Median 3Q Max
-1.6577 -0.8465 -0.1737 0.7169 1.9831

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.04091 0.2023
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.06893 0.2626
Residual 45.88681 6.7740
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

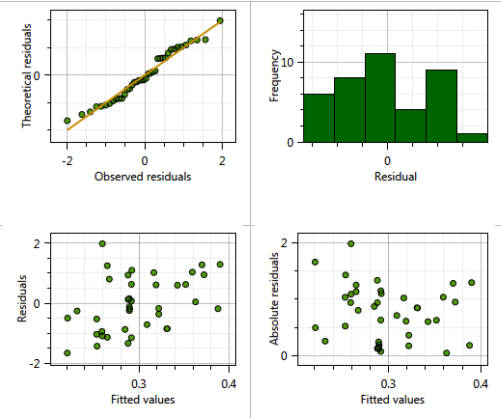
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.8597	0.1437	10.1336	-5.982	0.000128 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 6.774

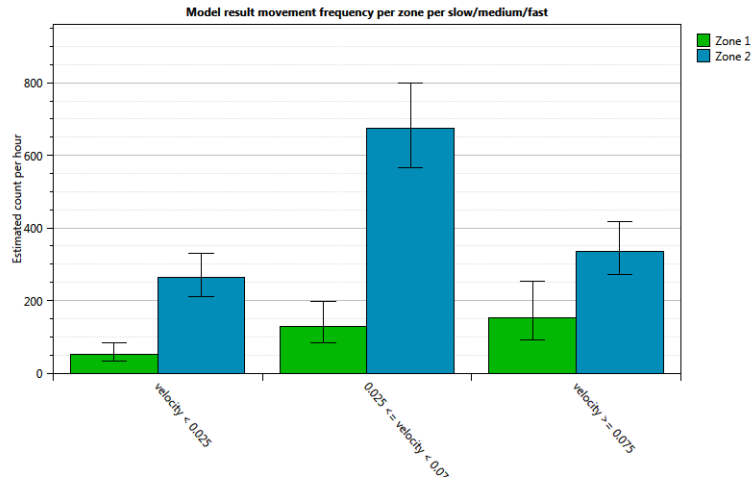
Model residuals

Statistic	Value
Sample skewness	0.1663
Sample excess kurtosis	-0.9196
Passed Shapiro Wilk normality test	Yes (p-value = 0.2829 > 0.05)



Movement frequency per zone per slow/medium/fast

Selected zones	Zone 1, Zone 2
Velocity categories	velocity < 0.025, 0.025 <= velocity < 0.075, velocity >= 0.075
Data transformation	Natural logarithm
Analysis	Zone difference analysis



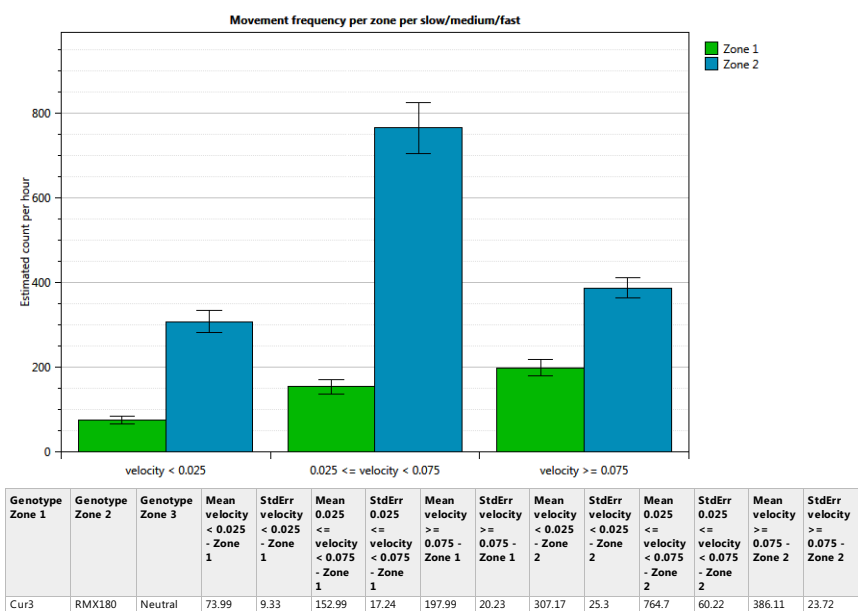
Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.		
Behaviour statistic	Cur3-RMX180	Remark
Movement frequency velocity < 0.025 (diff. Zone 1 - Zone 2)	p=5.69E-05*** [-1.88, -0.958]	CR
Movement frequency 0.025 <= velocity < 0.075 (diff. Zone 1 - Zone 2)	p=7.51E-05*** [-2.1, -1.1]	
Movement frequency velocity >= 0.075 (diff. Zone 1 - Zone 2)	p=3.56E-05*** [-0.897, -0.468]	

CR = Check residuals

The model predictions and 95% confidence intervals for each statistic.		
Statistic	Cur3-RMX180	Remark
Movement frequency (velocity < 0.025 - Zone 1)	51.7 [32.1, 83.4]	CR
Movement frequency (0.025 <= velocity < 0.075 - Zone 1)	129 [83.5, 199]	CR
Movement frequency (velocity >= 0.075 - Zone 1)	153 [92, 254]	CR
Movement frequency (velocity < 0.025 - Zone 2)	264 [211, 330]	
Movement frequency (0.025 <= velocity < 0.075 - Zone 2)	673 [567, 800]	
Movement frequency (velocity >= 0.075 - Zone 2)	336 [271, 417]	CR

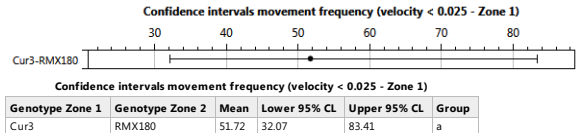
CR = Check residuals

Data summary



Analysis movement frequency (velocity < 0.025 - Zone 1)

Analysis model	Linear mixed model fit by REML: Movement_frequency_velocity_0_025_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_velocity_0_025_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 113.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.1319	-0.2760	0.2319	0.6168	1.2604

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.1892	0.4349
Residual		0.9903	0.9952

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

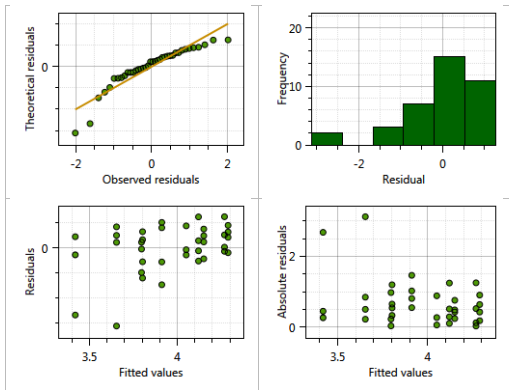
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	3.9459	0.2124	9.3310	18.58	1.1e-08 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

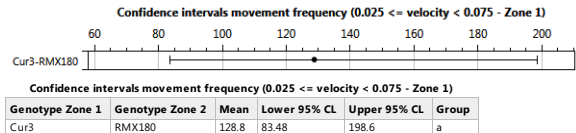
Model residuals

Statistic	Value
Sample skewness	-1.586
Sample excess kurtosis	3.284
Passed Shapiro Wilk normality test	No (p-value = 0.0004368 < 0.05)



Analysis movement frequency (0.025 <= velocity < 0.075 - Zone 1)

Analysis model	Linear mixed model fit by REML: Movement_frequency_velocity_0_025_velocity_0_075_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: Movement_frequency_0.025_velocity_0.075_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 85

Scaled residuals:
Min 1Q Median 3Q Max
-2.43866 -0.22146 -0.01825 0.44274 1.75614

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.1238 0.3519
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.1235 0.3515
Residual 0.3922 0.6263

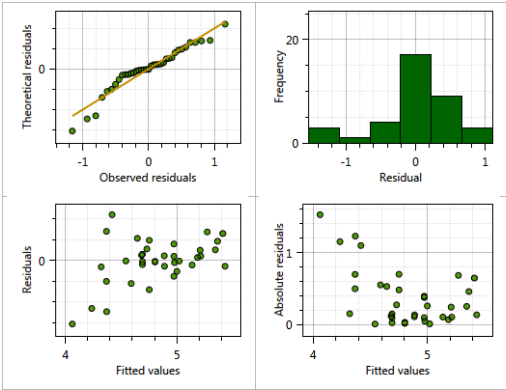
Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 4.8580 0.1889 8.2429 25.71 3.65e-09 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

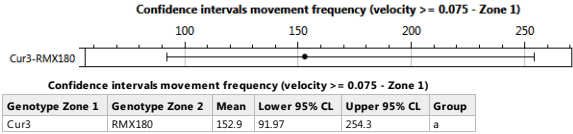
Model residuals

Statistic	Value
Sample skewness	-0.8413
Sample excess kurtosis	1.34
Passed Shapiro Wilk normality test	No (p-value = 0.04054 < 0.05)



Analysis movement frequency (velocity >= 0.075 - Zone 1)

Analysis model	Linear mixed model fit by REML: Movement_frequency_velocity_0.075_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_velocity_0.075_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 108.5

Scaled residuals:
Min 1Q Median 3Q Max
-4.3884 -0.1214 0.0344 0.5302 1.0545

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.17675 0.4204
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.03493 0.1869
Residual 0.83815 0.9155

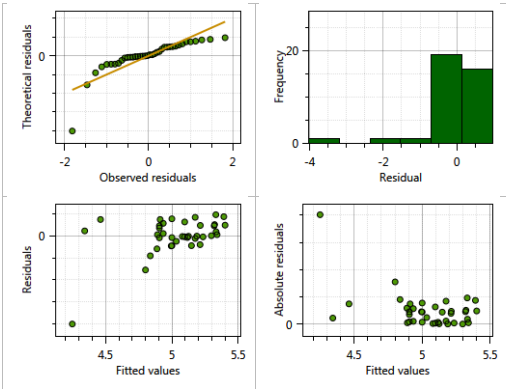
Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 5.0299 0.2083 6.0609 24.15 2.96e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

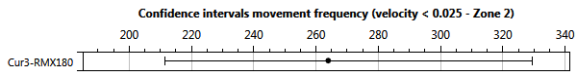
Model residuals

Statistic	Value
Sample skewness	-3.016
Sample excess kurtosis	13.09
Passed Shapiro Wilk normality test	No (p-value = 4.391E-07 < 0.05)



Analysis movement frequency (velocity < 0.025 - Zone 2)

Analysis model	Linear mixed model fit by REML: Movement_frequency_velocity_0_025_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	263.9	211.4	329.5	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_velocity_0_025_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 72.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.7447	-0.6024	0.2925	0.7026	1.7364

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000000	0.00000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.004163	0.06452
Residual		0.352148	0.59342

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

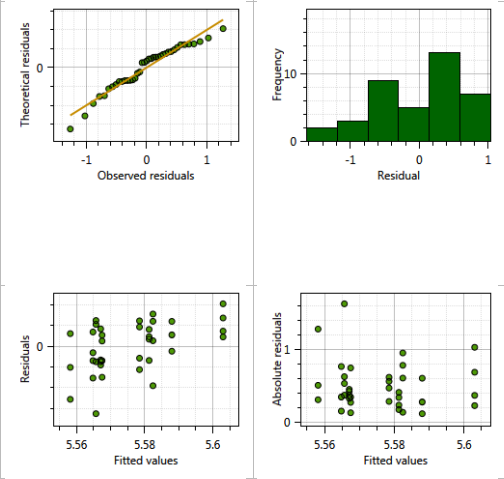
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	5.5756	0.0972	8.4512	57.36	2.99e-12 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

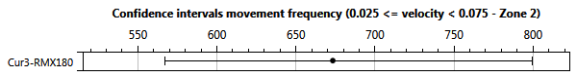
Model residuals

Statistic	Value
Sample skewness	-0.7276
Sample excess kurtosis	0.3187
Passed Shapiro Wilk normality test	Yes (p-value = 0.08693 > 0.05)



Analysis movement frequency (0.025 <= velocity < 0.075 - Zone 2)

Analysis model	Linear mixed model fit by REML: Movement_frequency_0_025_velocity_0_075_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	673.3	566.9	799.7	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_0_025_velocity_0_075_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 63.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.64900	-0.76023	0.04744	0.82343	1.83366

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	3.063e-18	1.750e-09
Genotype_Zone_2:Plant_Zone_2	(Intercept)	1.636e-15	4.045e-08
Residual		2.817e-01	5.308e-01

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

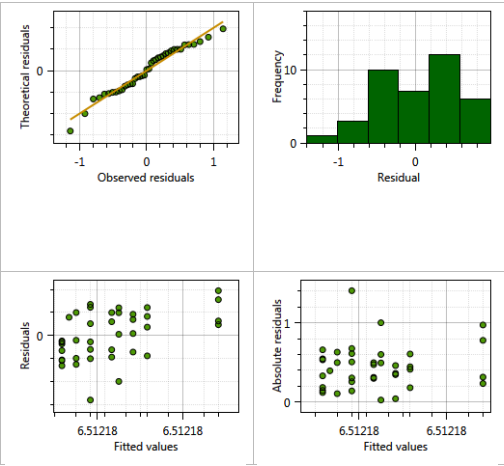
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	6.51218	0.08499	38.00000	76.62	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

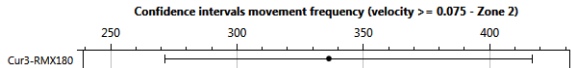
Model residuals

Statistic	Value
Sample skewness	-0.3959
Sample excess kurtosis	-0.1856
Passed Shapiro Wilk normality test	Yes (p-value = 0.3295 > 0.05)



Analysis movement frequency (velocity >= 0.075 - Zone 2)

Analysis model	Linear mixed model fit by REML: Movement_frequency_velocity_0.075_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals movement frequency (velocity >= 0.075 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	336.4	271.3	416.9	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Movement_frequency_velocity_0.075_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 80.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.6947	-0.1254	0.2652	0.5293	1.0817

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000	0.0000
Residual		0.439	0.6626

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

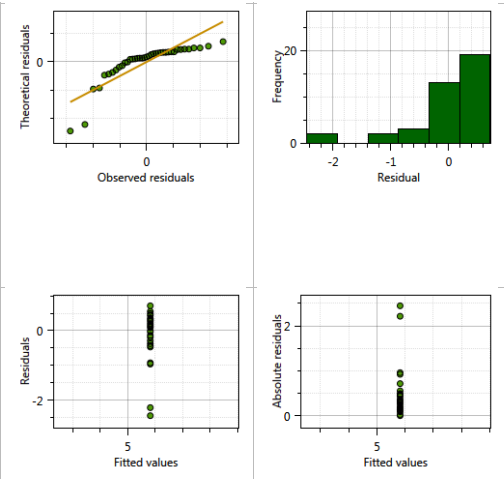
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	5.8182	0.1061	38.0000	54.84	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

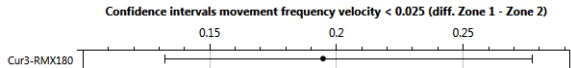
Model residuals

Statistic	Value
Sample skewness	-2.48
Sample excess kurtosis	6.739
Passed Shapiro Wilk normality test	No (p-value = 2.085E-07 < 0.05)



Analysis movement frequency velocity < 0.025 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Movement_frequency_velocity_0.025_Zone_1,Movement_frequency_velocity_0.025_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals movement frequency velocity < 0.025 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1947	0.1322	0.2773	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziformula
Data: data

Weights: wi

REML criterion at convergence: 122.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.27934	-0.67344	-0.03325	0.56201	2.30716

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.125	0.3536
Residual		67.620	8.2231

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

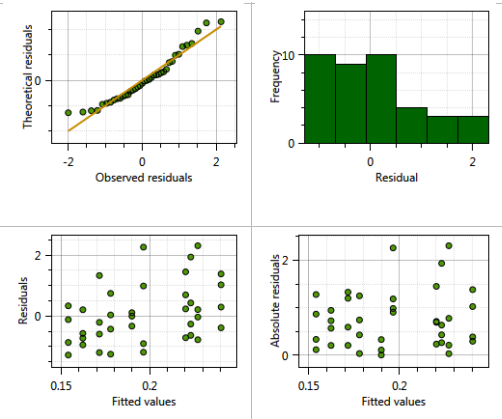
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.4198	0.2056	9.3900	-6.906	5.69e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 8.223

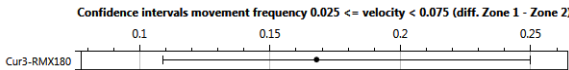
Model residuals

Statistic	Value
Sample skewness	0.7285
Sample excess kurtosis	-0.09359
Passed Shapiro Wilk normality test	No (p-value = 0.04083 < 0.05)



Analysis movement frequency 0.025 <= velocity < 0.075 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Movement_frequency_0_025_velocity_0_075_Zone_1,Movement_frequency_0_025_velocity_0_075_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals movement frequency 0.025 <= velocity < 0.075 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1678	0.1088	0.2499	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: ziFormula

Data: data

Weights: wi

REML criterion at convergence: 117.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.33509	-0.65226	0.03052	0.65600	2.25225

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.07596	0.2756
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.15497	0.3937
Residual		118.65865	10.8931

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

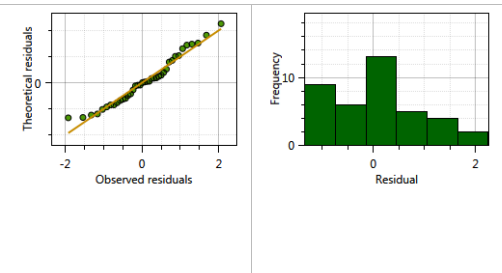
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.6010	0.2183	8.1228	-7.334	7.51e-05 ***

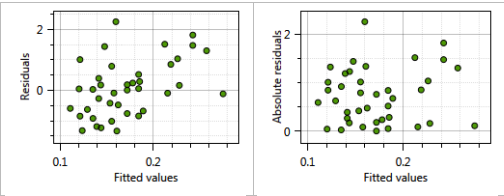
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 10.89

Model residuals

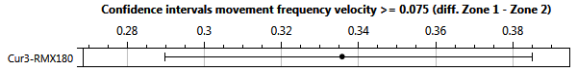
Statistic	Value
Sample skewness	0.4601
Sample excess kurtosis	-0.4624
Passed Shapiro Wilk normality test	Yes (p-value = 0.2195 > 0.05)





Analysis movement frequency velocity >= 0.075 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Movement_frequency_velocity_0.075_Zone_1,Movement_frequency_velocity_0.075_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals movement frequency velocity >= 0.075 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.3357	0.2897	0.3851	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 61.8

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.92929 -0.77525 -0.07534  0.44550  2.21891

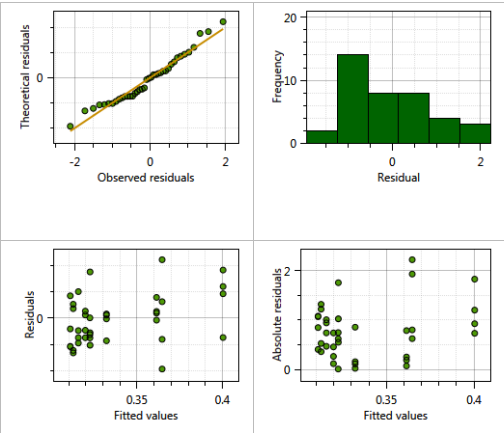
Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.03948 0.1987
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.00000 0.0000
Residual                                25.93783 5.0929
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error      df t value Pr(>|t|)
(Intercept) -0.68238    0.09605    9.84397  -7.105 3.56e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 5.093
```

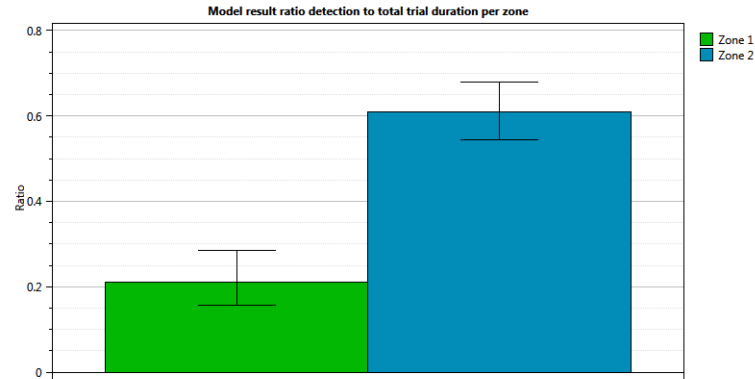
Model residuals

Statistic	Value
Sample skewness	0.5562
Sample excess kurtosis	-0.07423
Passed Shapiro Wilk normality test	Yes (p-value = 0.2294 > 0.05)



Ratio detection to total trial duration per zone

Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

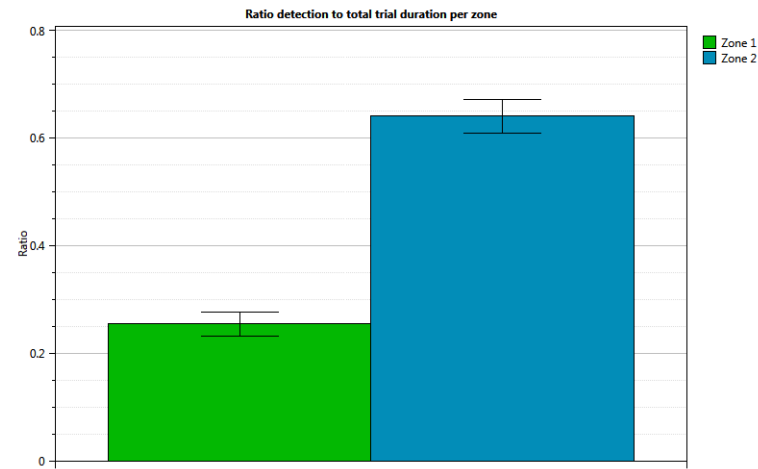
Behaviour statistic	Cur3-RMX180
Ratio detection to total trial duration (diff. Zone 1 - Zone 2)	p=0.00172** [-1.31, -0.541]

The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Ratio detection to total trial duration (Zone 1)	0.211 [0.156, 0.285]	CR
Ratio detection to total trial duration (Zone 2)	0.608 [0.544, 0.68]	

CR = Check residuals

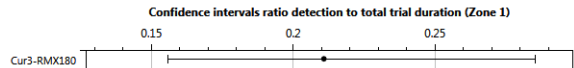
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean Zone 1	StdErr Zone 1	Mean Zone 2	StdErr Zone 2
Cur3	RMX180	Neutral	0.25	0.02	0.64	0.03

Analysis ratio detection to total trial duration (Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_detection_to_total_trial_duration_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2108	0.1557	0.2854	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_detection_to_total_trial_duration_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 92

Scaled residuals:
Min 1Q Median 3Q Max
-3.7942 -0.2809 0.2333 0.6354 1.2494

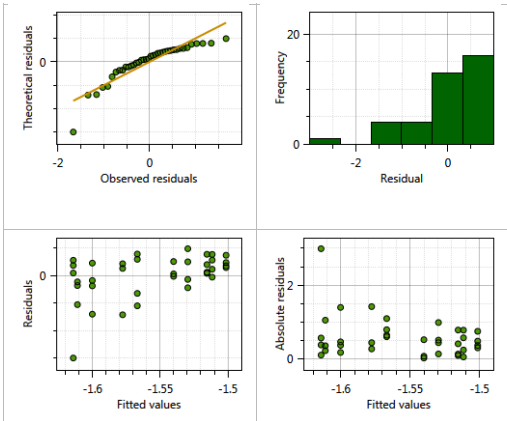
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.00000 0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.01829 0.1352
Residual 0.62139 0.7883
Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -1.5569 0.1349 9.4157 -11.54 7.23e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

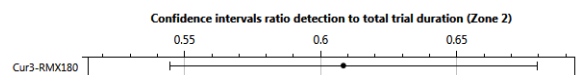
Model residuals

Statistic	Value
Sample skewness	-1.877
Sample excess kurtosis	4.855
Passed Shapiro Wilk normality test	No (p-value = 8.164E-05 < 0.05)



Analysis ratio detection to total trial duration (Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_detection_to_total_trial_duration_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.6083	0.5445	0.6796	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_detection_to_total_trial_duration_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) +
(1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 29.9

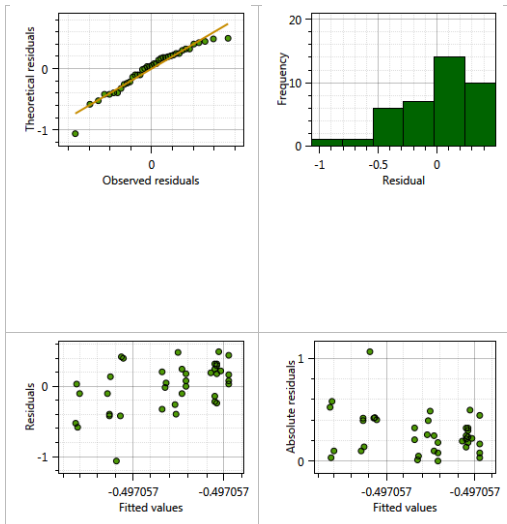
Scaled residuals:
    Min       1Q   Median       3Q      Max
-3.1105 -0.6627  0.1485  0.6891  1.4537

Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  5.168e-16  2.273e-08
Genotype_Zone_2:Plant_Zone_2 (Intercept)  2.150e-17  4.637e-09
Residual                                1.169e-01  3.419e-01
Number of obs: 39, groups:  Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -0.49706     0.05475  38.00000  -9.078  4.67e-11 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

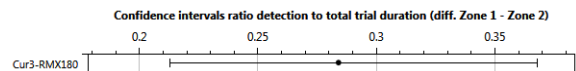
Model residuals

Statistic	Value
Sample skewness	-0.8693
Sample excess kurtosis	0.95
Passed Shapiro Wilk normality test	Yes (p-value = 0.05879 > 0.05)



Analysis ratio detection to total trial duration (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_detection_to_total_trial_duration_Zone_1,Ratio_detection_to_total_trial_duration_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.284	0.2127	0.368	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 99.5

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.7183 -0.6320  0.0032  0.7057  2.0312

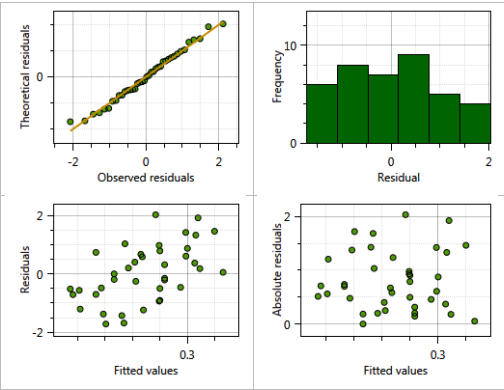
Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.009055  0.09516
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.032352  0.17987
Residual                                0.125427  0.35416
Number of obs: 39, groups:  Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -0.9248     0.1478   4.8410  -6.256  0.00172 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.3542
```

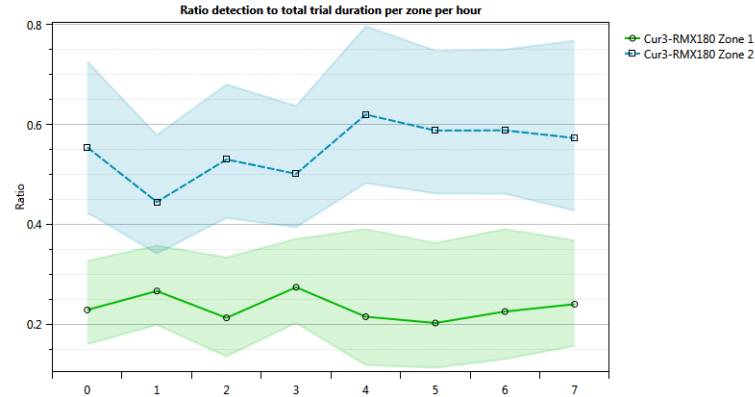
Model residuals

Statistic	Value
Sample skewness	0.1266
Sample excess kurtosis	-0.6308
Passed Shapiro Wilk normality test	Yes (p-value = 0.7825 > 0.05)



Ratio detection to total trial duration per zone per hour

Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

Behaviour statistic	Cur3-RMX180	Remark
Ratio detection to total trial duration H0 (diff. Zone 1 - Zone 2)	p=0.000125*** [-1.28, -0.457]	CR
Ratio detection to total trial duration H1 (diff. Zone 1 - Zone 2)	p=0.0181* [-0.864, -0.0857]	
Ratio detection to total trial duration H2 (diff. Zone 1 - Zone 2)	p=0.0191* [-1.32, -0.152]	CR
Ratio detection to total trial duration H3 (diff. Zone 1 - Zone 2)	p=0.013* [-1.31, -0.202]	CR
Ratio detection to total trial duration H4 (diff. Zone 1 - Zone 2)	p=0.02* [-1.62, -0.2]	CR
Ratio detection to total trial duration H5 (diff. Zone 1 - Zone 2)	p=3.09E-05**** [-1.62, -0.648]	CR
Ratio detection to total trial duration H6 (diff. Zone 1 - Zone 2)	p=3.4E-05**** [-1.66, -0.661]	CR
Ratio detection to total trial duration H7 (diff. Zone 1 - Zone 2)	p=0.00444** [-1.86, -0.533]	CR

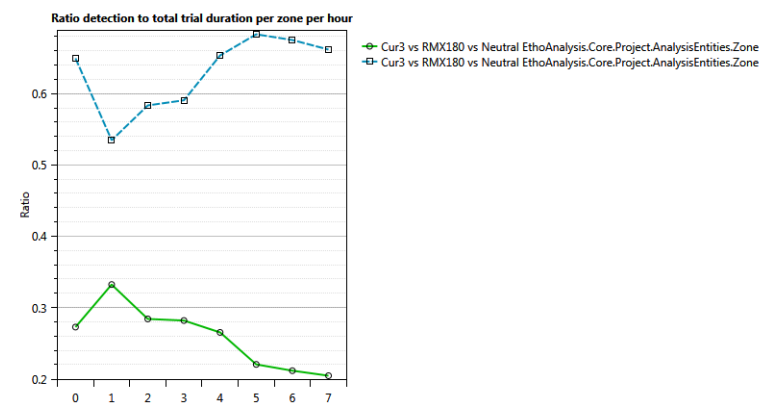
CR = Check residuals

The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Ratio detection to total trial duration (H0 - Zone 1)	0.229 [0.16, 0.327]	CR
Ratio detection to total trial duration (H0 - Zone 2)	0.554 [0.423, 0.726]	CR
Ratio detection to total trial duration (H1 - Zone 1)	0.267 [0.199, 0.358]	CR
Ratio detection to total trial duration (H1 - Zone 2)	0.445 [0.342, 0.579]	CR
Ratio detection to total trial duration (H2 - Zone 1)	0.213 [0.136, 0.334]	
Ratio detection to total trial duration (H2 - Zone 2)	0.53 [0.413, 0.68]	CR
Ratio detection to total trial duration (H3 - Zone 1)	0.274 [0.203, 0.371]	
Ratio detection to total trial duration (H3 - Zone 2)	0.501 [0.394, 0.637]	CR
Ratio detection to total trial duration (H4 - Zone 1)	0.215 [0.119, 0.391]	
Ratio detection to total trial duration (H4 - Zone 2)	0.62 [0.483, 0.796]	CR
Ratio detection to total trial duration (H5 - Zone 1)	0.203 [0.113, 0.363]	CR
Ratio detection to total trial duration (H5 - Zone 2)	0.588 [0.462, 0.748]	CR
Ratio detection to total trial duration (H6 - Zone 1)	0.226 [0.13, 0.391]	
Ratio detection to total trial duration (H6 - Zone 2)	0.588 [0.461, 0.75]	CR
Ratio detection to total trial duration (H7 - Zone 1)	0.24 [0.157, 0.368]	CR
Ratio detection to total trial duration (H7 - Zone 2)	0.573 [0.427, 0.768]	CR

CR = Check residuals

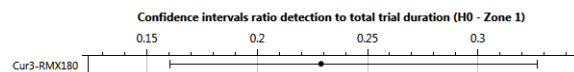
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean H0 - Zone 1	StdErr H0 - Zone 1	Mean H0 - Zone 2	StdErr H0 - Zone 2	Mean H1 - Zone 1	StdErr H1 - Zone 1	Mean H1 - Zone 2	StdErr H1 - Zone 2	Mean H2 - Zone 1	StdErr H2 - Zone 1	Mean H2 - Zone 2	StdErr H2 - Zone 2	Mean H3 - Zone 1	StdErr H3 - Zone 1	Mean H3 - Zone 2	StdErr H3 - Zone 2	Mean H4 - Zone 1	StdErr H4 - Zone 1	Mean H4 - Zone 2	StdErr H4 - Zone 2	Mean H5 - Zone 1	StdErr H5 - Zone 1	Mean H5 - Zone 2	StdErr H5 - Zone 2	Mean H6 - Zone 1	StdErr H6 - Zone 1	Mean H6 - Zone 2	StdErr H6 - Zone 2
Cur3	RMX180	Neutral	0.27	0.04	0.65	0.04	0.33	0.04	0.53	0.04	0.28	0.04	0.58	0.05	0.28	0.04	0.59	0.05	0.27	0.05	0.65	0.05	0.22	0.04	0.68	0.05	0.21	0.04	0.68	0.05

Analysis ratio detection to total trial duration (H0 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_detection_to_total_trial_duration_H0_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio detection to total trial duration (H0 - Zone 1)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2289	0.1602	0.327	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_detection_to_total_trial_duration_H0_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 94.7

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.1115	-0.4201	0.2351	0.7360	1.3933

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000	0.000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000	0.000
Residual		1.012	1.006

Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

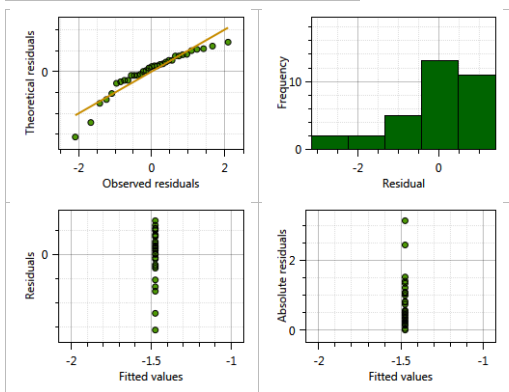
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.4745	0.1752	32.0000	-8.418	1.28e-09 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

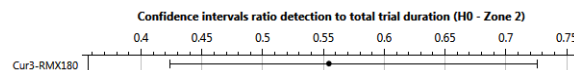
Model residuals

Statistic	Value
Sample skewness	-1.381
Sample excess kurtosis	2.317
Passed Shapiro Wilk normality test	No (p-value = 0.004081 < 0.05)



Analysis ratio detection to total trial duration (H0 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_detection_to_total_trial_duration_H0_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio detection to total trial duration (H0 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5544	0.4234	0.726	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_detection_to_total_trial_duration_H0_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 86.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.9904	-0.3409	0.2473	0.6244	0.9084

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.01107	0.1052
Residual		0.51238	0.7158

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

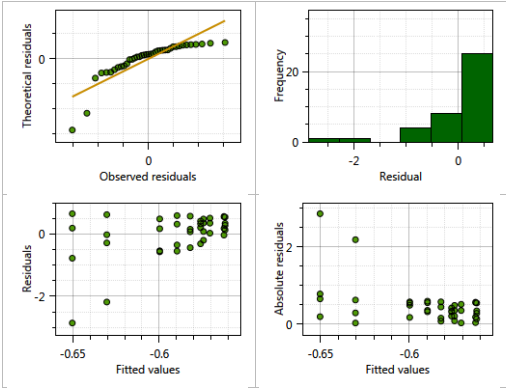
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.5898	0.1194	9.0852	-4.941	0.000779 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

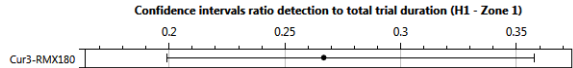
Model residuals

Statistic	Value
Sample skewness	-2.55
Sample excess kurtosis	7.848
Passed Shapiro Wilk normality test	No (p-value = 3.993E-07 < 0.05)



Analysis ratio detection to total trial duration (H1 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_detection_to_total_trial_duration_H1_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2667	0.1989	0.3578	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_detection_to_total_trial_duration_H1_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 96.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.7283	-0.3852	0.2067	0.6905	1.5004

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		0.7757	0.8807

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

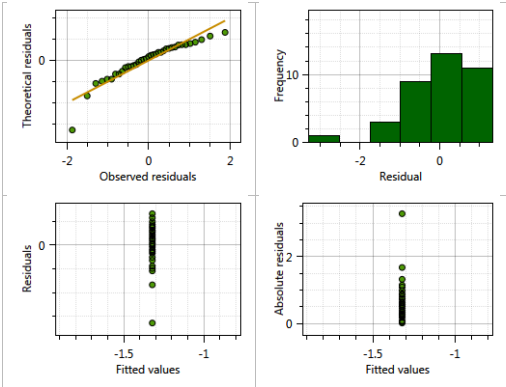
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.3215	0.1448	36.0000	-9.127	6.73e-11 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

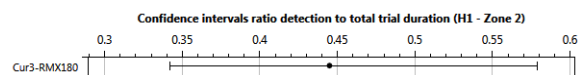
Model residuals

Statistic	Value
Sample skewness	-1.561
Sample excess kurtosis	4.163
Passed Shapiro Wilk normality test	No (p-value = 0.002193 < 0.05)



Analysis ratio detection to total trial duration (H1 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_detection_to_total_trial_duration_H1_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4449	0.3418	0.579	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method [`lmerModLmerTest`]
Formula: `Ratio_detection_to_total_trial_duration_H1_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)`
Data: data

REML criterion at convergence: 92.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.3629	-0.3870	0.3200	0.6346	1.0101

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000	0.0000
Residual		0.643	0.8019

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

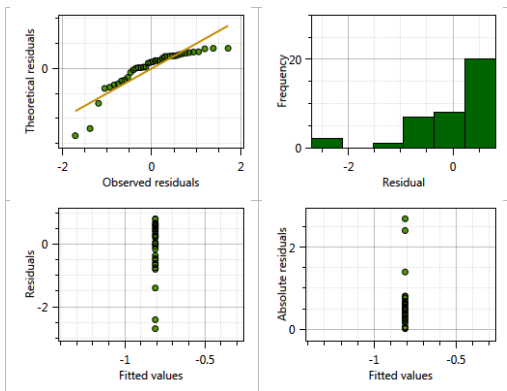
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.8100	0.1301	37.0000	-6.227	3.1e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

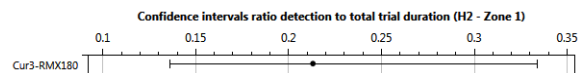
Model residuals

Statistic	Value
Sample skewness	-1.894
Sample excess kurtosis	3.974
Passed Shapiro Wilk normality test	No (p-value = 1.233E-05 < 0.05)



Analysis ratio detection to total trial duration (H2 - Zone 1)

Analysis model	Linear mixed model fit by REML: <code>Ratio_detection_to_total_trial_duration_H2_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)</code>
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2131	0.1359	0.334	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method [`lmerModLmerTest`]
Formula: `Ratio_detection_to_total_trial_duration_H2_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)`
Data: data

REML criterion at convergence: 92.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.90355	-0.77323	0.07446	0.59519	1.68757

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.2239	0.4732
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		0.5584	0.7473

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

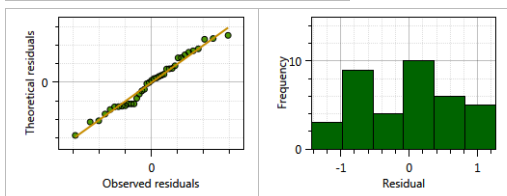
Fixed effects:

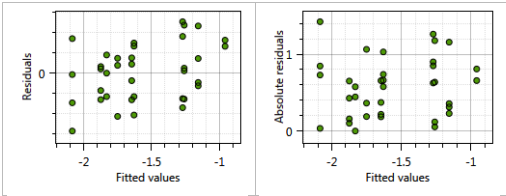
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.5461	0.1945	7.8868	-7.949	4.95e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

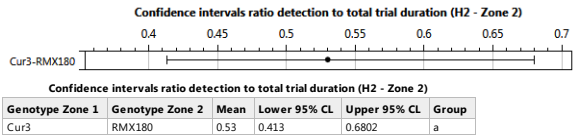
Statistic	Value
Sample skewness	0.03008
Sample excess kurtosis	-0.8086
Passed Shapiro Wilk normality test	Yes (p-value = 0.5394 > 0.05)





Analysis ratio detection to total trial duration (H2 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_detection_to_total_trial_duration_H2_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_detection_to_total_trial_duration_H2_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 74.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.9198	-0.1466	0.3677	0.6390	1.0315

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.004643	0.06814
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000000	0.00000
Residual		0.412281	0.64209

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

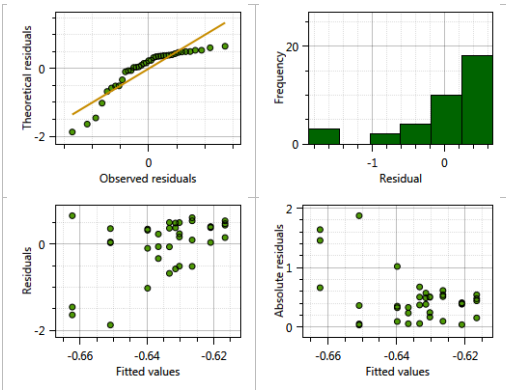
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.6349	0.1078	7.8205	-5.891	0.000398 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

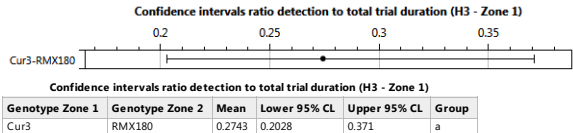
Model residuals

Statistic	Value
Sample skewness	-1.587
Sample excess kurtosis	1.977
Passed Shapiro Wilk normality test	No (p-value = 2.174E-05 < 0.05)



Analysis ratio detection to total trial duration (H3 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_detection_to_total_trial_duration_H3_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_detection_to_total_trial_duration_H3_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 71.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.6093	-0.6155	0.1061	0.6392	1.5419

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	4.599e-18	2.145e-09
Genotype_Zone_2:Plant_Zone_2	(Intercept)	1.341e-02	1.158e-01
Residual		5.106e-01	7.146e-01

Number of obs: 32, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

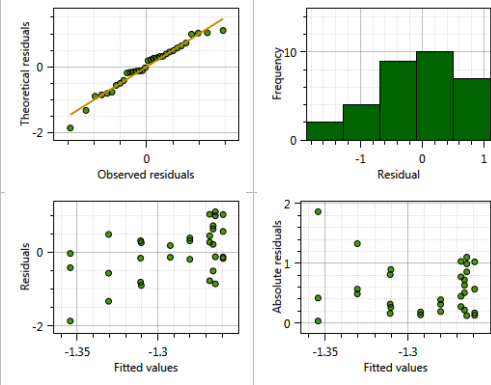
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.2936	0.1318	8.2898	-9.816	7.58e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

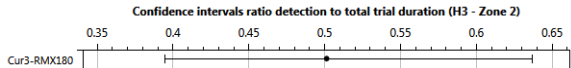
Model residuals

Statistic	Value
Sample skewness	-0.5762
Sample excess kurtosis	0.2564
Passed Shapiro Wilk normality test	Yes (p-value = 0.3726 > 0.05)



Analysis ratio detection to total trial duration (H3 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_detection_to_total_trial_duration_H3_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5012	0.3944	0.637	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_detection_to_total_trial_duration_H3_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 78.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.4777	-0.4240	0.1801	0.7568	1.0724

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000000	0.00000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.004121	0.06419
Residual		0.417374	0.64604

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

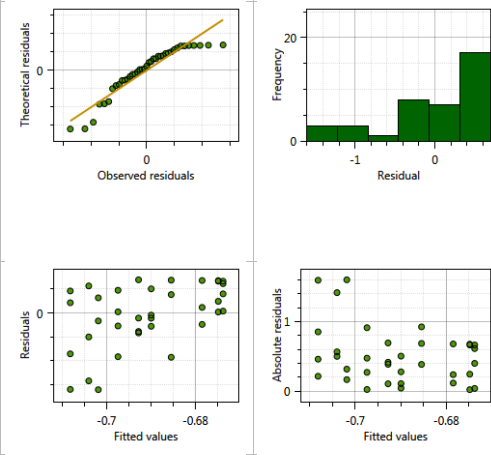
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.6907	0.1054	8.7070	-6.551	0.000122 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

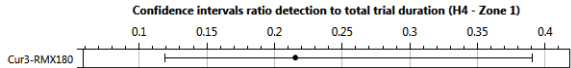
Model residuals

Statistic	Value
Sample skewness	-1.074
Sample excess kurtosis	0.5468
Passed Shapiro Wilk normality test	No (p-value = 0.0007359 < 0.05)



Analysis ratio detection to total trial duration (H4 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_detection_to_total_trial_duration_H4_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2154	0.1187	0.3906	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_detection_to_total_trial_duration_H4_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 88.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.53383	-0.45489	-0.06424	0.59276	1.67802

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.2857	0.5345
Residual		0.8921	0.9445

Number of obs: 30, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

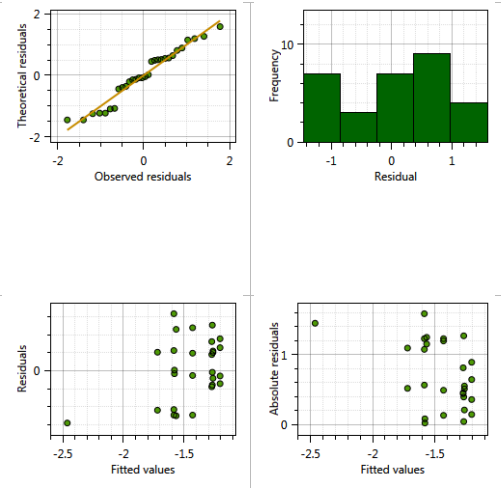
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.5355	0.2436	6.0203	-6.304	0.000733 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

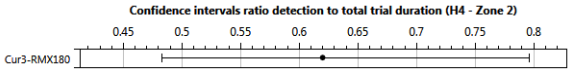
Model residuals

Statistic	Value
Sample skewness	-0.1622
Sample excess kurtosis	-0.9099
Passed Shapiro Wilk normality test	Yes (p-value = 0.1648 > 0.05)



Analysis ratio detection to total trial duration (H4 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_detection_to_total_trial_duration_H4_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.6199	0.4825	0.7964	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_detection_to_total_trial_duration_H4_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 59.5

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.1287	-0.4517	0.2667	0.6606	1.0981

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.03251	0.1803
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.02458	0.1568
Residual		0.23127	0.4809

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

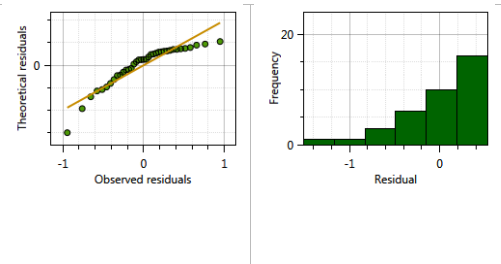
Fixed effects:

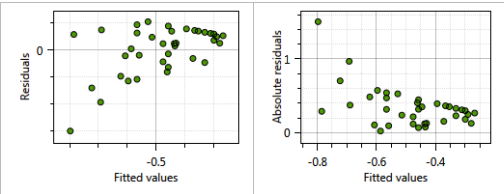
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.4782	0.1098	8.5227	-4.355	0.00209 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

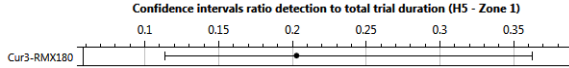
Statistic	Value
Sample skewness	-1.482
Sample excess kurtosis	2.477
Passed Shapiro Wilk normality test	No (p-value = 0.0003936 < 0.05)





Analysis ratio detection to total trial duration (H5 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_detection_to_total_trial_duration_H5_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio detection to total trial duration (H5 - Zone 1)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2028	0.1133	0.3628	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_detection_to_total_trial_duration_H5_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 86.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.4516	-0.4766	0.2782	0.6566	1.3289

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.3009	0.5485
Residual		0.9346	0.9668

Number of obs: 29, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

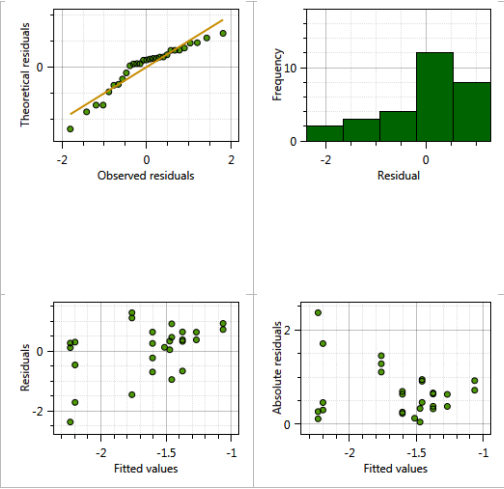
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.5957	0.2522	7.9901	-6.326	0.000227 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

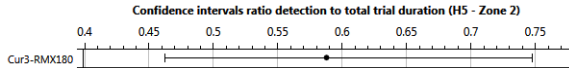
Model residuals

Statistic	Value
Sample skewness	-1.063
Sample excess kurtosis	0.6642
Passed Shapiro Wilk normality test	No (p-value = 0.0133 < 0.05)



Analysis ratio detection to total trial duration (H5 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_detection_to_total_trial_duration_H5_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio detection to total trial duration (H5 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5878	0.462	0.7478	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_detection_to_total_trial_duration_H5_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 76.5

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.5891	-0.3794	0.4274	0.7686	0.9352

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	1.156e-16	1.075e-08
Genotype_Zone_2:Plant_Zone_2	(Intercept)	1.463e-02	1.209e-01
Residual		3.851e-01	6.206e-01

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

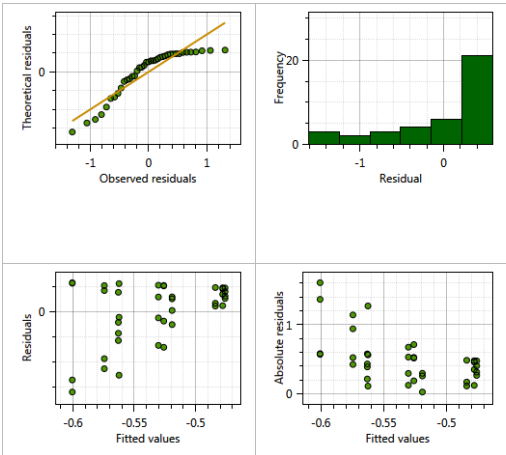
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.5314	0.1065	9.0462	-4.989	0.000739 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

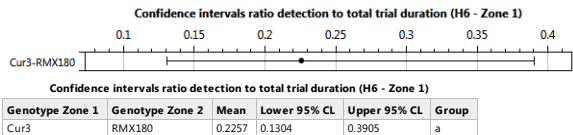
Model residuals

Statistic	Value
Sample skewness	-1.215
Sample excess kurtosis	0.4714
Passed Shapiro Wilk normality test	No (p-value = 4.342E-05 < 0.05)



Analysis ratio detection to total trial duration (H6 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_detection_to_total_trial_duration_H6_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



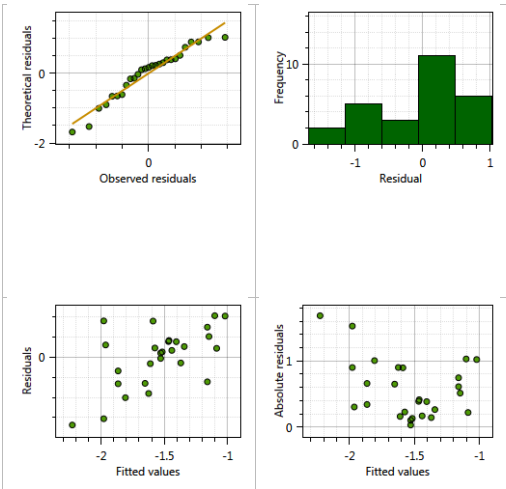
Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_detection_to_total_trial_duration_H6_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data
REML criterion at convergence: 73.3
Scaled residuals:
Min IQ Median 3Q Max
-2.0698 -0.5853 0.2072 0.4936 1.2656
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.08166 0.2858
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.17827 0.4222
Residual 0.66201 0.8136
Number of obs: 27, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -1.4886 0.2302 6.7571 -6.466 4e-04 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

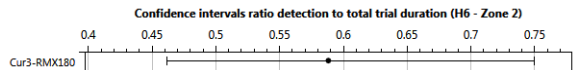
Model residuals

Statistic	Value
Sample skewness	-0.705
Sample excess kurtosis	0.04792
Passed Shapiro Wilk normality test	Yes (p-value = 0.1392 > 0.05)



Analysis ratio detection to total trial duration (H6 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_detection_to_total_trial_duration_H6_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio detection to total trial duration (H6 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5881	0.4613	0.7498	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_detection_to_total_trial_duration_H6_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 86.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.0268	-0.3563	0.3108	0.7183	0.7183

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.000
Residual		0.5461	0.739

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

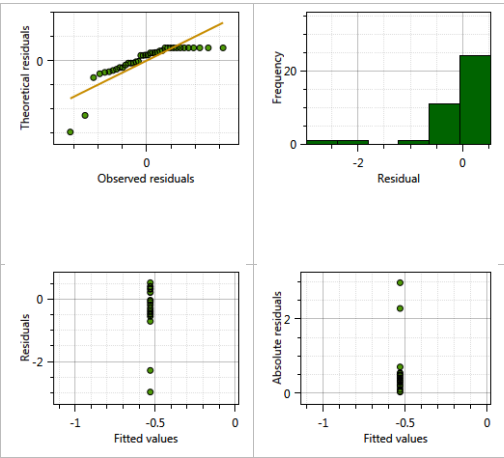
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.5308	0.1199	37.0000	-4.428	8.13e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

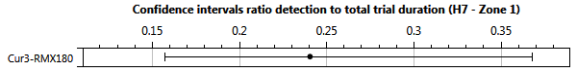
Model residuals

Statistic	Value
Sample skewness	-2.618
Sample excess kurtosis	8.16
Passed Shapiro Wilk normality test	No (p-value = 1.17E-07 < 0.05)



Analysis ratio detection to total trial duration (H7 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_detection_to_total_trial_duration_H7_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio detection to total trial duration (H7 - Zone 1)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2404	0.1571	0.368	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_detection_to_total_trial_duration_H7_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 60.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.8253	-0.8450	0.1462	0.8812	1.2143

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.1338	0.3658
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Residual		0.4729	0.6877

Number of obs: 26, groups: Genotype_Zone_2:Plant_Zone_2, 10; Genotype_Zone_1:Plant_Zone_1, 9

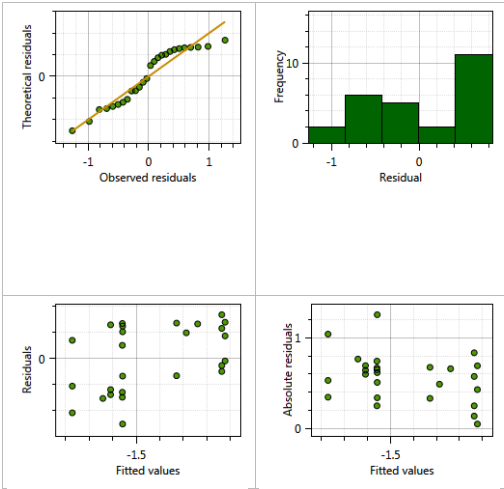
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.4254	0.1831	7.6338	-7.787	6.84e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

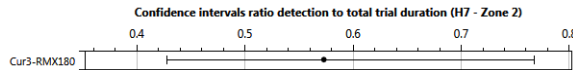
Model residuals

Statistic	Value
Sample skewness	-0.3609
Sample excess kurtosis	-1.277
Passed Shapiro Wilk normality test	No (p-value = 0.01941 < 0.05)



Analysis ratio detection to total trial duration (H7 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_detection_to_total_trial_duration_H7_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5729	0.4275	0.7678	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_detection_to_total_trial_duration_H7_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 72.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.4722	-0.5564	0.2865	0.9194	0.9337

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0005236	0.02288
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0001804	0.01343
Residual		0.3586888	0.59891

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

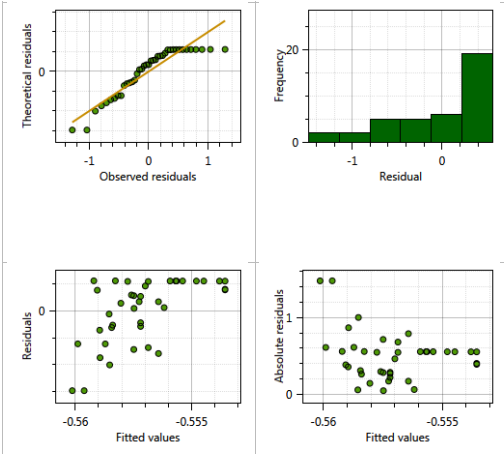
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.55704	0.09627	3.26481	-5.786	0.0081 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

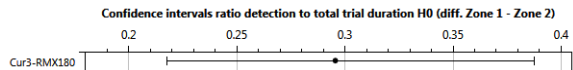
Model residuals

Statistic	Value
Sample skewness	-0.9717
Sample excess kurtosis	0.0272
Passed Shapiro Wilk normality test	No (p-value = 0.0001446 < 0.05)



Analysis ratio detection to total trial duration H0 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_detection_to_total_trial_duration_H0_Zone_1,Ratio_detection_to_total_trial_duration_H0_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2955	0.2175	0.3877	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziformula
Data: data

Weights: wi

REML criterion at convergence: 129.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.1641	-0.8159	-0.1309	0.6177	2.5983

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		0.3096	0.5564

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

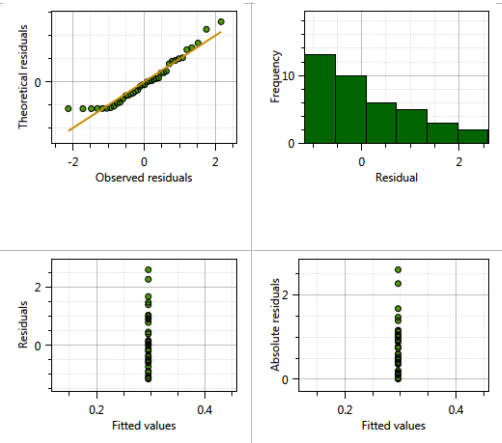
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.8687	0.2033	38.0000	-4.273	0.000125 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.5564

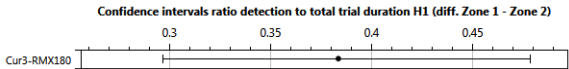
Model residuals

Statistic	Value
Sample skewness	0.7694
Sample excess kurtosis	0.03535
Passed Shapiro Wilk normality test	No (p-value = 0.01346 < 0.05)



Analysis ratio detection to total trial duration H1 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_detection_to_total_trial_duration_H1_Zone_1,Ratio_detection_to_total_trial_duration_H1_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals ratio detection to total trial duration H1 (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.3835	0.2965	0.4786	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: ziFormula

Data: data

Weights: wi

REML criterion at convergence: 125.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.4522	-0.7141	-0.1003	0.7887	2.3348

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	3.832e-17	6.191e-09
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000e+00	0.000e+00
Residual		2.949e-01	5.431e-01

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

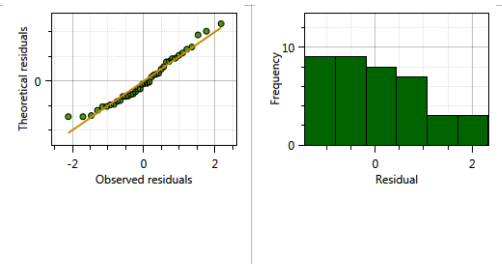
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.4748	0.1922	38.0000	-2.47	0.0181 *

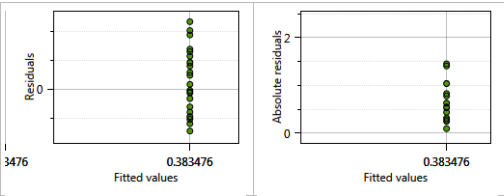
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.5431

Model residuals

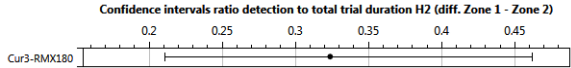
Statistic	Value
Sample skewness	0.5024
Sample excess kurtosis	-0.4993
Passed Shapiro Wilk normality test	Yes (p-value = 0.1762 > 0.05)





Analysis ratio detection to total trial duration H2 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_detection_to_total_trial_duration_H2_Zone_1:Ratio_detection_to_total_trial_duration_H2_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.3237	0.2106	0.4621	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 135.1

Scaled residuals:
Min 1Q Median 3Q Max
-1.5051 -0.7487 -0.3157 0.4712 2.2142

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 2.496e-01 4.996e-01
Genotype_Zone_2:Plant_Zone_2 (Intercept) 3.337e-15 5.777e-08
Residual 3.049e-01 5.522e-01
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

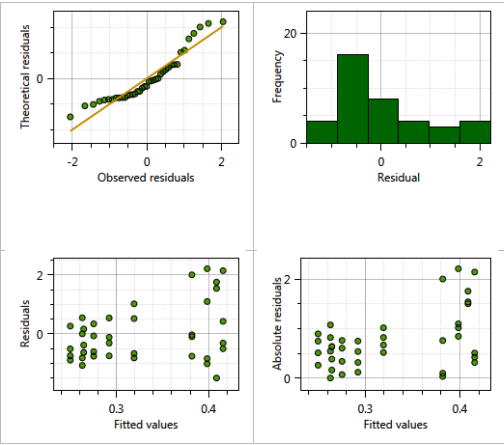
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -0.7366 0.2589 9.0773 -2.846 0.0191 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.5522

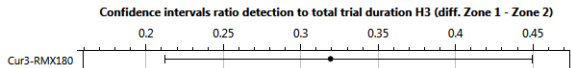
Model residuals

Statistic	Value
Sample skewness	0.9731
Sample excess kurtosis	0.1738
Passed Shapiro Wilk normality test	No (p-value = 0.002093 < 0.05)



Analysis ratio detection to total trial duration H3 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_detection_to_total_trial_duration_H3_Zone_1:Ratio_detection_to_total_trial_duration_H3_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.3192	0.212	0.4497	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 130

Scaled residuals:
Min 1Q Median 3Q Max
-1.33960 -0.88186 0.05801 0.73774 1.86709

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0000 0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.2402 0.4902
Residual 0.2639 0.5137
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

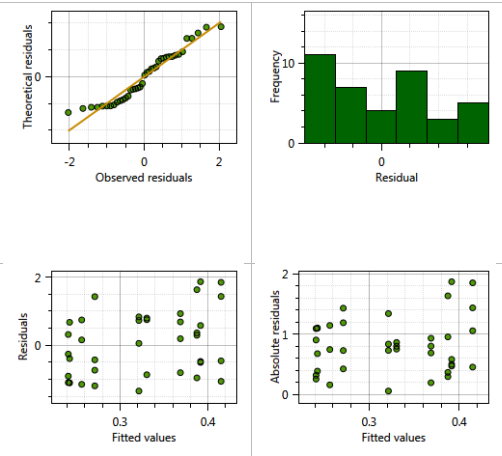
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)

(Intercept) -0.7575 0.2463 9.1691 -3.075 0.013 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Dispersion: 0.5137

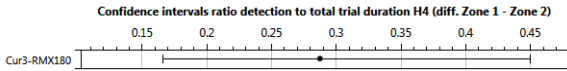
Model residuals

Statistic	Value
Sample skewness	0.3258
Sample excess kurtosis	-1.032
Passed Shapiro Wilk normality test	No (p-value = 0.01985 < 0.05)



Analysis ratio detection to total trial duration H4 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_detection_to_total_trial_duration_H4_Zone_1,Ratio_detection_to_total_trial_duration_H4_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2873	0.1657	0.4501	a

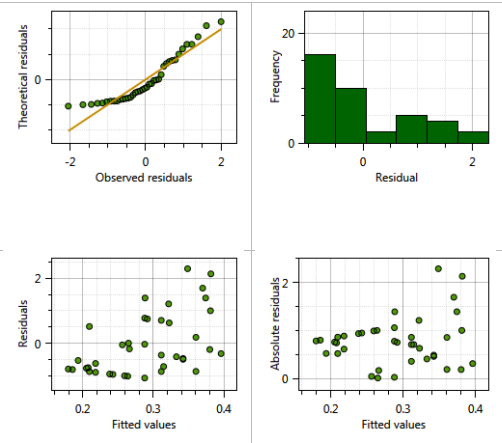
Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi
REML criterion at convergence: 141.9
Scaled residuals:
Min 1Q Median 3Q Max
-1.0600 -0.7917 -0.3571 0.6688 2.2913
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.09714 0.3117
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.25089 0.5009
Residual 0.35597 0.5966
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -0.9083 0.2906 6.1081 -3.125 0.02 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Dispersion: 0.5966

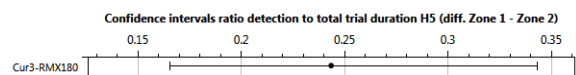
Model residuals

Statistic	Value
Sample skewness	0.9578
Sample excess kurtosis	-0.09638
Passed Shapiro Wilk normality test	No (p-value = 0.0005458 < 0.05)



Analysis ratio detection to total trial duration H5 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_detection_to_total_trial_duration_H5_Zone_1,Ratio_detection_to_total_trial_duration_H5_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals ratio detection to total trial duration H5 (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2435	0.1653	0.3434	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 142.5

Scaled residuals:
    Min       1Q   Median       3Q      Max
-0.9287 -0.9002 -0.3260  0.6615  2.4329

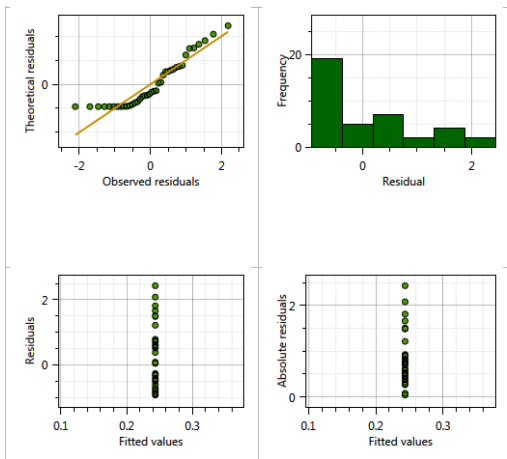
Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0000  0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.0000  0.0000
Residual                      0.3731  0.6108
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -1.1337     0.2398 38.0000  -4.729 3.09e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.6108
```

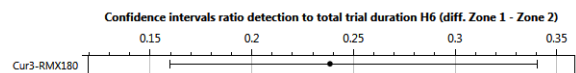
Model residuals

Statistic	Value
Sample skewness	0.8257
Sample excess kurtosis	-0.4485
Passed Shapiro Wilk normality test	No (p-value = 0.0002664 < 0.05)



Analysis ratio detection to total trial duration H6 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_detection_to_total_trial_duration_H6_Zone_1,Ratio_detection_to_total_trial_duration_H6_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals ratio detection to total trial duration H6 (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2384	0.1595	0.3405	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 145.5

Scaled residuals:
    Min       1Q   Median       3Q      Max
-0.9034 -0.9034 -0.2593  0.5986  2.8858

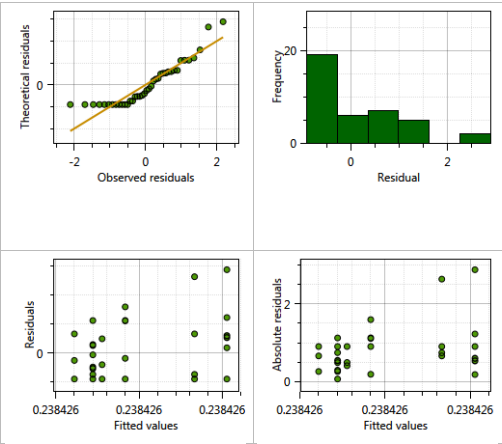
Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 1.703e-15 4.126e-08
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.000e+00 0.000e+00
Residual                      3.836e-01 6.193e-01
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -1.1613     0.2472 38.0000  -4.697 3.4e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.6193
```

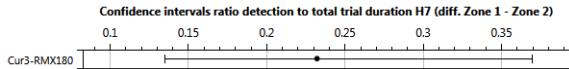
Model residuals

Statistic	Value
Sample skewness	1.12
Sample excess kurtosis	0.9587
Passed Shapiro Wilk normality test	No (p-value = 0.0001356 < 0.05)



Analysis ratio detection to total trial duration H7 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_detection_to_total_trial_duration_H7_Zone_1,Ratio_detection_to_total_trial_duration_H7_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals ratio detection to total trial duration H7 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2321	0.1347	0.3698	a

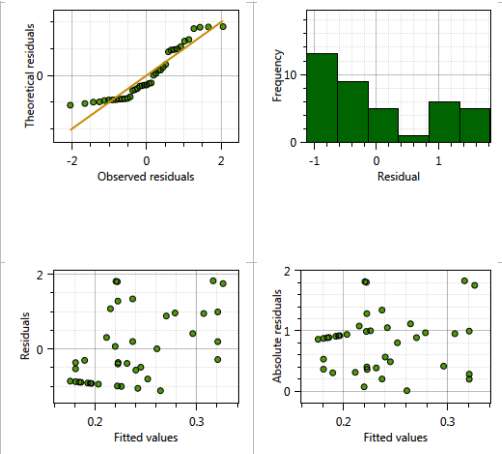
Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi
REML criterion at convergence: 141
Scaled residuals:
Min 1Q Median 3Q Max
-1.1158 -0.8799 -0.3593 0.9196 1.8290
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.05914 0.2432
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.19393 0.4404
Residual 0.28856 0.5372
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -1.1964 0.2718 6.0633 -4.403 0.00444 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Dispersion: 0.5372

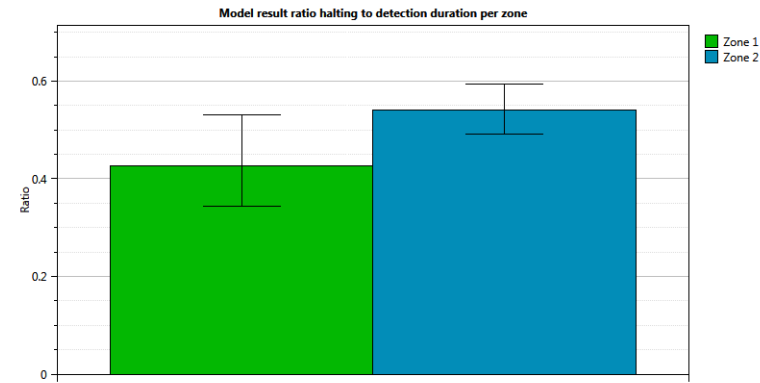
Model residuals

Statistic	Value
Sample skewness	0.6683
Sample excess kurtosis	-0.8967
Passed Shapiro Wilk normality test	No (p-value = 0.0006093 < 0.05)



Ratio halting to detection duration per zone

Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



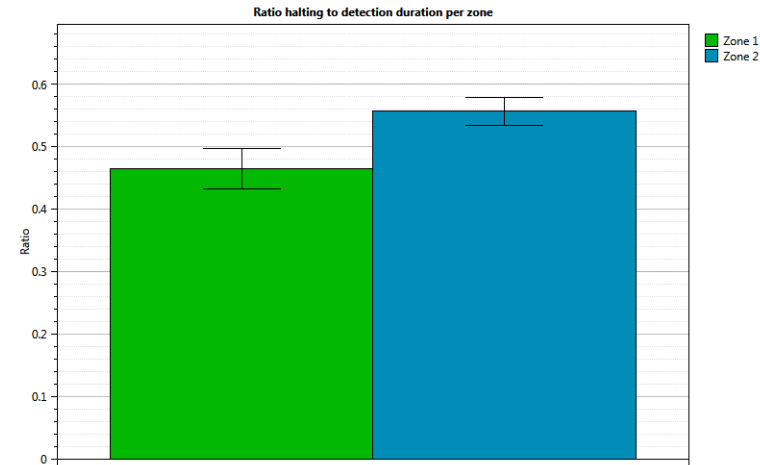
Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

Behaviour statistic	Cur3-RMX180
Ratio halting to detection duration (diff. Zone 1 - Zone 2)	p=0.0291* [-0.341, -0.0247]

The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180
Ratio halting to detection duration (Zone 1)	0.427 [0.344, 0.531]
Ratio halting to detection duration (Zone 2)	0.541 [0.492, 0.594]

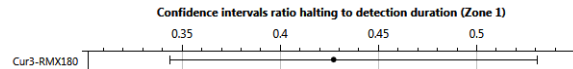
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean Zone 1	StdErr Zone 1	Mean Zone 2	StdErr Zone 2
Cur3	RMX180	Neutral	0.46	0.03	0.56	0.02

Analysis ratio halting to detection duration (Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_detection_duration_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4271	0.3436	0.531	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_detection_duration_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 47.1

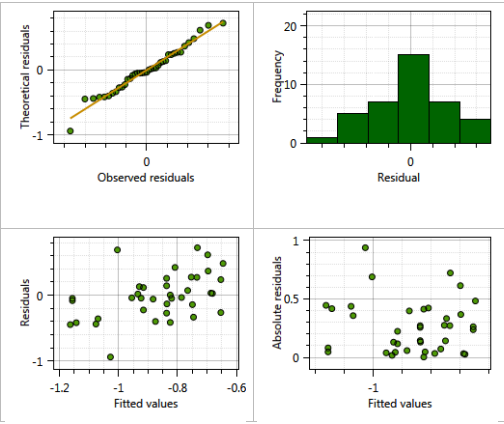
Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.46050 -0.63800 -0.09042  0.62306  1.89379

Random effects:
Groups                Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.01670  0.1253
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.03653  0.1911
Residual                                0.14558  0.3815
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept) -0.85065    0.09474  8.18513 -8.979 1.63e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

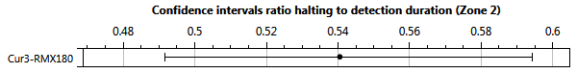
Model residuals

Statistic	Value
Sample skewness	-0.05161
Sample excess kurtosis	0.4666
Passed Shapiro Wilk normality test	Yes (p-value = 0.6025 > 0.05)



Analysis ratio halting to detection duration (Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_detection_duration_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio halting to detection duration (Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5405	0.4915	0.5944	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_detection_duration_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 6.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.55646	-0.49021	-0.00856	0.50148	2.21447

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000000	0.00000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.001539	0.03923
Residual		0.061502	0.24800

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

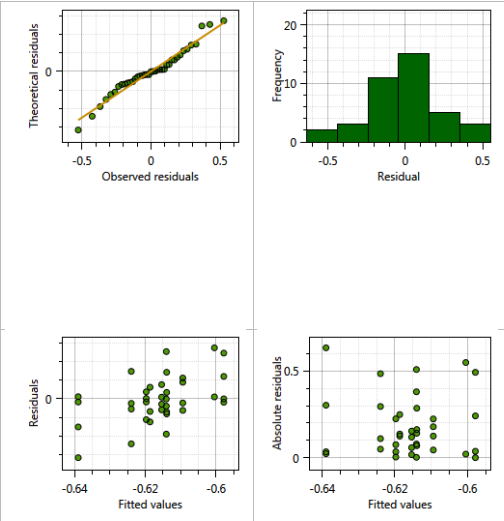
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.61525	0.04161	8.51374	-14.79	2.29e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

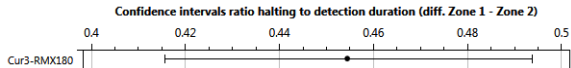
Model residuals

Statistic	Value
Sample skewness	0.02118
Sample excess kurtosis	0.9433
Passed Shapiro Wilk normality test	Yes (p-value = 0.2975 > 0.05)



Analysis ratio halting to detection duration (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_halting_to_detection_duration_Zone_1:Ratio_halting_to_detection_duration_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals ratio halting to detection duration (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4544	0.4155	0.4938	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziformula
Data: data

Weights: wi

REML criterion at convergence: 41.4

Scaled residuals:

Min1QMedian3QMax

-2.2198-0.6027-0.13520.54762.7637

Random effects:

Groups

Name

Variance

Std.Dev.

Genotype_Zone_1:Plant_Zone_1 (Intercept)

3.379e-18

1.838e-09

Genotype_Zone_2:Plant_Zone_2 (Intercept)

7.247e-03

8.513e-02

Residual

3.701e-02

1.924e-01

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

Estimate

Std. Error

df

t value

Pr(>|t|)

(Intercept)

-0.18291

0.06694

7.02259

-2.733

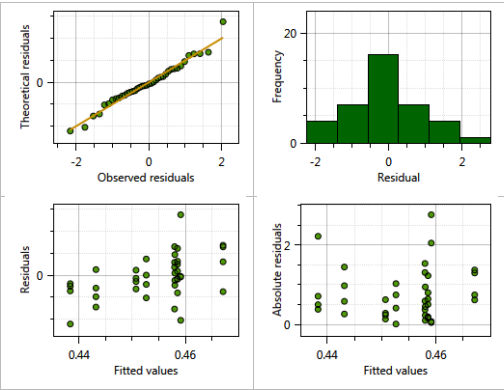
0.0291 *

Signif. codes: 0 '****' 0.001 '***' 0.01 '**' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.1924

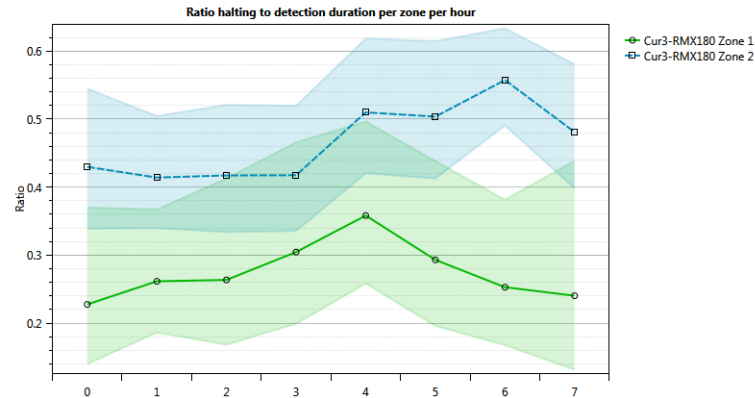
Model residuals

Statistic	Value
Sample skewness	0.2507
Sample excess kurtosis	1.048
Passed Shapiro Wilk normality test	Yes (p-value = 0.6726 > 0.05)



Ratio halting to detection duration per zone per hour

Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

Behaviour statistic	Cur3-RMX180
Ratio halting to detection duration H0 (diff. Zone 1 - Zone 2)	p=0.0322* [-0.73, -0.0401]
Ratio halting to detection duration H1 (diff. Zone 1 - Zone 2)	p=0.0484* [-0.557, -0.00206]
Ratio halting to detection duration H2 (diff. Zone 1 - Zone 2)	p=0.244 [-0.653, 0.199]
Ratio halting to detection duration H3 (diff. Zone 1 - Zone 2)	p=0.432 [-0.534, 0.259]
Ratio halting to detection duration H4 (diff. Zone 1 - Zone 2)	p=0.197 [-0.51, 0.11]
Ratio halting to detection duration H5 (diff. Zone 1 - Zone 2)	p=0.198 [-0.583, 0.136]
Ratio halting to detection duration H6 (diff. Zone 1 - Zone 2)	p=0.00164** [-0.91, -0.237]
Ratio halting to detection duration H7 (diff. Zone 1 - Zone 2)	p=0.0326* [-1.05, -0.0576]

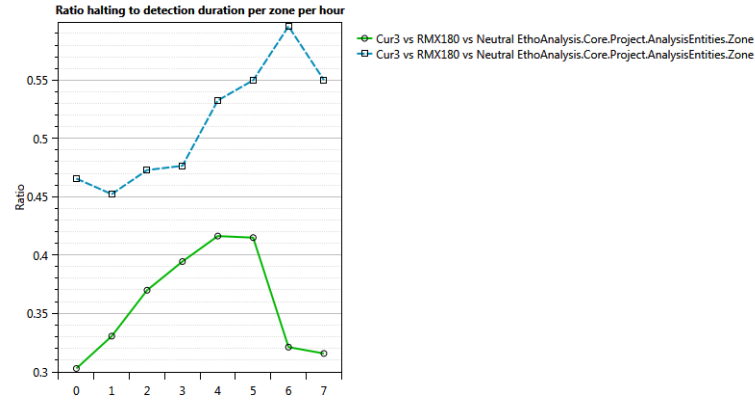
The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Ratio halting to detection duration (H0 - Zone 1)	0.228 [0.14, 0.37]	CR
Ratio halting to detection duration (H0 - Zone 2)	0.43 [0.339, 0.545]	CR
Ratio halting to detection duration (H1 - Zone 1)	0.262 [0.186, 0.367]	CR
Ratio halting to detection duration (H1 - Zone 2)	0.414 [0.34, 0.505]	CR
Ratio halting to detection duration (H2 - Zone 1)	0.264 [0.168, 0.413]	CR
Ratio halting to detection duration (H2 - Zone 2)	0.417 [0.334, 0.521]	CR
Ratio halting to detection duration (H3 - Zone 1)	0.305 [0.199, 0.466]	CR
Ratio halting to detection duration (H3 - Zone 2)	0.418 [0.336, 0.52]	CR
Ratio halting to detection duration (H4 - Zone 1)	0.358 [0.258, 0.497]	

Statistic	Cur3-RMX180	Remark
Ratio halting to detection duration (H4 - Zone 2)	0.51 [0.421, 0.619]	CR
Ratio halting to detection duration (H5 - Zone 1)	0.293 [0.196, 0.438]	CR
Ratio halting to detection duration (H5 - Zone 2)	0.504 [0.413, 0.615]	CR
Ratio halting to detection duration (H6 - Zone 1)	0.253 [0.168, 0.382]	
Ratio halting to detection duration (H6 - Zone 2)	0.558 [0.491, 0.634]	
Ratio halting to detection duration (H7 - Zone 1)	0.24 [0.132, 0.439]	CR
Ratio halting to detection duration (H7 - Zone 2)	0.481 [0.398, 0.581]	CR

CR = Check residuals

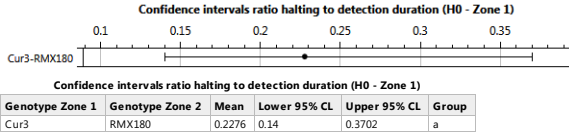
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean H0 - Zone 1	StdErr H0 - Zone 1	Mean H0 - Zone 2	StdErr H0 - Zone 2	Mean H1 - Zone 1	StdErr H1 - Zone 1	Mean H1 - Zone 2	StdErr H1 - Zone 2	Mean H2 - Zone 1	StdErr H2 - Zone 1	Mean H2 - Zone 2	StdErr H2 - Zone 2	Mean H3 - Zone 1	StdErr H3 - Zone 1	Mean H3 - Zone 2	StdErr H3 - Zone 2	Mean H4 - Zone 1	StdErr H4 - Zone 1	Mean H4 - Zone 2	StdErr H4 - Zone 2	Mean H5 - Zone 1	StdErr H5 - Zone 1	Mean H5 - Zone 2	StdErr H5 - Zone 2	Mean H6 - Zone 1	StdErr H6 - Zone 1	Mean H6 - Zone 2	StdErr H6 - Zone 2
Cur3	RMX180	Neutral	0.3	0.04	0.47	0.04	0.33	0.04	0.45	0.03	0.37	0.05	0.47	0.03	0.39	0.04	0.48	0.03	0.42	0.05	0.53	0.03	0.41	0.05	0.55	0.03	0.32	0.05	0.6	0.03

Analysis ratio halting to detection duration (H0 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_detection_duration_H0_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_detection_duration_H0_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 91.2

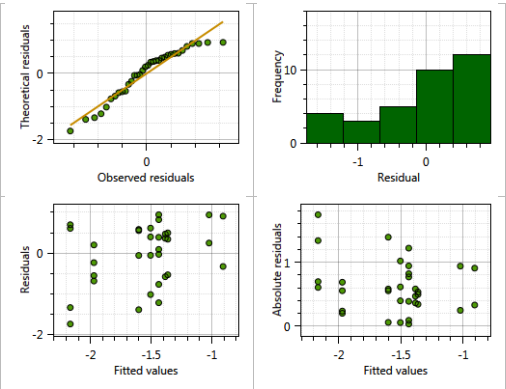
Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.1410 -0.6733  0.2738  0.7037  1.1571

Random effects:
Groups:                               Name      Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.2560  0.5059
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.0000  0.0000
Residual                                0.6647  0.8153
Number of obs: 34, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -1.4800    0.2136   8.6311  -6.929 8.39e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

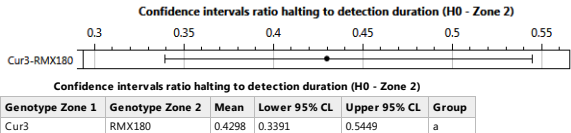
Model residuals

Statistic	Value
Sample skewness	-0.711
Sample excess kurtosis	-0.4544
Passed Shapiro Wilk normality test	No (p-value = 0.0225 < 0.05)



Analysis ratio halting to detection duration (H0 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_detection_duration_H0_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_detection_duration_H0_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 59.7

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.7402	-0.3629	0.0645	0.4772	1.5841

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.01627	0.12755
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.00127	0.03564
Residual		0.25117	0.50117

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

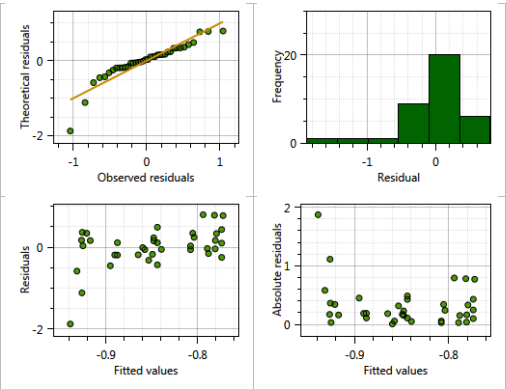
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.84434	0.09154	4.87694	-9.223	0.000287 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

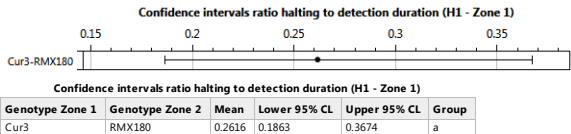
Model residuals

Statistic	Value
Sample skewness	-1.613
Sample excess kurtosis	5.363
Passed Shapiro Wilk normality test	No (p-value = 0.0004495 < 0.05)



Analysis ratio halting to detection duration (H1 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_detection_duration_H1_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_detection_duration_H1_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 92

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.7203	-0.4818	0.0996	0.6134	1.4976

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.03162	0.1778
Residual		0.70403	0.8391

Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

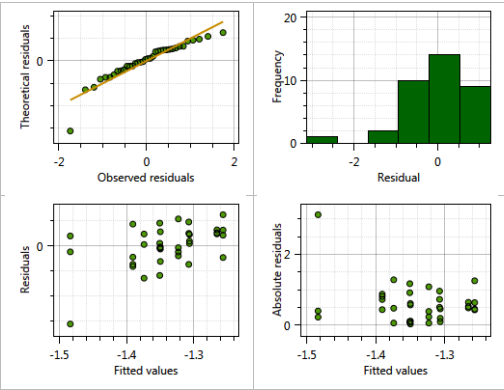
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.3408	0.1509	9.3277	-8.886	7.46e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

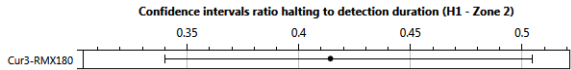
Model residuals

Statistic	Value
Sample skewness	-1.562
Sample excess kurtosis	4.654
Passed Shapiro Wilk normality test	No (p-value = 0.002481 < 0.05)



Analysis ratio halting to detection duration (H1 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_detection_duration_H1_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio halting to detection duration (H1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4142	0.3399	0.5047	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_detection_duration_H1_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 71

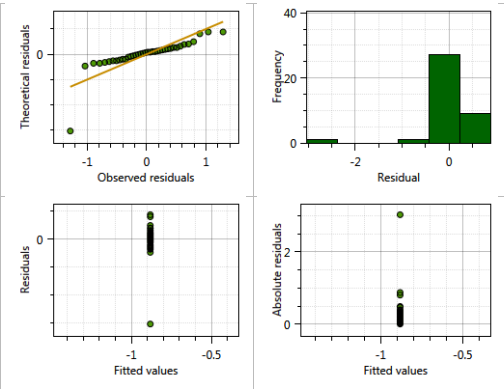
Scaled residuals:
  Min       1Q   Median       3Q      Max
-5.0400 -0.3281  0.1193  0.3704  1.4660

Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  5.613e-23  7.492e-12
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.000e+00  0.000e+00
Residual                                3.616e-01  6.013e-01
Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -0.88150    0.09754  37.00000  -9.037  6.73e-11 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

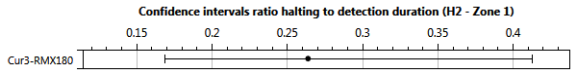
Model residuals

Statistic	Value
Sample skewness	-3.397
Sample excess kurtosis	17.71
Passed Shapiro Wilk normality test	No (p-value = 5.268E-08 < 0.05)



Analysis ratio halting to detection duration (H2 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_detection_duration_H2_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio halting to detection duration (H2 - Zone 1)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2637	0.1684	0.4128	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_detection_duration_H2_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 99

Scaled residuals:
  Min       1Q   Median       3Q      Max
-2.22115 -0.65939  0.05342  0.88391  1.57706

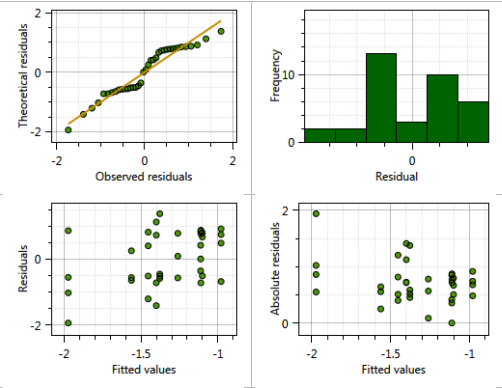
Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.0000  0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.1836  0.4285
```

Residual 0.7631 0.8735
Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -1.3330 0.1994 9.3607 -6.687 7.47e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

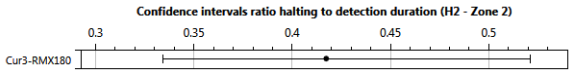
Model residuals

Statistic	Value
Sample skewness	-0.2995
Sample excess kurtosis	-0.7955
Passed Shapiro Wilk normality test	No (p-value = 0.03028 < 0.05)



Analysis ratio halting to detection duration (H2 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_detection_duration_H2_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4173	0.334	0.5212	a

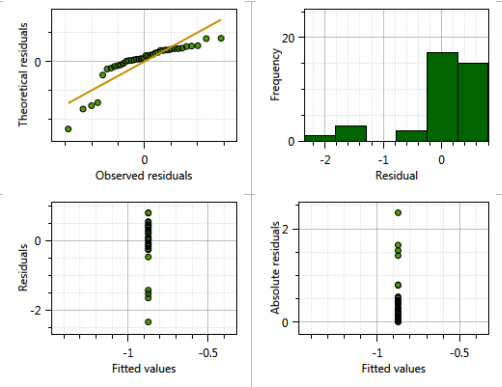
Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_detection_duration_H2_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data
REML criterion at convergence: 79.8
Scaled residuals:
Min 1Q Median 3Q Max
-3.4645 -0.1582 0.2203 0.5851 1.1841
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0000 0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.0000 0.0000
Residual 0.4581 0.6768
Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -0.8740 0.1098 37.0000 -7.961 1.55e-09 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

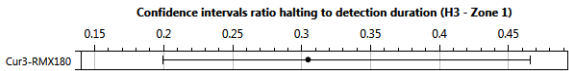
Model residuals

Statistic	Value
Sample skewness	-2.018
Sample excess kurtosis	4.125
Passed Shapiro Wilk normality test	No (p-value = 2.357E-06 < 0.05)



Analysis ratio halting to detection duration (H3 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_detection_duration_H3_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.3046	0.1991	0.466	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_detection_duration_H3_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 96.5

Scaled residuals:
Min 1Q Median 3Q Max
-3.2794 -0.2611 0.2530 0.6781 0.9783

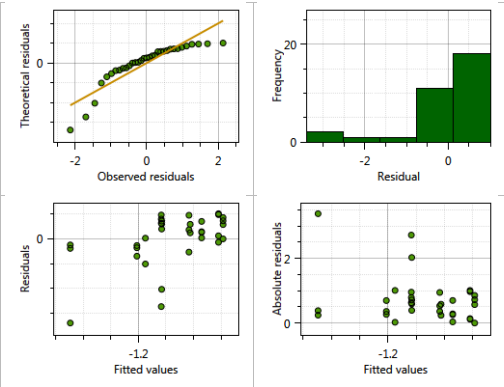
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.000000 0.00000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.009578 0.09787
Residual 1.062553 1.03080
Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -1.1886 0.1822 7.5052 -6.523 0.000243 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

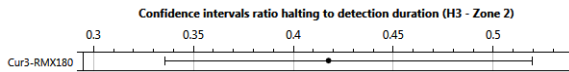
Model residuals

Statistic	Value
Sample skewness	-1.902
Sample excess kurtosis	3.805
Passed Shapiro Wilk normality test	No (p-value = 2.92E-05 < 0.05)



Analysis ratio halting to detection duration (H3 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_detection_duration_H3_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio halting to detection duration (H3 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4176	0.3355	0.5197	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_detection_duration_H3_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 70.5

Scaled residuals:
Min 1Q Median 3Q Max
-3.2928 -0.3904 0.1841 0.5709 1.3581

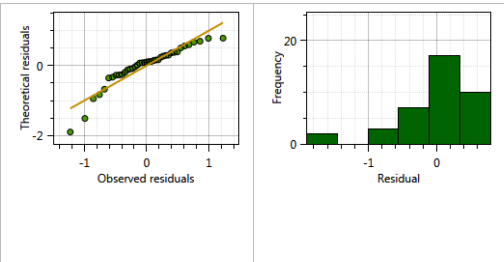
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.000000 0.00000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.007702 0.08776
Residual 0.332865 0.57694
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

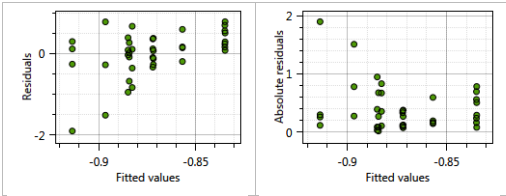
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -0.87328 0.09649 8.87856 -9.051 8.94e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

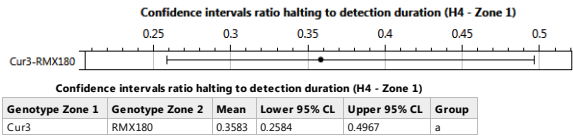
Statistic	Value
Sample skewness	-1.461
Sample excess kurtosis	2.925
Passed Shapiro Wilk normality test	No (p-value = 0.0009034 < 0.05)





Analysis ratio halting to detection duration (H4 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_detection_duration_H4_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_detection_duration_H4_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 66.4

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-2.9378	-0.4891	0.1697	0.7103	1.2783

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000000	0.00000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.002378	0.04876
Residual		0.553081	0.74369

Number of obs: 29, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

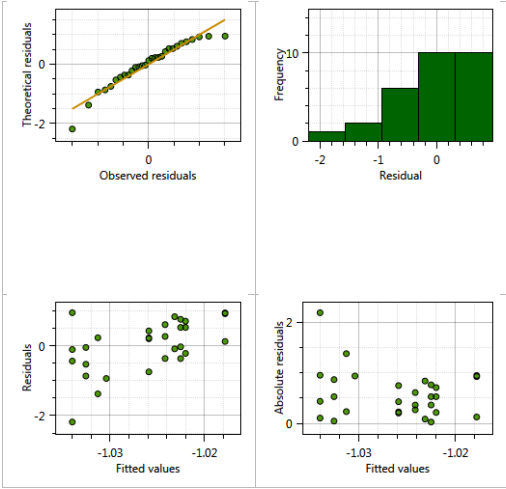
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.026	0.139	7.229	-7.382	0.000129 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

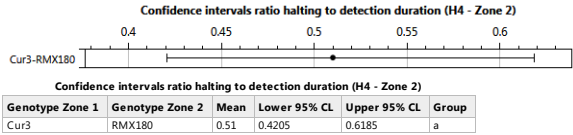
Model residuals

Statistic	Value
Sample skewness	-1.007
Sample excess kurtosis	1.305
Passed Shapiro Wilk normality test	Yes (p-value = 0.06406 > 0.05)



Analysis ratio halting to detection duration (H4 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_detection_duration_H4_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_detection_duration_H4_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 43.5

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-2.87100	-0.37801	0.07416	0.49088	1.54358

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000000	0.00000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.02867	0.1693
Residual		0.15588	0.3948

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

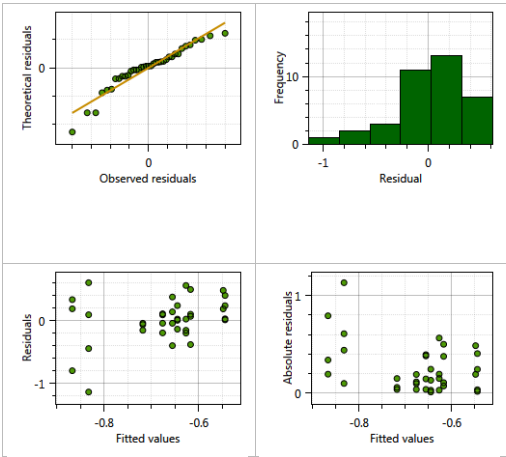
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.6733	0.0845	8.4857	-7.968	3.21e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

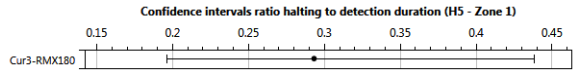
Model residuals

Statistic	Value
Sample skewness	-1.017
Sample excess kurtosis	1.673
Passed Shapiro Wilk normality test	No (p-value = 0.02033 < 0.05)



Analysis ratio halting to detection duration (H5 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_detection_duration_H5_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2931	0.196	0.4384	a

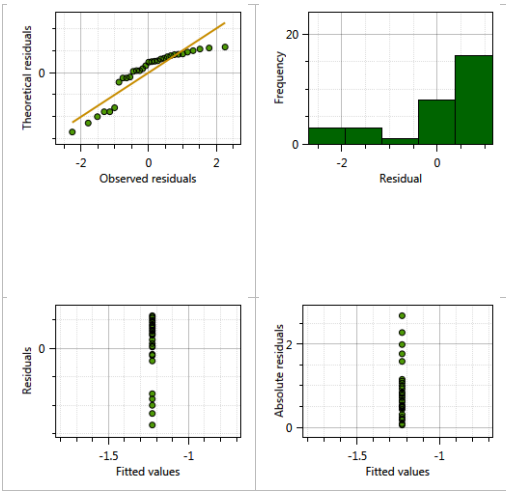
Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_detection_duration_H5_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data
REML criterion at convergence: 94.1
Scaled residuals:
Min IQ Median 3Q Max
-2.4465 -0.2210 0.4302 0.7183 1.0520
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.000 0.000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.000 0.000
Residual 1.204 1.097
Number of obs: 31, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -1.2271 0.1971 30.0000 -6.226 7.44e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

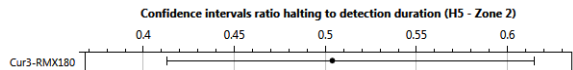
Model residuals

Statistic	Value
Sample skewness	-1.209
Sample excess kurtosis	0.311
Passed Shapiro Wilk normality test	No (p-value = 0.0002069 < 0.05)



Analysis ratio halting to detection duration (H5 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_detection_duration_H5_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio halting to detection duration (H5 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5038	0.4127	0.6148	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_detection_duration_H5_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 50.6

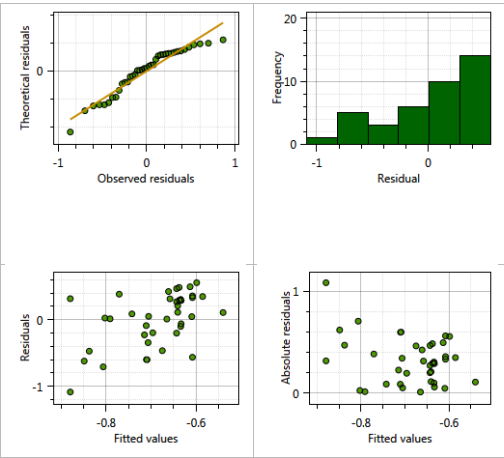
Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.5663 -0.5054  0.1217  0.7476  1.3173

Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.018039 0.1343
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.008557 0.0925
Residual                                0.179245 0.4234
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error      df t value Pr(>|t|)
(Intercept) -0.68567      0.08526    7.42788  -8.043 6.37e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

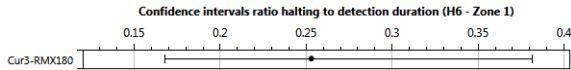
Model residuals

Statistic	Value
Sample skewness	-0.7741
Sample excess kurtosis	-0.08685
Passed Shapiro Wilk normality test	No (p-value = 0.01742 < 0.05)



Analysis ratio halting to detection duration (H6 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_detection_duration_H6_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio halting to detection duration (H6 - Zone 1)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.253	0.1677	0.3816	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_detection_duration_H6_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 67.6

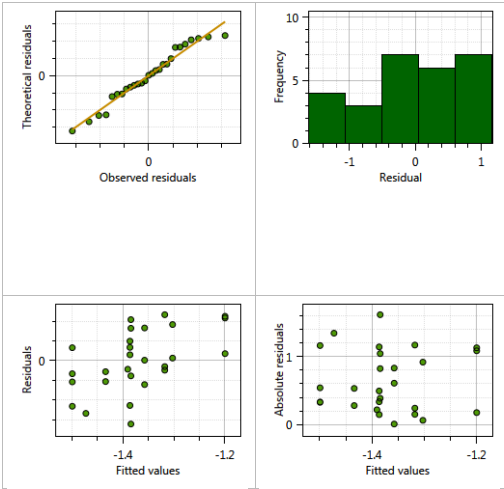
Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.99228 -0.56855  0.01287  0.81404  1.44288

Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 4.547e-18 2.132e-09
Genotype_Zone_2:Plant_Zone_2 (Intercept) 4.794e-02 2.189e-01
Residual                                6.542e-01 8.088e-01
Number of obs: 27, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error      df t value Pr(>|t|)
(Intercept)  -1.3745      0.1724    6.7149  -7.972 0.000116 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

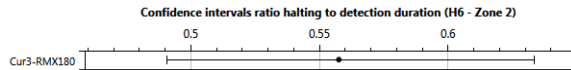
Model residuals

Statistic	Value
Sample skewness	-0.2385
Sample excess kurtosis	-0.6454
Passed Shapiro Wilk normality test	Yes (p-value = 0.3345 > 0.05)



Analysis ratio halting to detection duration (H6 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_detection_duration_H6_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5575	0.4906	0.6336	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_detection_duration_H6_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 38.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.5081	-0.3713	0.1235	0.8543	1.4489

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		0.1516	0.3893

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

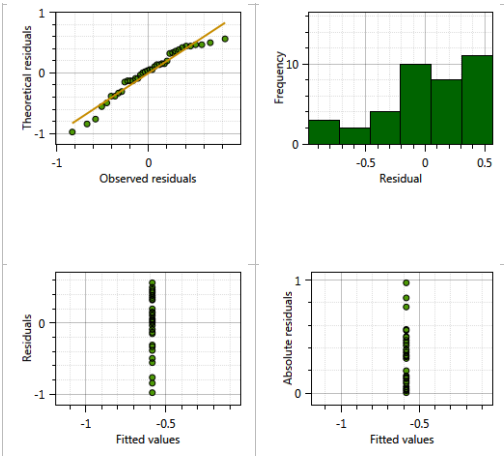
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.58426	0.06315	37.00000	-9.252	3.66e-11 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

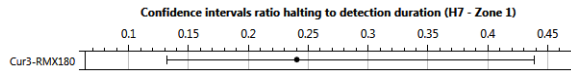
Model residuals

Statistic	Value
Sample skewness	-0.7234
Sample excess kurtosis	0.07446
Passed Shapiro Wilk normality test	Yes (p-value = 0.05615 > 0.05)



Analysis ratio halting to detection duration (H7 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_detection_duration_H7_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2404	0.1316	0.4389	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_detection_duration_H7_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 78.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.2721	-0.2587	0.3612	0.6101	1.0102

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.21809	0.4670
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.05644	0.2376
Residual		0.84488	0.9192

Number of obs: 27, groups: Genotype_Zone_2:Plant_Zone_2, 10; Genotype_Zone_1:Plant_Zone_1, 9

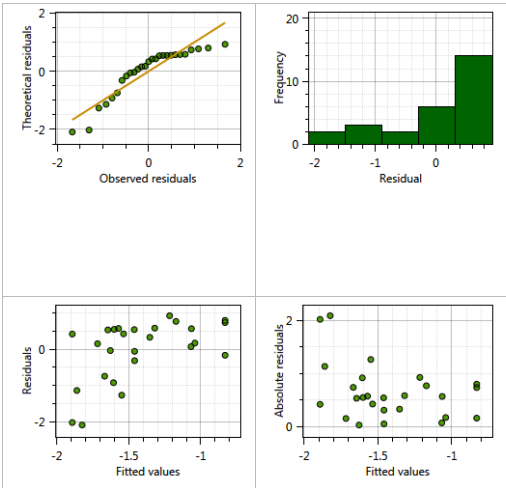
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.4255	0.2506	6.4918	-5.688	0.00097 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

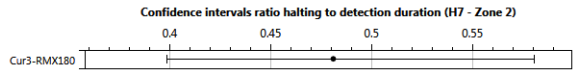
Model residuals

Statistic	Value
Sample skewness	-1.308
Sample excess kurtosis	0.9146
Passed Shapiro Wilk normality test	No (p-value = 0.0007432 < 0.05)



Analysis ratio halting to detection duration (H7 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_detection_duration_H7_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.481	0.3984	0.5808	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_detection_duration_H7_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 70.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.3880	-0.4519	0.3801	0.6571	1.2063

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		0.3381	0.5814

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

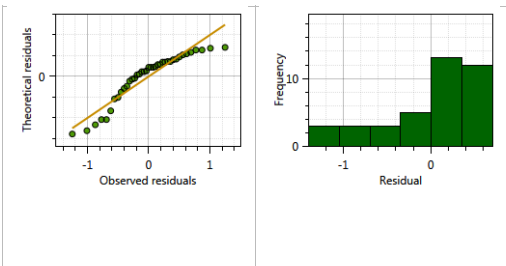
Fixed effects:

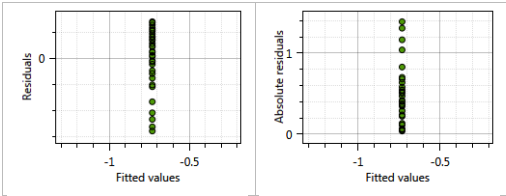
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.7318	0.0931	38.0000	-7.861	1.74e-09 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

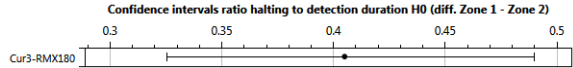
Statistic	Value
Sample skewness	-1.059
Sample excess kurtosis	0.1837
Passed Shapiro Wilk normality test	No (p-value = 0.0006131 < 0.05)





Analysis ratio halting to detection duration H0 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_halting_to_detection_duration_H0_Zone_1:Ratio_halting_to_detection_duration_H0_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4049	0.3253	0.49	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 91.3

Scaled residuals:
Min 1Q Median 3Q Max
-1.7277 -0.8362 -0.2580 0.4439 2.0717

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.04848 0.2202
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.00000 0.0000
Residual 0.11612 0.3408
Number of obs: 35, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

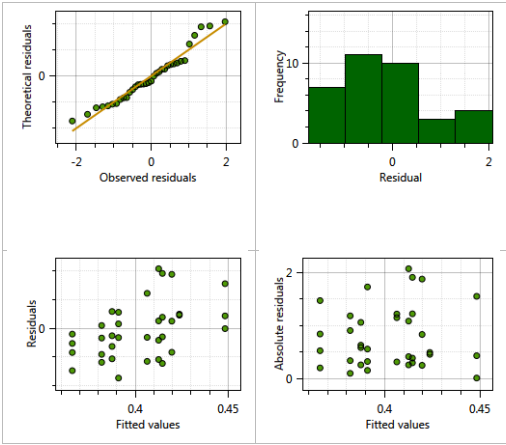
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -0.3849 0.1540 9.6380 -2.5 0.0322 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.3408

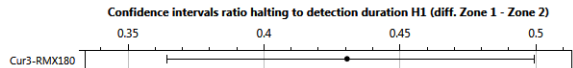
Model residuals

Statistic	Value
Sample skewness	0.5899
Sample excess kurtosis	-0.09388
Passed Shapiro Wilk normality test	Yes (p-value = 0.14 > 0.05)



Analysis ratio halting to detection duration H1 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_halting_to_detection_duration_H1_Zone_1:Ratio_halting_to_detection_duration_H1_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4305	0.3642	0.4995	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 94.8

Scaled residuals:
Min 1Q Median 3Q Max
-1.8258 -0.8547 -0.1824 0.4755 2.7434

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0000 0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.0000 0.0000
Residual 0.1303 0.3609
Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

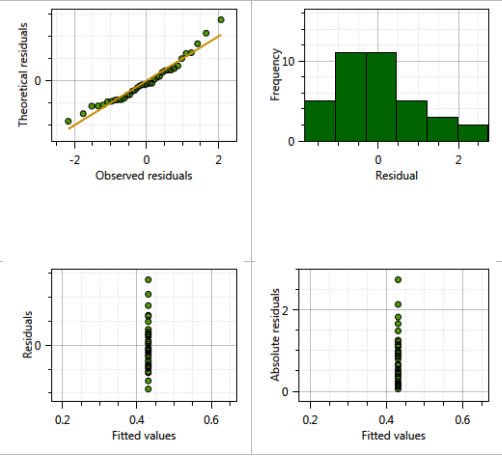
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)

(Intercept) -0.2797 0.1369 36.0000 -2.043 0.0484 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Dispersion: 0.3609

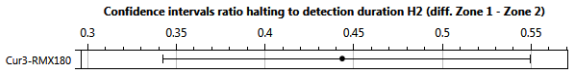
Model residuals

Statistic	Value
Sample skewness	0.8261
Sample excess kurtosis	0.7497
Passed Shapiro Wilk normality test	Yes (p-value = 0.1452 > 0.05)



Analysis ratio halting to detection duration H2 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_halting_to_detection_duration_H2_Zone_1Ratio_halting_to_detection_duration_H2_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



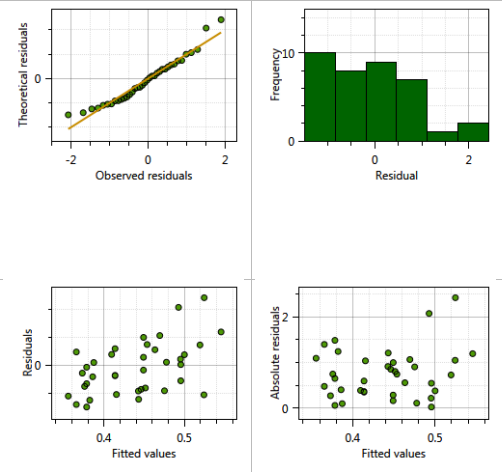
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4435	0.3422	0.5496	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi
REML criterion at convergence: 99.7
Scaled residuals:
Min 1Q Median 3Q Max
-1.4851 -0.8542 -0.1670 0.4800 2.4158
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.1100 0.3317
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.0277 0.1664
Residual 0.1272 0.3566
Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -0.2271 0.1769 6.3983 -1.284 0.244
Dispersion: 0.3566

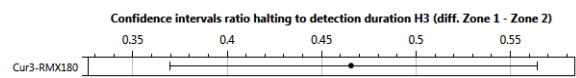
Model residuals

Statistic	Value
Sample skewness	0.7077
Sample excess kurtosis	0.3479
Passed Shapiro Wilk normality test	Yes (p-value = 0.1315 > 0.05)



Analysis ratio halting to detection duration H3 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_halting_to_detection_duration_H3_Zone_1Ratio_halting_to_detection_duration_H3_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals ratio halting to detection duration H3 (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4656	0.3695	0.5643	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 87.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.94141	-0.43274	0.09906	0.49703	1.96665

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.1014	0.3184
Residual		0.1165	0.3413

Number of obs: 35, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

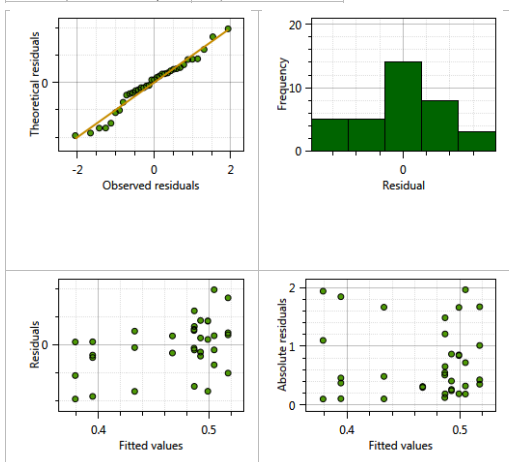
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.1379	0.1645	6.3913	-0.838	0.432

Dispersion: 0.3413

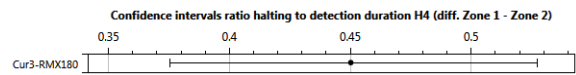
Model residuals

Statistic	Value
Sample skewness	-0.2433
Sample excess kurtosis	-0.07021
Passed Shapiro Wilk normality test	Yes (p-value = 0.373 > 0.05)



Analysis ratio halting to detection duration H4 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_halting_to_detection_duration_H4_Zone_1,Ratio_halting_to_detection_duration_H4_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals ratio halting to detection duration H4 (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4502	0.3752	0.5274	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 76.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.9057	-0.5388	-0.2574	0.4896	2.7274

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		0.1511	0.3887

Number of obs: 30, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

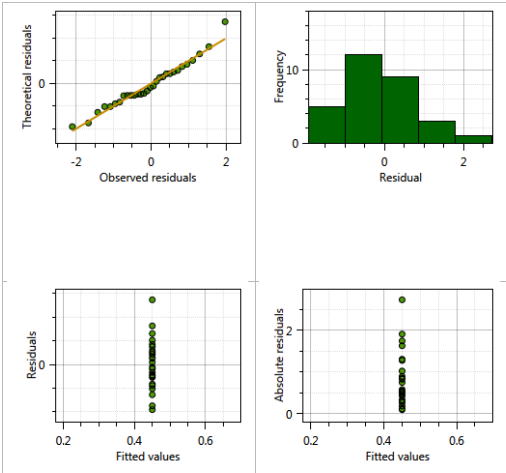
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.2000	0.1515	29.0000	-1.32	0.197

Dispersion: 0.3887

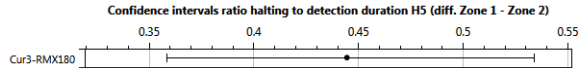
Model residuals

Statistic	Value
Sample skewness	0.6124
Sample excess kurtosis	0.9307
Passed Shapiro Wilk normality test	Yes (p-value = 0.5387 > 0.05)



Analysis ratio halting to detection duration H5 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_halting_to_detection_duration_H5_Zone_1,Ratio_halting_to_detection_duration_H5_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4444	0.3583	0.534	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 84.4

Scaled residuals:
Min IQ Median 3Q Max
-1.95774 -0.63602 0.05103 0.62301 1.38105

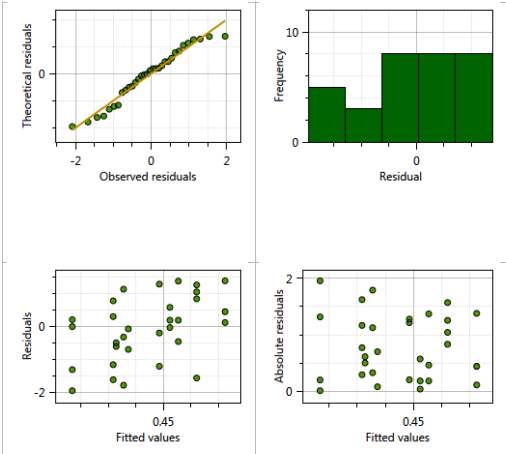
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 3.487e-02 1.867e-01
Genotype_Zone_2:Plant_Zone_2 (Intercept) 1.606e-17 4.006e-09
Residual 1.659e-01 4.073e-01
Number of obs: 32, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -0.2232 0.1623 10.4459 -1.375 0.198

Dispersion: 0.4073

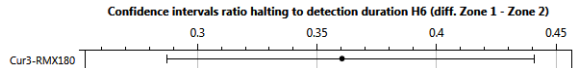
Model residuals

Statistic	Value
Sample skewness	-0.3232
Sample excess kurtosis	-0.8033
Passed Shapiro Wilk normality test	Yes (p-value = 0.1941 > 0.05)



Analysis ratio halting to detection duration H6 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_halting_to_detection_duration_H6_Zone_1,Ratio_halting_to_detection_duration_H6_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.3604	0.287	0.441	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data

Weights: wi

REML criterion at convergence: 74

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.5898	-0.6364	-0.2858	0.8025	2.1887

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	4.017e-16	2.004e-08
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000e+00	0.000e+00
Residual		1.449e-01	3.807e-01

Number of obs: 28, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

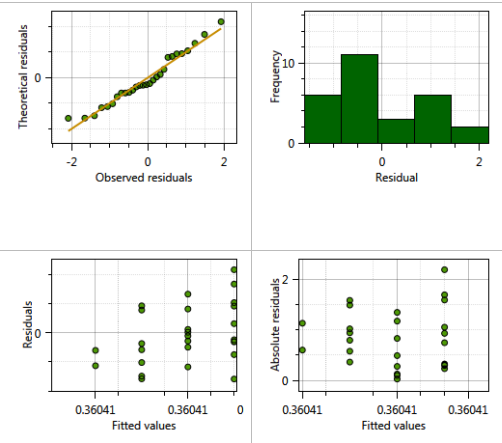
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.5736	0.1639	27.0000	-3.499	0.00164 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.3807

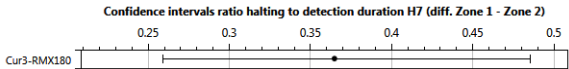
Model residuals

Statistic	Value
Sample skewness	0.4698
Sample excess kurtosis	-0.3719
Passed Shapiro Wilk normality test	Yes (p-value = 0.3533 > 0.05)



Analysis ratio halting to detection duration H7 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_halting_to_detection_duration_H7_Zone_1,Ratio_halting_to_detection_duration_H7_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.3648	0.2588	0.4856	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: ziFormula

Data: data

Weights: wi

REML criterion at convergence: 85.1

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.4128	-0.7734	-0.1050	0.6669	1.5803

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.2225	0.4717
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Residual		0.1336	0.3655

Number of obs: 30, groups: Genotype_Zone_2:Plant_Zone_2, 10; Genotype_Zone_1:Plant_Zone_1, 9

Fixed effects:

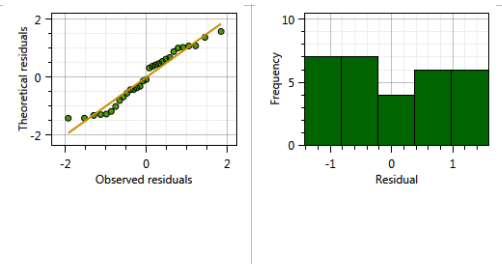
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.5548	0.2193	8.8791	-2.53	0.0326 *

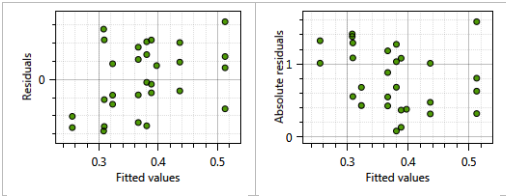
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.3655

Model residuals

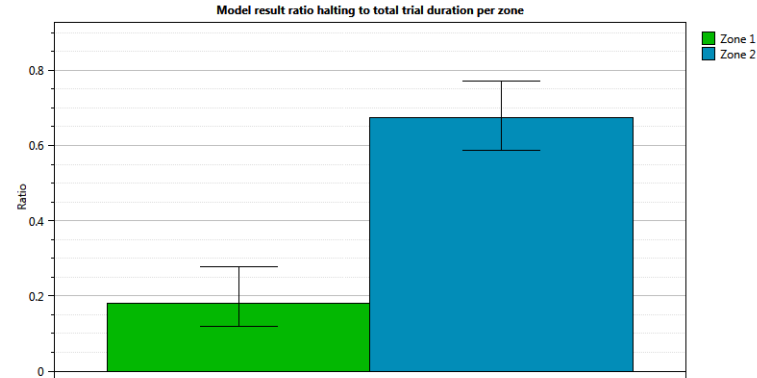
Statistic	Value
Sample skewness	-0.01012
Sample excess kurtosis	-1.262
Passed Shapiro Wilk normality test	Yes (p-value = 0.09701 > 0.05)





Ratio halting to total trial duration per zone

Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

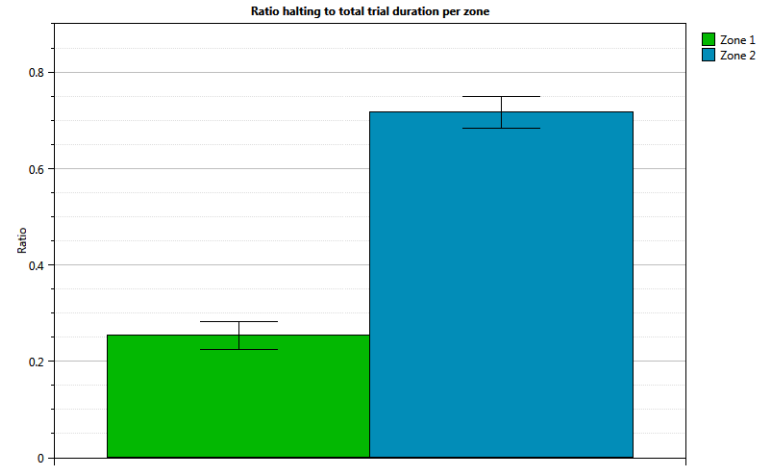
Behaviour statistic	Cur3-RMX180
Ratio halting to total trial duration (diff. Zone 1 - Zone 2)	p=0.000283*** [-1.45, -0.631]

The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Ratio halting to total trial duration (Zone 1)	0.181 [0.118, 0.278]	CR
Ratio halting to total trial duration (Zone 2)	0.673 [0.587, 0.772]	CR

CR = Check residuals

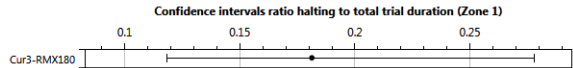
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean Zone 1	StdErr Zone 1	Mean Zone 2	StdErr Zone 2
Cur3	RMX180	Neutral	0.25	0.03	0.72	0.03

Analysis ratio halting to total trial duration (Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_total_trial_duration_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1813	0.1182	0.2781	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_total_trial_duration_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 112.6

Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.7369 -0.3294  0.2530  0.6067  1.2204

Random effects:
              Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.00000 0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.08948 0.2991
Residual                                1.03961 1.0196
```

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

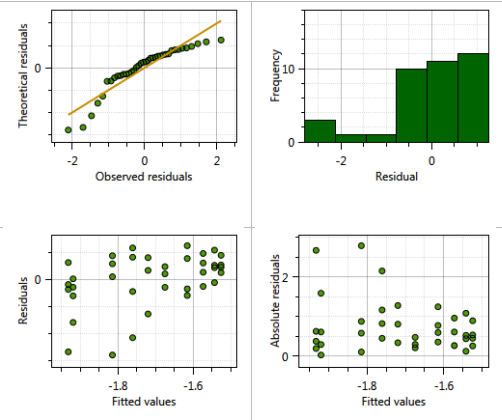
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.7078	0.1907	9.5207	-8.953	6.09e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

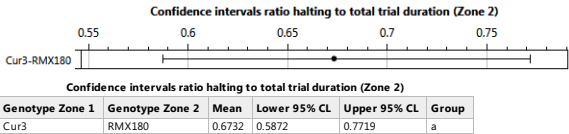
Model residuals

Statistic	Value
Sample skewness	-1.408
Sample excess kurtosis	1.798
Passed Shapiro Wilk normality test	No (p-value = 0.0003123 < 0.05)



Analysis ratio halting to total trial duration (Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_total_trial_duration_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_total_trial_duration_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 45.9

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-4.5190	-0.2928	0.1591	0.6481	0.9376

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.000
Residual		0.1781	0.422

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

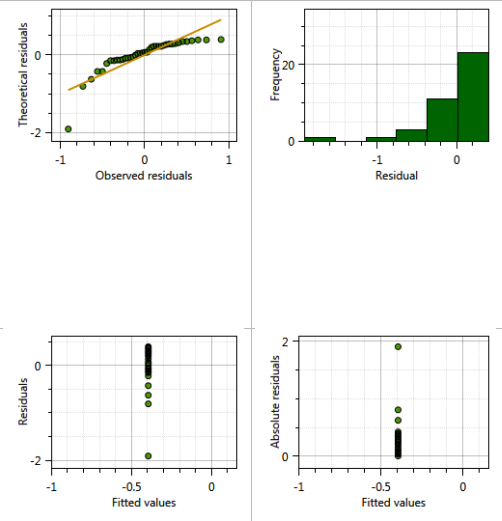
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.39565	0.06757	38.00000	-5.855	8.99e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

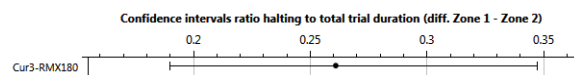
Model residuals

Statistic	Value
Sample skewness	-2.729
Sample excess kurtosis	10.39
Passed Shapiro Wilk normality test	No (p-value = 6.762E-07 < 0.05)



Analysis ratio halting to total trial duration (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_halting_to_total_trial_duration_Zone_1,Ratio_halting_to_total_trial_duration_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals ratio halting to total trial duration (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2609	0.1897	0.3474	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 112.1

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.33206 -0.73969 -0.03082  0.50843  2.48961

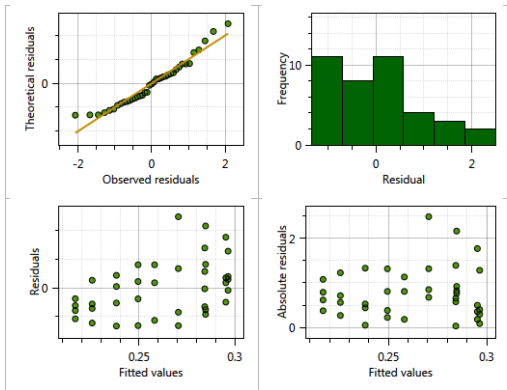
Random effects:
Groups              Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.00000  0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.08699  0.2949
Residual                                0.17614  0.4197
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -1.0411     0.1814   8.9763  -5.739 0.000283 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.4197
```

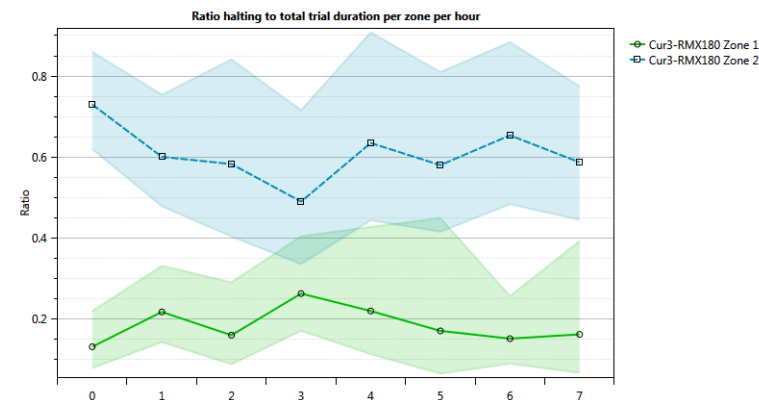
Model residuals

Statistic	Value
Sample skewness	0.7043
Sample excess kurtosis	0.1095
Passed Shapiro Wilk normality test	Yes (p-value = 0.06503 > 0.05)



Ratio halting to total trial duration per zone per hour

Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

Behaviour statistic	Cur3-RMX180	Remark
Ratio halting to total trial duration H0 (diff. Zone 1 - Zone 2)	p=5.49E-05*** [-1.67, -0.64]	CR
Ratio halting to total trial duration H1 (diff. Zone 1 - Zone 2)	p=0.00827** [-1.12, -0.178]	CR
Ratio halting to total trial duration H2 (diff. Zone 1 - Zone 2)	p=0.0124* [-1.55, -0.251]	CR
Ratio halting to total trial duration H3 (diff. Zone 1 - Zone 2)	p=0.0315* [-1.3, -0.0767]	CR
Ratio halting to total trial duration H4 (diff. Zone 1 - Zone 2)	p=0.00968*** [-1.61, -0.298]	CR
Ratio halting to total trial duration H5 (diff. Zone 1 - Zone 2)	p=0.006** [-1.72, -0.386]	CR
Ratio halting to total trial duration H6 (diff. Zone 1 - Zone 2)	p=0.000819*** [-2.11, -0.762]	CR
Ratio halting to total trial duration H7 (diff. Zone 1 - Zone 2)	p=0.00404** [-1.86, -0.474]	CR

CR = Check residuals

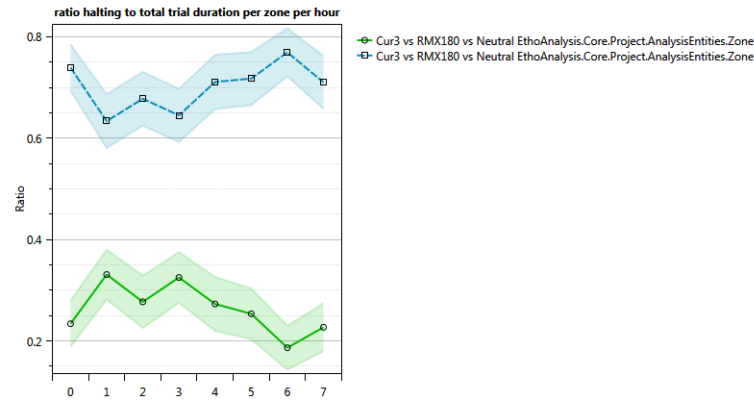
The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Ratio halting to total trial duration (H0 - Zone 1)	0.131	CR

Statistic	Cur3-RMX180	Remark
Ratio halting to total trial duration (H0 - Zone 2)	[0.0786, 0.219]	
	0.73	CR
Ratio halting to total trial duration (H1 - Zone 1)	[0.619, 0.86]	
	0.217	CR
Ratio halting to total trial duration (H1 - Zone 2)	[0.142, 0.332]	
	0.601	CR
Ratio halting to total trial duration (H2 - Zone 1)	[0.478, 0.754]	
	0.16	
Ratio halting to total trial duration (H2 - Zone 2)	[0.0879, 0.291]	
	0.583	CR
Ratio halting to total trial duration (H3 - Zone 1)	[0.404, 0.841]	
	0.263	CR
Ratio halting to total trial duration (H3 - Zone 2)	[0.171, 0.404]	
	0.49	CR
Ratio halting to total trial duration (H4 - Zone 1)	[0.335, 0.716]	
	0.22	
Ratio halting to total trial duration (H4 - Zone 2)	[0.113, 0.428]	
	0.635	CR
Ratio halting to total trial duration (H5 - Zone 1)	[0.444, 0.908]	
	0.17	
Ratio halting to total trial duration (H5 - Zone 2)	[0.0646, 0.45]	
	0.58	CR
Ratio halting to total trial duration (H6 - Zone 1)	[0.415, 0.81]	
	0.151	
Ratio halting to total trial duration (H6 - Zone 2)	[0.0892, 0.257]	
	0.654	CR
Ratio halting to total trial duration (H7 - Zone 1)	[0.483, 0.884]	
	0.162	CR
Ratio halting to total trial duration (H7 - Zone 2)	[0.0667, 0.393]	
	0.587	CR
	[0.445, 0.775]	

CR = Check residuals

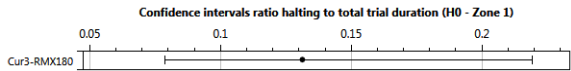
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean H0 - Zone 1	StdErr H0 - Zone 1	Mean H0 - Zone 2	StdErr H0 - Zone 2	Mean H1 - Zone 1	StdErr H1 - Zone 1	Mean H1 - Zone 2	StdErr H1 - Zone 2	Mean H2 - Zone 1	StdErr H2 - Zone 1	Mean H2 - Zone 2	StdErr H2 - Zone 2	Mean H3 - Zone 1	StdErr H3 - Zone 1	Mean H3 - Zone 2	StdErr H3 - Zone 2	Mean H4 - Zone 1	StdErr H4 - Zone 1	Mean H4 - Zone 2	StdErr H4 - Zone 2	Mean H5 - Zone 1	StdErr H5 - Zone 1	Mean H5 - Zone 2	StdErr H5 - Zone 2	Mean H6 - Zone 1	StdErr H6 - Zone 1	Mean H6 - Zone 2	StdErr H6 - Zone 2
Cur3	RMX180	Neutral	0.23	0.05	0.74	0.05	0.33	0.05	0.63	0.05	0.28	0.05	0.68	0.05	0.33	0.05	0.65	0.05	0.27	0.05	0.71	0.05	0.25	0.05	0.72	0.05	0.19	0.04	0.77	0.05

Analysis ratio halting to total trial duration (H0 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_total_trial_duration_H0_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1313	0.07858	0.2193	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_total_trial_duration_H0_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 118

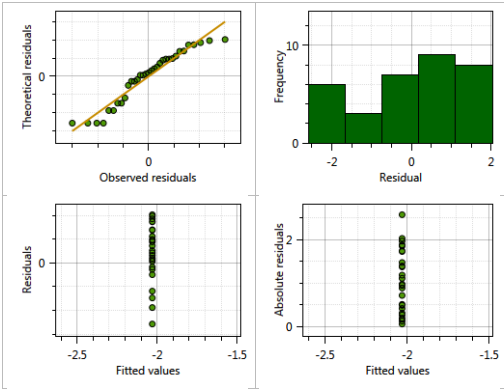
Scaled residuals:
  Min       1Q   Median       3Q      Max
-1.7789 -0.8211  0.1366  0.6774  1.4027

Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.000    0.000
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.000    0.000
Residual                                2.095    1.447
Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   -2.030      0.252 32.000  -8.058 3.36e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

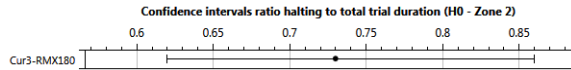
Model residuals

Statistic	Value
Sample skewness	-0.5082
Sample excess kurtosis	-0.8382
Passed Shapiro Wilk normality test	No (p-value = 0.02272 < 0.05)



Analysis ratio halting to total trial duration (H0 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_total_trial_duration_H0_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.7299	0.6195	0.86	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_total_trial_duration_H0_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 44.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.4657	-0.2658	0.3535	0.6889	0.8866

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.006092	0.07805
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000000	0.00000
Residual		0.175355	0.41875

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

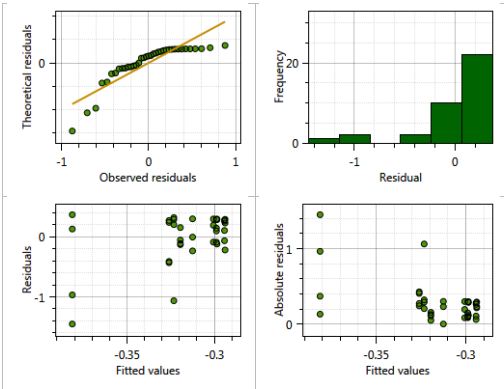
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.31487	0.07319	9.59662	-4.302	0.00171 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

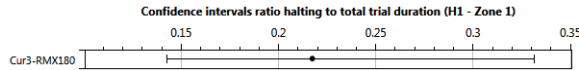
Model residuals

Statistic	Value
Sample skewness	-2.057
Sample excess kurtosis	4.387
Passed Shapiro Wilk normality test	No (p-value = 1.508E-06 < 0.05)



Analysis ratio halting to total trial duration (H1 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_total_trial_duration_H1_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2173	0.1425	0.3315	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_total_trial_duration_H1_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 114.1

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.5046	-0.5573	0.3640	0.8124	1.2416

Random effects:

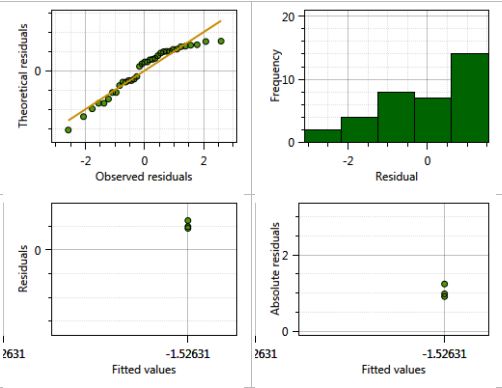
Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000e+00	0.000e+00
Genotype_Zone_2:Plant_Zone_2	(Intercept)	6.165e-17	7.852e-09

Residual 1.511e+00 1.229e+00
Number of obs: 35, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -1.5263 0.2078 34.0000 -7.346 1.64e-08 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

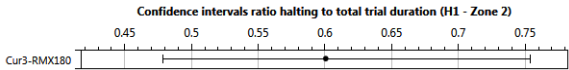
Model residuals

Statistic	Value
Sample skewness	-0.744
Sample excess kurtosis	-0.3347
Passed Shapiro Wilk normality test	No (p-value = 0.01334 < 0.05)



Analysis ratio halting to total trial duration (H1 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_total_trial_duration_H1_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.6005	0.4783	0.754	a

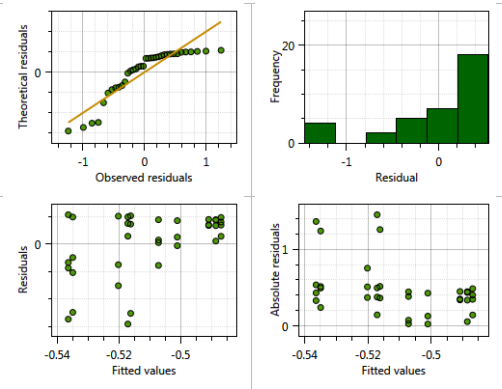
Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_total_trial_duration_H1_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data
REML criterion at convergence: 66.6
Scaled residuals:
Min 1Q Median 3Q Max
-2.4535 -0.5777 0.4095 0.7438 0.9082
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.000000 0.00000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.005814 0.07625
Residual 0.348829 0.59062
Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -0.5099 0.1014 9.4806 -5.029 0.000606 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

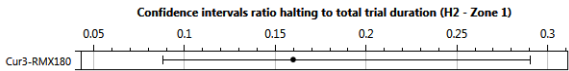
Model residuals

Statistic	Value
Sample skewness	-1.303
Sample excess kurtosis	0.7027
Passed Shapiro Wilk normality test	No (p-value = 2.223E-05 < 0.05)



Analysis ratio halting to total trial duration (H2 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_total_trial_duration_H2_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1598	0.08792	0.2905	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_total_trial_duration_H2_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 116.9

Scaled residuals:
Min 1Q Median 3Q Max
-1.7472 -0.7432 0.1648 0.6700 1.3397

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.2568 0.5068
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.0000 0.0000
Residual 1.4481 1.2034

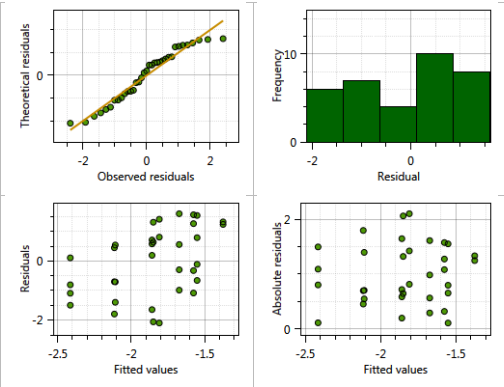
Number of obs: 35, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -1.8337 0.2602 8.1890 -7.047 9.59e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

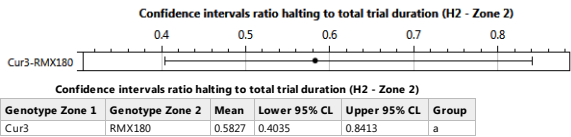
Model residuals

Statistic	Value
Sample skewness	-0.2854
Sample excess kurtosis	-1.115
Passed Shapiro Wilk normality test	Yes (p-value = 0.05806 > 0.05)



Analysis ratio halting to total trial duration (H2 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_total_trial_duration_H2_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_total_trial_duration_H2_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 89.8

Scaled residuals:
Min 1Q Median 3Q Max
-2.9312 -0.1626 0.3074 0.5389 1.3260

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0921 0.3035
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.0000 0.0000
Residual 0.5717 0.7561

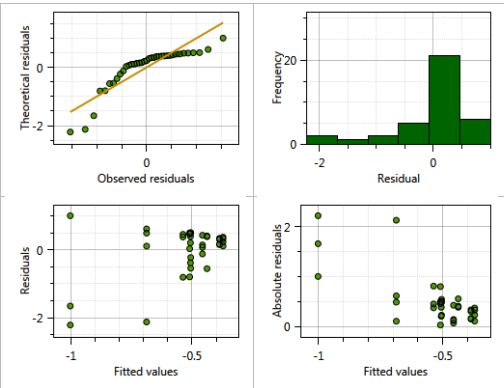
Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -0.5401 0.1573 7.4676 -3.433 0.0099 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

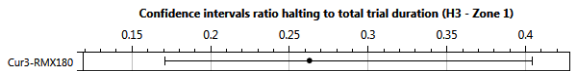
Model residuals

Statistic	Value
Sample skewness	-1.888
Sample excess kurtosis	3.425
Passed Shapiro Wilk normality test	No (p-value = 3.341E-06 < 0.05)



Analysis ratio halting to total trial duration (H3 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_total_trial_duration_H3_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2627	0.1706	0.4044	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_total_trial_duration_H3_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 98.3

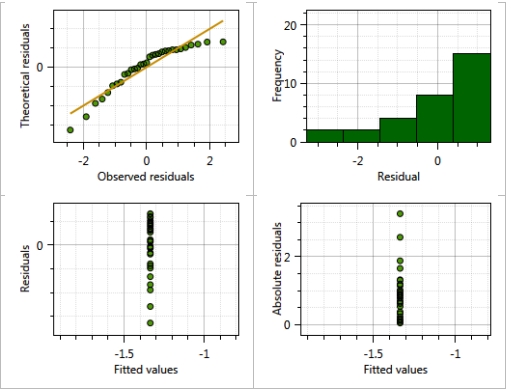
Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.7786 -0.4938  0.1939  0.7501  1.1192

Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.000      0.000
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.000      0.000
Residual                                1.384      1.176
Number of obs: 31, groups:  Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -1.3367      0.2113 30.0000  -6.327 5.61e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

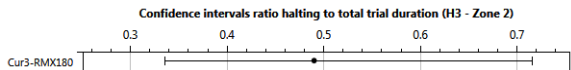
Model residuals

Statistic	Value
Sample skewness	-1.176
Sample excess kurtosis	0.8915
Passed Shapiro Wilk normality test	No (p-value = 0.003136 < 0.05)



Analysis ratio halting to total trial duration (H3 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_total_trial_duration_H3_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4899	0.3353	0.716	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_total_trial_duration_H3_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 110.9

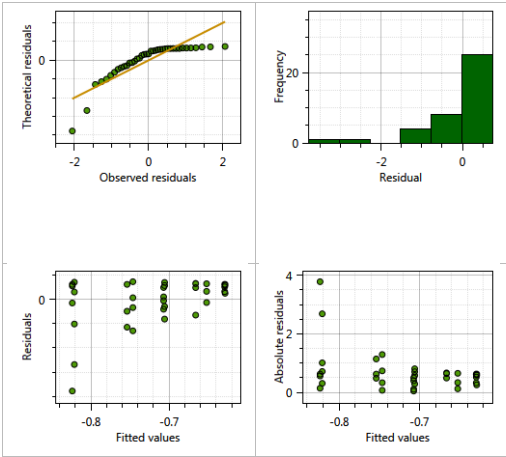
Scaled residuals:
    Min       1Q   Median       3Q      Max
-3.8769 -0.3182  0.3461  0.6432  0.7550

Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  5.350e-17 7.314e-09
Genotype_Zone_2:Plant_Zone_2 (Intercept)  3.839e-02 1.959e-01
Residual                                9.513e-01 9.753e-01
Number of obs: 39, groups:  Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -0.7135      0.1681  9.1382  -4.245  0.00209 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

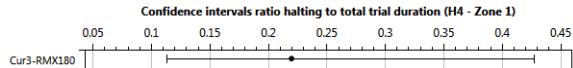
Model residuals

Statistic	Value
Sample skewness	-2.335
Sample excess kurtosis	6.409
Passed Shapiro Wilk normality test	No (p-value = 3.04E-07 < 0.05)



Analysis ratio halting to total trial duration (H4 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_total_trial_duration_H4_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2197	0.1129	0.4275	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_total_trial_duration_H4_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 92

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.29100	-0.66085	0.01235	0.81416	1.32386

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.2587	0.5086
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		1.3593	1.1659

Number of obs: 28, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 9

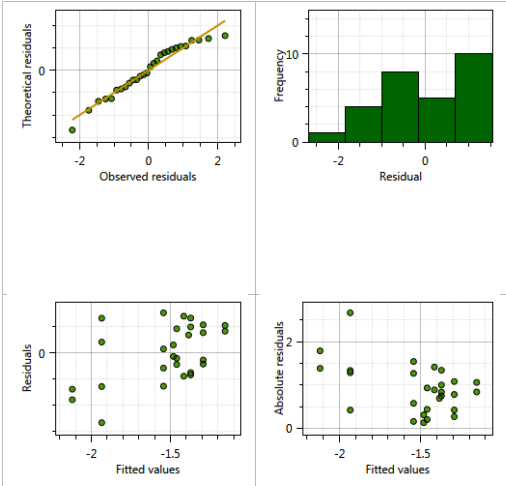
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.5156	0.2777	6.5463	-5.458	0.00118 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

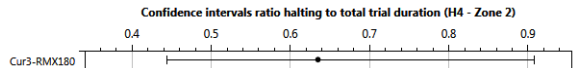
Model residuals

Statistic	Value
Sample skewness	-0.4995
Sample excess kurtosis	-0.4037
Passed Shapiro Wilk normality test	Yes (p-value = 0.2291 > 0.05)



Analysis ratio halting to total trial duration (H4 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_total_trial_duration_H4_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.6347	0.4436	0.9082	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_total_trial_duration_H4_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 86

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.7717	-0.0954	0.3617	0.5280	0.9480

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.03409	0.1846
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.05740	0.2396
Residual		0.50199	0.7085

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

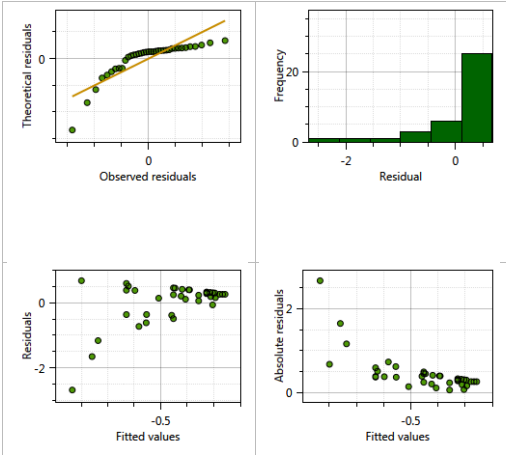
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.4545	0.1513	6.9543	-3.004	0.02 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

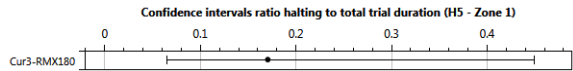
Model residuals

Statistic	Value
Sample skewness	-2.448
Sample excess kurtosis	6.968
Passed Shapiro Wilk normality test	No (p-value = 4.295E-07 < 0.05)



Analysis ratio halting to total trial duration (H5 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_total_trial_duration_H5_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1705	0.06465	0.4496	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_total_trial_duration_H5_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 101.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.0300	-0.4217	0.1774	0.4584	1.1581

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.5983	0.7735
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.7034	0.8387
Residual		1.2972	1.1389

Number of obs: 28, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

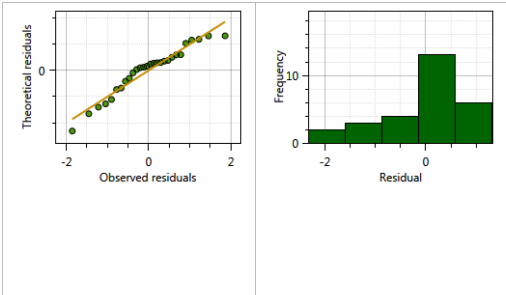
Fixed effects:

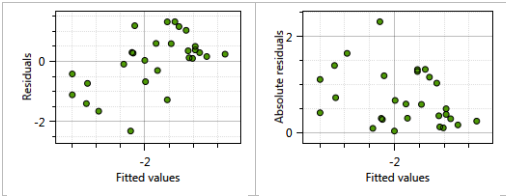
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.7691	0.4251	8.5353	-4.162	0.00274 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

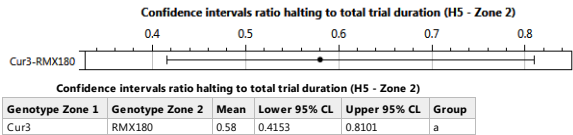
Statistic	Value
Sample skewness	-0.7206
Sample excess kurtosis	0.1911
Passed Shapiro Wilk normality test	Yes (p-value = 0.1179 > 0.05)





Analysis ratio halting to total trial duration (H5 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_total_trial_duration_H5_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_total_trial_duration_H5_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 95.6

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-2.5868	-0.2176	0.4130	0.5626	1.0267

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	4.564e-19	6.756e-10
Genotype_Zone_2:Plant_Zone_2	(Intercept)	6.355e-02	2.521e-01
Residual		6.062e-01	7.786e-01

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

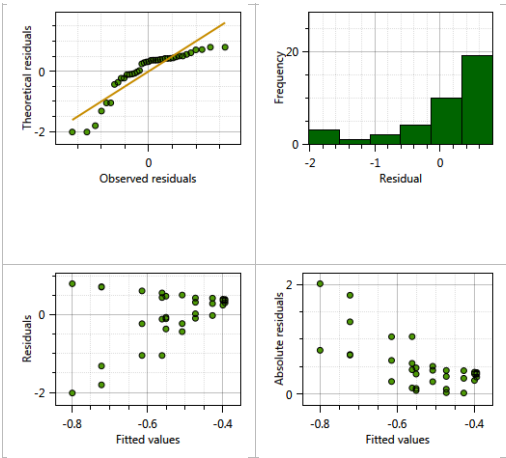
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.5447	0.1481	9.1540	-3.678	0.00494 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

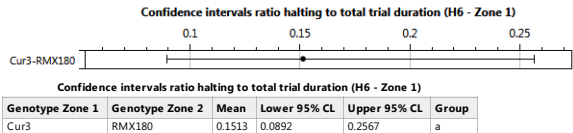
Model residuals

Statistic	Value
Sample skewness	-1.548
Sample excess kurtosis	1.684
Passed Shapiro Wilk normality test	No (p-value = 9.356E-06 < 0.05)



Analysis ratio halting to total trial duration (H6 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_total_trial_duration_H6_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_total_trial_duration_H6_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 87.6

Scaled residuals:

	Min	1Q	Median	3Q	Max
	-2.0763	-0.4646	0.1533	0.6384	1.4431

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000	0.000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000	0.000
Residual		1.712	1.309

Number of obs: 26, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

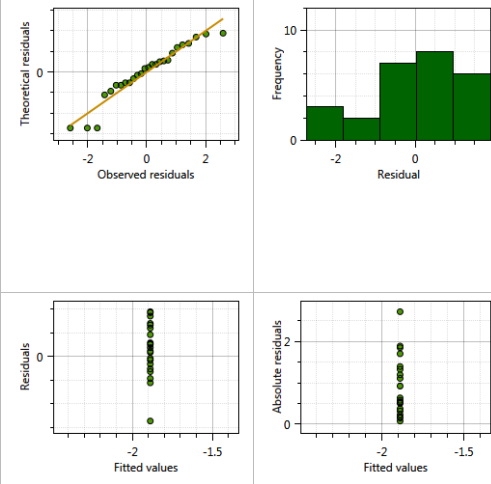
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.8883	0.2566	25.0000	-7.358	1.04e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

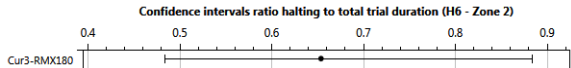
Model residuals

Statistic	Value
Sample skewness	-0.7165
Sample excess kurtosis	0.2273
Passed Shapiro Wilk normality test	Yes (p-value = 0.061 > 0.05)



Analysis ratio halting to total trial duration (H6 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_total_trial_duration_H6_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.6536	0.4833	0.884	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_total_trial_duration_H6_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 102.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.5511	0.1424	0.3050	0.4629	0.4629

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		0.8435	0.9184

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

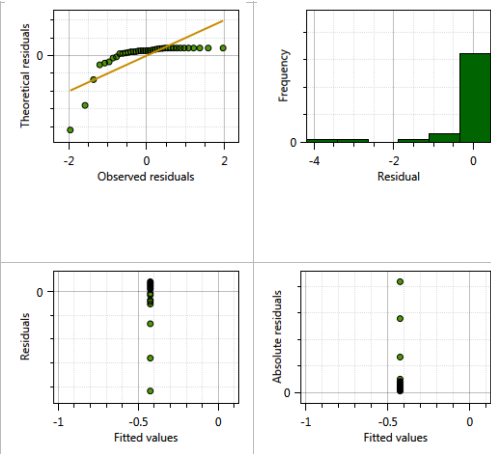
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.4252	0.1490	37.0000	-2.854	0.00704 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

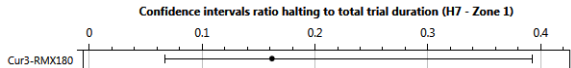
Model residuals

Statistic	Value
Sample skewness	-3.542
Sample excess kurtosis	13.28
Passed Shapiro Wilk normality test	No (p-value = 2.8E-10 < 0.05)



Analysis ratio halting to total trial duration (H7 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_total_trial_duration_H7_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio halting to total trial duration (H7 - Zone 1)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1618	0.06669	0.3927	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_total_trial_duration_H7_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 94.7

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.6714	-0.7657	0.3403	0.8563	1.1057

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.42897	0.6550
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.01083	0.1041
Residual		1.93498	1.3910

Number of obs: 26, groups: Genotype_Zone_2:Plant_Zone_2, 10; Genotype_Zone_1:Plant_Zone_1, 9

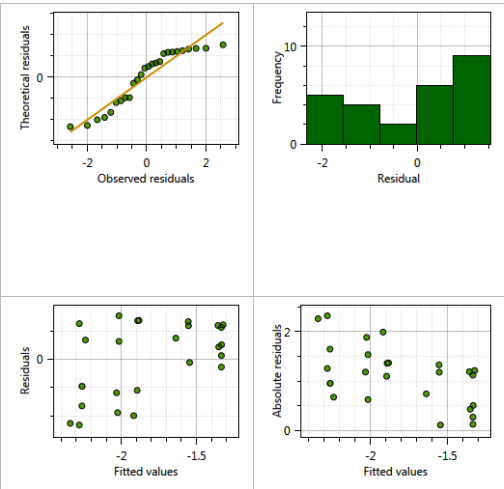
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.8212	0.3539	5.4752	-5.146	0.00279 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

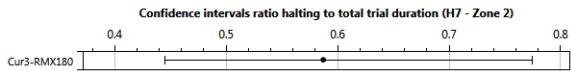
Model residuals

Statistic	Value
Sample skewness	-0.5369
Sample excess kurtosis	-1.199
Passed Shapiro Wilk normality test	No (p-value = 0.006784 < 0.05)



Analysis ratio halting to total trial duration (H7 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_halting_to_total_trial_duration_H7_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio halting to total trial duration (H7 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.587	0.4447	0.7748	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_halting_to_total_trial_duration_H7_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 89.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.8366	-0.4133	0.4918	0.6876	0.7563

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	2.937e-16	1.714e-08
Genotype_Zone_2:Plant_Zone_2	(Intercept)	8.749e-03	9.354e-02
Residual		5.478e-01	7.401e-01

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

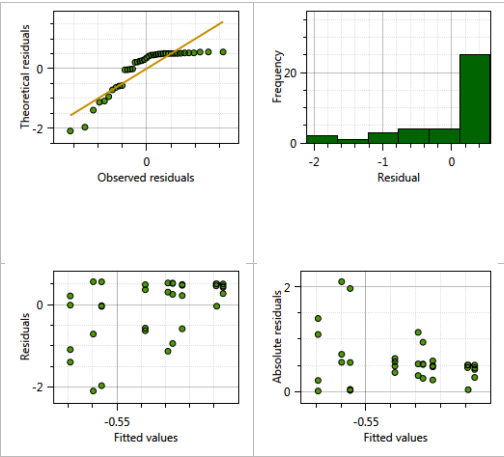
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.5327	0.1222	8.7561	-4.361	0.00194 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

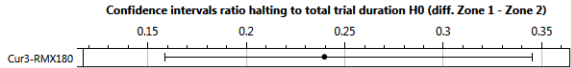
Model residuals

Statistic	Value
Sample skewness	-1.507
Sample excess kurtosis	1.405
Passed Shapiro Wilk normality test	No (p-value = 1.095E-06 < 0.05)



Analysis ratio halting to total trial duration H0 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_halting_to_total_trial_duration_H0_Zone_1,Ratio_halting_to_total_trial_duration_H0_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals ratio halting to total trial duration H0 (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2397	0.1585	0.3453	a

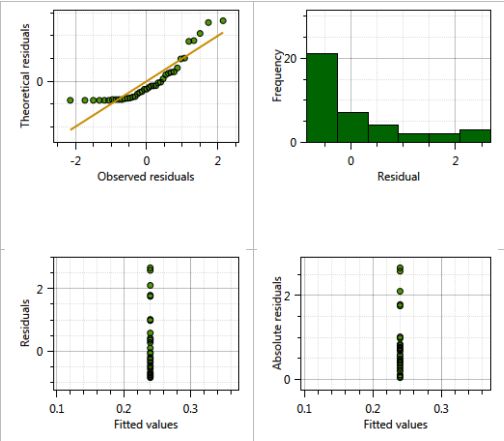
Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi
REML criterion at convergence: 146.7
Scaled residuals:
Min IQ Median 3Q Max
-0.8397 -0.7848 -0.3492 0.3742 2.6638
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 3.620e-17 6.017e-09
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.000e+00 0.000e+00
Residual 4.471e-01 6.686e-01
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -1.1545 0.2542 38.0000 -4.542 5.49e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Dispersion: 0.6686

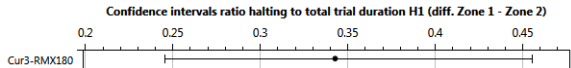
Model residuals

Statistic	Value
Sample skewness	1.415
Sample excess kurtosis	1.149
Passed Shapiro Wilk normality test	No (p-value = 8.499E-06 < 0.05)



Analysis ratio halting to total trial duration H1 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_halting_to_total_trial_duration_H1_Zone_1,Ratio_halting_to_total_trial_duration_H1_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals ratio halting to total trial duration H1 (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.3427	0.2452	0.4556	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data

Weights: wi

REML criterion at convergence: 140.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.0617	-0.8728	-0.2061	0.7639	2.0361

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		0.4626	0.6801

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

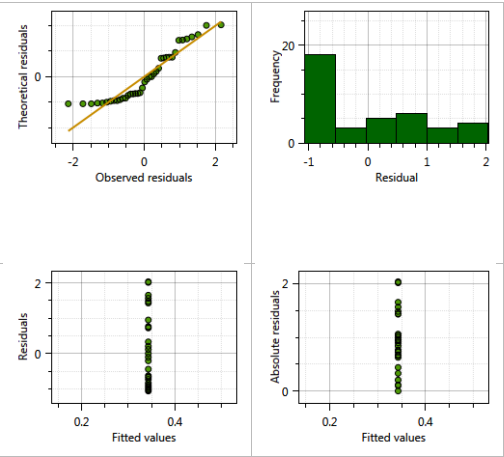
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.6512	0.2337	38.0000	-2.787	0.00827 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.6801

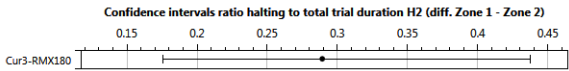
Model residuals

Statistic	Value
Sample skewness	0.6227
Sample excess kurtosis	-0.9676
Passed Shapiro Wilk normality test	No (p-value = 0.0005821 < 0.05)



Analysis ratio halting to total trial duration H2 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_halting_to_total_trial_duration_H2_Zone_1,Ratio_halting_to_total_trial_duration_H2_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2892	0.1754	0.4376	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: ziFormula

Data: data

Weights: wi

REML criterion at convergence: 147

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.1140	-0.7559	-0.3947	0.2989	2.0822

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	1.984e-01	4.454e-01
Genotype_Zone_2:Plant_Zone_2	(Intercept)	8.423e-16	2.902e-08
Residual		4.578e-01	6.766e-01

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

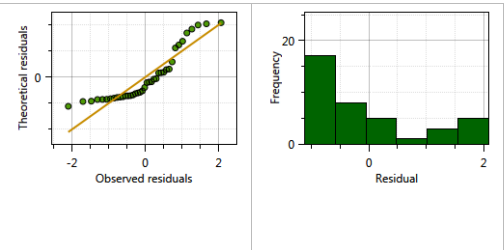
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.8994	0.2833	8.3540	-3.175	0.0124 *

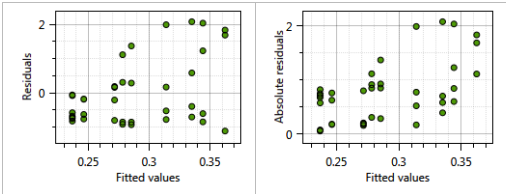
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.6766

Model residuals

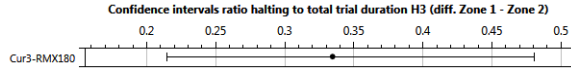
Statistic	Value
Sample skewness	1.056
Sample excess kurtosis	-0.1525
Passed Shapiro Wilk normality test	No (p-value = 4.6E-05 < 0.05)





Analysis ratio halting to total trial duration H3 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_halting_to_total_trial_duration_H3_Zone_1,Ratio_halting_to_total_trial_duration_H3_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals ratio halting to total trial duration H3 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.3346	0.2144	0.4808	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 140.3

Scaled residuals:
  Min       1Q   Median       3Q      Max
-1.2113 -0.9132 -0.1675  0.8075  1.8966

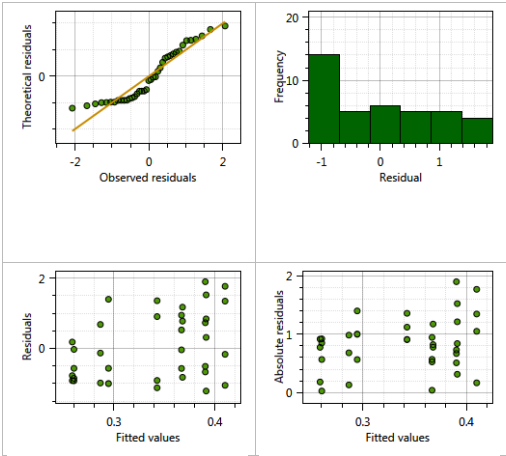
Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  5.262e-16  2.294e-08
Genotype_Zone_2:Plant_Zone_2 (Intercept)  2.220e-01  4.711e-01
Residual                                4.158e-01  6.448e-01
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -0.6876     0.2691  8.7996  -2.555   0.0315 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.6448
```

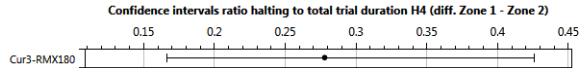
Model residuals

Statistic	Value
Sample skewness	0.4867
Sample excess kurtosis	-1.197
Passed Shapiro Wilk normality test	No (p-value = 0.001491 < 0.05)



Analysis ratio halting to total trial duration H4 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_halting_to_total_trial_duration_H4_Zone_1,Ratio_halting_to_total_trial_duration_H4_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals ratio halting to total trial duration H4 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2778	0.1662	0.4261	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 150.4

Scaled residuals:
  Min       1Q   Median       3Q      Max
-0.8852 -0.7531 -0.4046  0.7761  2.1739

Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  1.185e-15  3.443e-08
Genotype_Zone_2:Plant_Zone_2 (Intercept)  1.518e-01  3.896e-01
Residual                                5.205e-01  7.215e-01
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

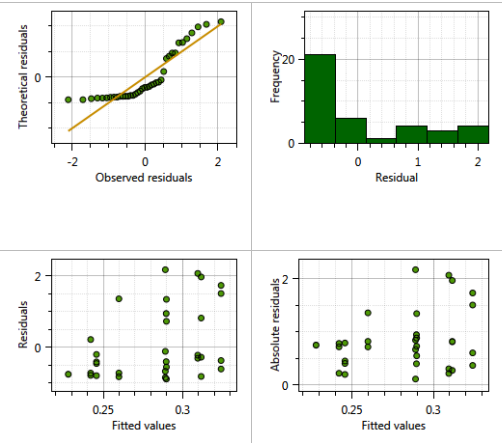
Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
```

```
(Intercept)  -0.9555    0.2884  8.5621  -3.313  0.00968 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.7215
```

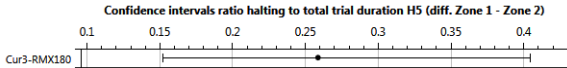
Model residuals

Statistic	Value
Sample skewness	1.072
Sample excess kurtosis	-0.2959
Passed Shapiro Wilk normality test	No (p-value = 6.873E-06 < 0.05)



Analysis ratio halting to total trial duration H5 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_halting_to_total_trial_duration_H5_Zone_1,Ratio_halting_to_total_trial_duration_H5_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2586	0.1519	0.4046	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 150.7

Scaled residuals:
Min IQ Median 3Q Max
-0.9826 -0.7569 -0.5539 0.5572 2.2565

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.1931 0.4394
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.0000 0.0000
Residual 0.4885 0.6990
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

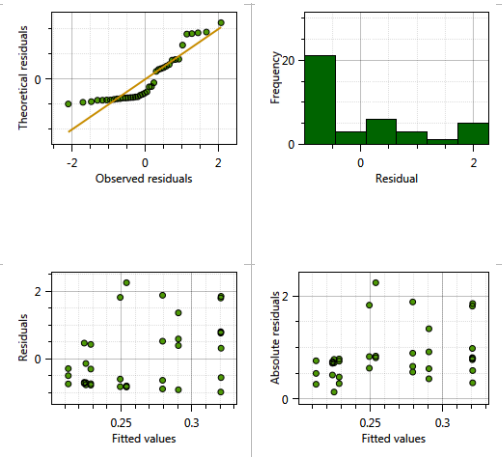
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -1.0533 0.2948 9.0019 -3.573 0.006 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.699

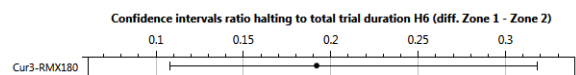
Model residuals

Statistic	Value
Sample skewness	0.9853
Sample excess kurtosis	-0.2973
Passed Shapiro Wilk normality test	No (p-value = 2.555E-05 < 0.05)



Analysis ratio halting to total trial duration H6 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_halting_to_total_trial_duration_H6_Zone_1,Ratio_halting_to_total_trial_duration_H6_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals ratio halting to total trial duration H6 (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.1918	0.1077	0.3183	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 153

Scaled residuals:
    Min       1Q   Median       3Q      Max
-0.9864 -0.6962 -0.4308  0.2813  2.6698

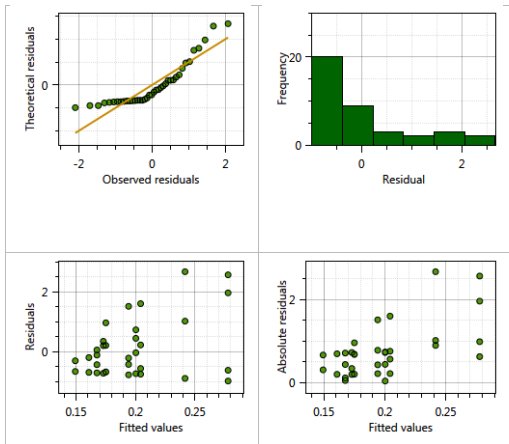
Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0000  0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.2309  0.4805
Residual                      0.3952  0.6287
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -1.4381     0.3028  9.8326  -4.749 0.000819 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.6287
```

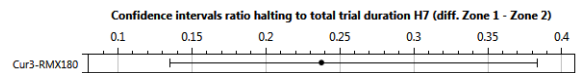
Model residuals

Statistic	Value
Sample skewness	1.431
Sample excess kurtosis	1.315
Passed Shapiro Wilk normality test	No (p-value = 1.59E-05 < 0.05)



Analysis ratio halting to total trial duration H7 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_halting_to_total_trial_duration_H7_Zone_1,Ratio_halting_to_total_trial_duration_H7_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals ratio halting to total trial duration H7 (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.2375	0.1348	0.3836	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 152.5

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.0109 -0.7510 -0.5683  0.6351  2.0049

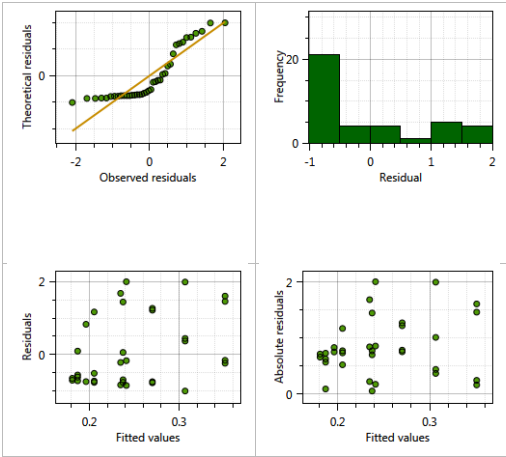
Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0000  0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.2833  0.5323
Residual                      0.4327  0.6578
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -1.1665     0.3073  9.2471  -3.796 0.00404 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.6578
```

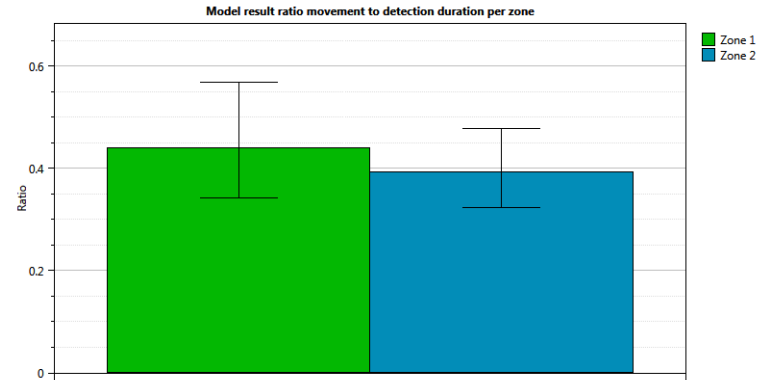
Model residuals

Statistic	Value
Sample skewness	0.9396
Sample excess kurtosis	-0.6459
Passed Shapiro Wilk normality test	No (p-value = 1.075E-05 < 0.05)



Ratio movement to detection duration per zone

Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

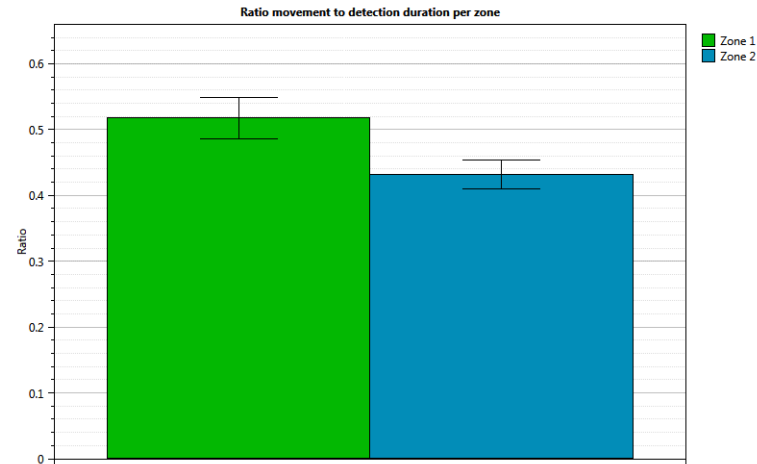
Behaviour statistic	Cur3-RMX180
Ratio movement to detection duration (diff. Zone 1 - Zone 2)	p=0.00335** [0.0655, 0.305]

The model predictions and 95% confidence intervals for each statistic.

Statistic	Cur3-RMX180	Remark
Ratio movement to detection duration (Zone 1)	0.441 [0.342, 0.569]	CR
Ratio movement to detection duration (Zone 2)	0.393 [0.323, 0.479]	CR

CR = Check residuals

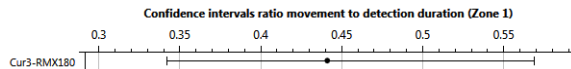
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean Zone 1	StdErr Zone 1	Mean Zone 2	StdErr Zone 2
Cur3	RMX180	Neutral	0.52	0.03	0.43	0.02

Analysis ratio movement to detection duration (Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_detection_duration_Zone_1 ~ 1 + (1 Genotype_Zone_1 Plant_Zone_1) + (1 Genotype_Zone_2 Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.441	0.3418	0.569	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_detection_duration_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 93.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.8166	-0.1277	0.3264	0.4928	0.8347

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	6.512e-16	2.552e-08
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000e+00	0.000e+00
Residual		6.180e-01	7.861e-01

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

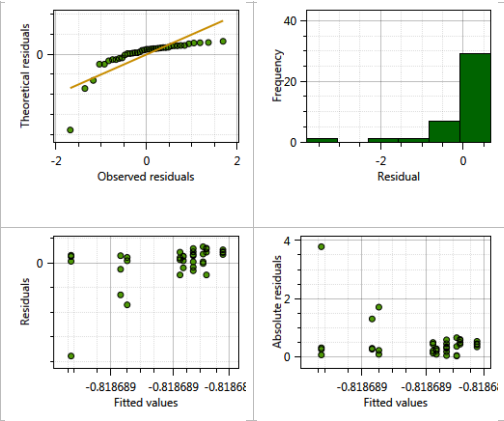
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.8187	0.1259	38.0000	-6.504	1.16e-07 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

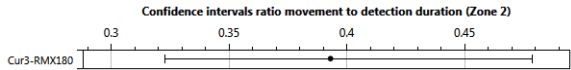
Model residuals

Statistic	Value
Sample skewness	-3.427
Sample excess kurtosis	14.34
Passed Shapiro Wilk normality test	No (p-value = 1.01E-08 < 0.05)



Analysis ratio movement to detection duration (Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_detection_duration_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.3931	0.3227	0.4788	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_detection_duration_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 61.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.9425	-0.0516	0.2745	0.4943	1.0883

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	1.940e-16	1.393e-08
Genotype_Zone_2:Plant_Zone_2	(Intercept)	2.802e-03	5.293e-02
Residual		2.684e-01	5.181e-01

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

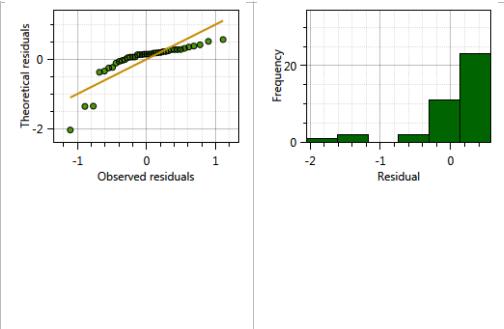
Fixed effects:

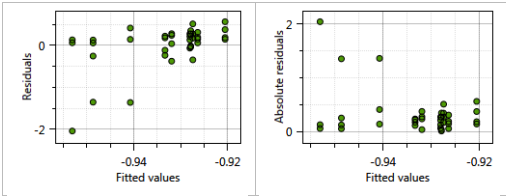
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.93379	0.08464	7.51787	-11.03	6.55e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

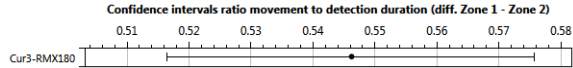
Statistic	Value
Sample skewness	-2.627
Sample excess kurtosis	7.437
Passed Shapiro Wilk normality test	No (p-value = 6.637E-08 < 0.05)





Analysis ratio movement to detection duration (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_movement_to_detection_duration_Zone_1,Ratio_movement_to_detection_duration_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals ratio movement to detection duration (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5462	0.5164	0.5757	a

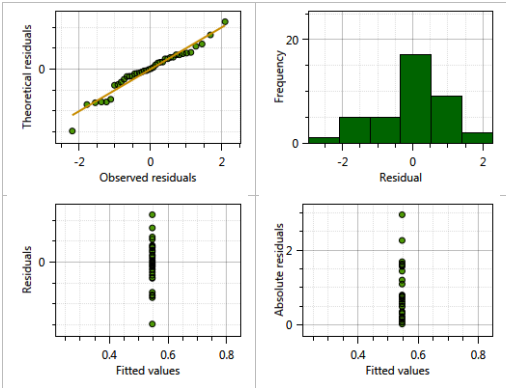
Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1
REML criterion at convergence: 39.6
Scaled residuals:
Min 1Q Median 3Q Max
-2.95413 -0.41781 -0.01872 0.56486 2.26367
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.00000 0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.00000 0.0000
Residual 0.03218 0.1794
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 0.18539 0.05923 38.00000 3.13 0.00335 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Dispersion: 0.1794

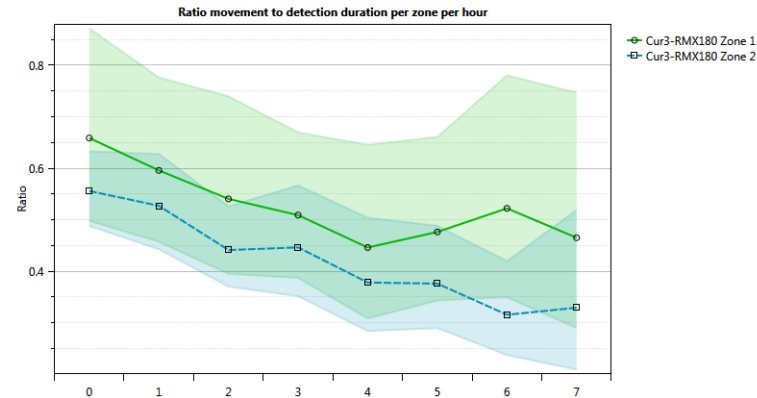
Model residuals

Statistic	Value
Sample skewness	-0.5259
Sample excess kurtosis	1.154
Passed Shapiro Wilk normality test	Yes (p-value = 0.2331 > 0.05)



Ratio movement to detection duration per zone per hour

Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

Behaviour statistic	Cur3-RMX180	Remark
Ratio movement to detection duration H0 (diff. Zone 1 - Zone 2)	p=0.0076** [0.0614, 0.37]	CR

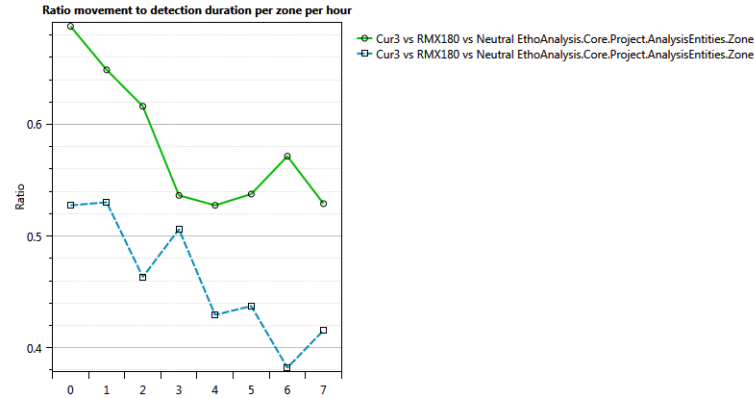
Behaviour statistic	Cur3-RMX180	Remark
Ratio movement to detection duration H1 (diff. Zone 1 - Zone 2)	p=0.0233* [0.0254, 0.327]	
Ratio movement to detection duration H2 (diff. Zone 1 - Zone 2)	p=0.00569** [0.0795, 0.433]	
Ratio movement to detection duration H3 (diff. Zone 1 - Zone 2)	p=0.844 [-0.22, 0.181]	
Ratio movement to detection duration H4 (diff. Zone 1 - Zone 2)	p=0.166 [-0.0866, 0.429]	
Ratio movement to detection duration H5 (diff. Zone 1 - Zone 2)	p=0.367 [-0.19, 0.464]	
Ratio movement to detection duration H6 (diff. Zone 1 - Zone 2)	p=0.0353* [0.0221, 0.576]	
Ratio movement to detection duration H7 (diff. Zone 1 - Zone 2)	p=0.441 [-0.251, 0.51]	

CR = Check residuals

The model predictions and 95% confidence intervals for each statistic.		
Statistic	Cur3-RMX180	Remark
Ratio movement to detection duration (H0 - Zone 1)	0.659 [0.498, 0.872]	CR
Ratio movement to detection duration (H0 - Zone 2)	0.556 [0.488, 0.633]	
Ratio movement to detection duration (H1 - Zone 1)	0.596 [0.457, 0.776]	CR
Ratio movement to detection duration (H1 - Zone 2)	0.527 [0.443, 0.628]	CR
Ratio movement to detection duration (H2 - Zone 1)	0.541 [0.395, 0.74]	CR
Ratio movement to detection duration (H2 - Zone 2)	0.441 [0.37, 0.526]	CR
Ratio movement to detection duration (H3 - Zone 1)	0.509 [0.387, 0.67]	
Ratio movement to detection duration (H3 - Zone 2)	0.446 [0.352, 0.567]	CR
Ratio movement to detection duration (H4 - Zone 1)	0.446 [0.308, 0.646]	CR
Ratio movement to detection duration (H4 - Zone 2)	0.378 [0.284, 0.504]	CR
Ratio movement to detection duration (H5 - Zone 1)	0.476 [0.343, 0.661]	CR
Ratio movement to detection duration (H5 - Zone 2)	0.376 [0.29, 0.488]	CR
Ratio movement to detection duration (H6 - Zone 1)	0.522 [0.35, 0.78]	CR
Ratio movement to detection duration (H6 - Zone 2)	0.316 [0.237, 0.42]	CR
Ratio movement to detection duration (H7 - Zone 1)	0.465 [0.29, 0.747]	CR
Ratio movement to detection duration (H7 - Zone 2)	0.329 [0.209, 0.519]	CR

CR = Check residuals

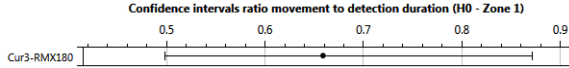
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean H0 - Zone 1	StdErr H0 - Zone 1	Mean H0 - Zone 2	StdErr H0 - Zone 2	Mean H1 - Zone 1	StdErr H1 - Zone 1	Mean H1 - Zone 2	StdErr H1 - Zone 2	Mean H2 - Zone 1	StdErr H2 - Zone 1	Mean H2 - Zone 2	StdErr H2 - Zone 2	Mean H3 - Zone 1	StdErr H3 - Zone 1	Mean H3 - Zone 2	StdErr H3 - Zone 2	Mean H4 - Zone 1	StdErr H4 - Zone 1	Mean H4 - Zone 2	StdErr H4 - Zone 2	Mean H5 - Zone 1	StdErr H5 - Zone 1	Mean H5 - Zone 2	StdErr H5 - Zone 2	Mean H6 - Zone 1	StdErr H6 - Zone 1	Mean H6 - Zone 2	StdErr H6 - Zone 2
Cur3	RMX180	Neutral	0.69	0.04	0.53	0.03	0.65	0.04	0.53	0.03	0.62	0.05	0.46	0.03	0.54	0.05	0.51	0.03	0.53	0.05	0.43	0.03	0.54	0.05	0.44	0.03	0.57	0.06	0.38	0.03

Analysis ratio movement to detection duration (H0 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_detection_duration_H0_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.6588	0.4979	0.8717	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_detection_duration_H0_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 40.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.9423	-0.2410	0.1371	0.5034	1.2674

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0909	0.3015
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		0.1343	0.3665

Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

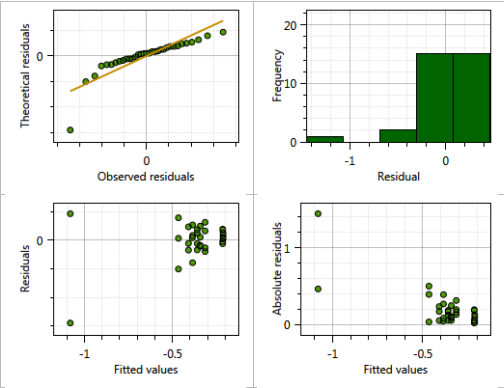
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.4174	0.1165	6.4696	-3.583	0.0102 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

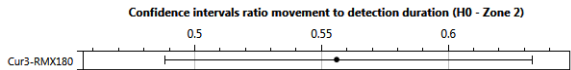
Model residuals

Statistic	Value
Sample skewness	-2.727
Sample excess kurtosis	11.1
Passed Shapiro Wilk normality test	No (p-value = 7.09E-06 < 0.05)



Analysis ratio movement to detection duration (H0 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_detection_duration_H0_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5559	0.4881	0.6332	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_detection_duration_H0_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 10.5

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.2893	-0.5360	0.1256	0.4088	1.9777

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.01547	0.1244
Residual		0.06035	0.2457

Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

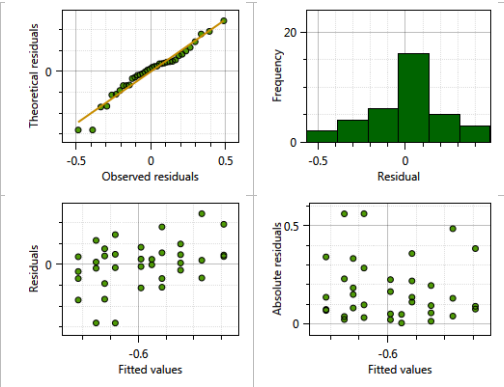
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.58711	0.05706	8.55735	-10.29	4.15e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

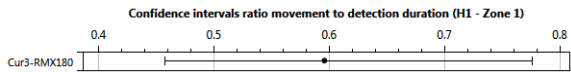
Model residuals

Statistic	Value
Sample skewness	-0.4822
Sample excess kurtosis	0.8256
Passed Shapiro Wilk normality test	Yes (p-value = 0.2839 > 0.05)



Analysis ratio movement to detection duration (H1 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_detection_duration_H1_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5958	0.4572	0.7764	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_detection_duration_H1_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 64.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-----	----	--------	----	-----

-4.3455 -0.1795 0.2740 0.5615 0.7718

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.04514	0.2125
Residual		0.29938	0.5472

Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

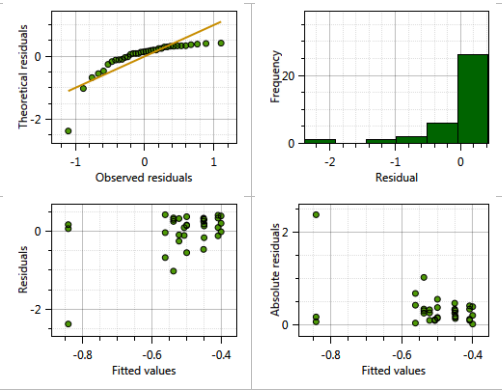
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.5178	0.1135	7.5171	-4.562	0.00217 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

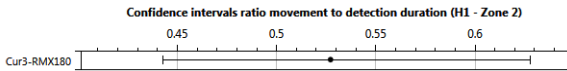
Model residuals

Statistic	Value
Sample skewness	-3.096
Sample excess kurtosis	12.08
Passed Shapiro Wilk normality test	No (p-value = 1.074E-07 < 0.05)



Analysis ratio movement to detection duration (H1 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_detection_duration_H1_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5272	0.4426	0.628	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_detection_duration_H1_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 40.7

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.8511	-0.1745	0.1093	0.4000	1.5033

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	1.400e-17	3.742e-09
Genotype_Zone_2:Plant_Zone_2	(Intercept)	8.840e-03	9.402e-02
Residual		1.566e-01	3.957e-01

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

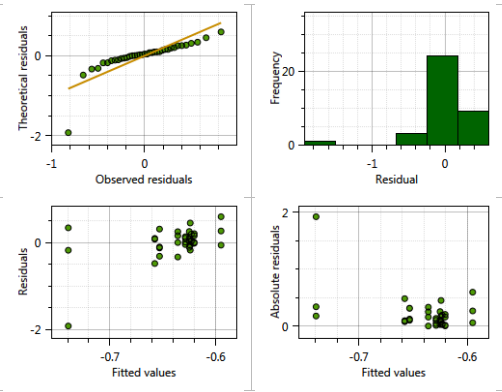
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.64023	0.07161	6.03967	-8.94	0.000105 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

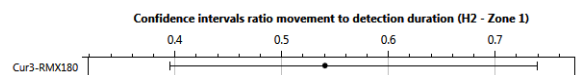
Model residuals

Statistic	Value
Sample skewness	-3.451
Sample excess kurtosis	17
Passed Shapiro Wilk normality test	No (p-value = 1.079E-07 < 0.05)



Analysis ratio movement to detection duration (H2 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_detection_duration_H2_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio movement to detection duration (H2 - Zone 1)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5405	0.395	0.7397	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_detection_duration_H2_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 71

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.0585	-0.4411	0.3481	0.5708	1.4531

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.1004	0.3168
Residual		0.3328	0.5769

Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

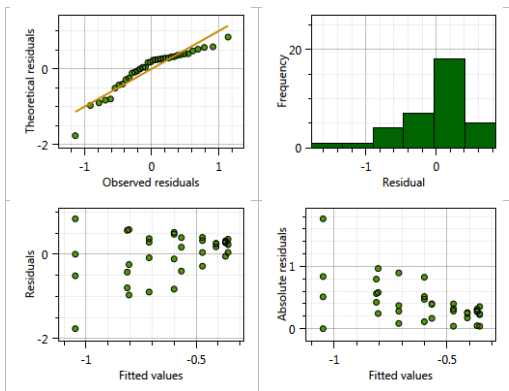
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.6152	0.1392	9.2324	-4.42	0.00157 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

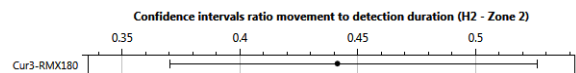
Model residuals

Statistic	Value
Sample skewness	-1.342
Sample excess kurtosis	2.099
Passed Shapiro Wilk normality test	No (p-value = 0.001793 < 0.05)



Analysis ratio movement to detection duration (H2 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_detection_duration_H2_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio movement to detection duration (H2 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4413	0.3701	0.5262	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_detection_duration_H2_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 59.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.4868	-0.4389	0.1983	0.5176	1.3285

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		0.2788	0.5281

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

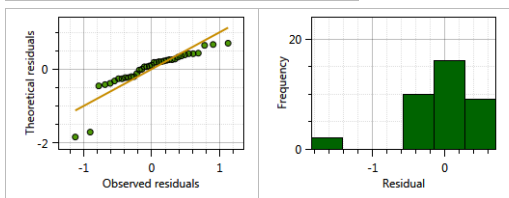
Fixed effects:

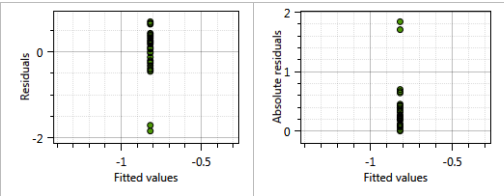
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.81805	0.08681	36.00000	-9.423	2.96e-11 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

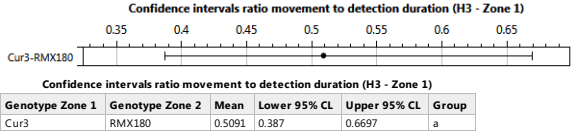
Statistic	Value
Sample skewness	-2.03
Sample excess kurtosis	5.557
Passed Shapiro Wilk normality test	No (p-value = 1.62E-05 < 0.05)





Analysis ratio movement to detection duration (H3 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_detection_duration_H3_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_detection_duration_H3_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 54.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.3647	-0.5421	0.2401	0.5972	1.6333

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.01696	0.1302
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.04675	0.2162
Residual		0.24138	0.4913

Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

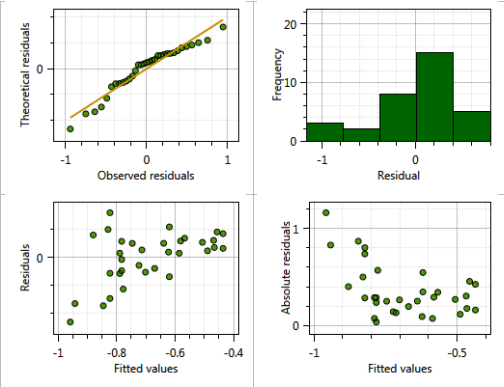
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.6752	0.1179	7.6118	-5.728	0.000528 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

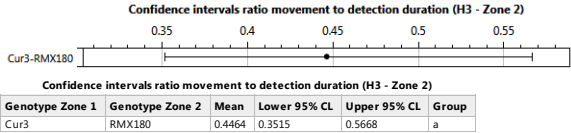
Model residuals

Statistic	Value
Sample skewness	-0.8167
Sample excess kurtosis	0.2945
Passed Shapiro Wilk normality test	Yes (p-value = 0.06869 > 0.05)



Analysis ratio movement to detection duration (H3 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_detection_duration_H3_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_detection_duration_H3_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 72

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.5281	-0.1882	0.2662	0.5888	1.1442

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.02689	0.1640
Residual		0.33167	0.5759

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

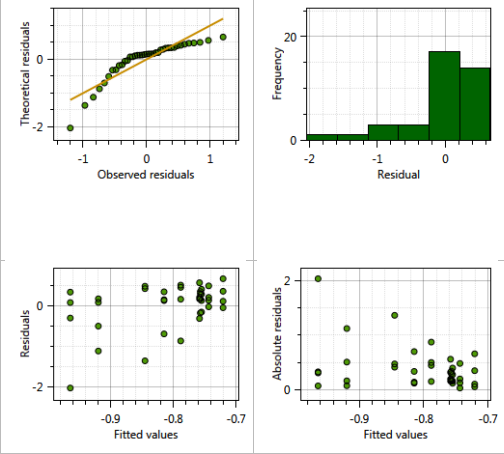
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.8066	0.1059	9.1706	-7.62	2.94e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

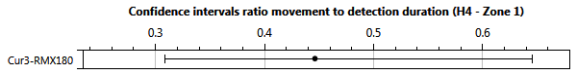
Model residuals

Statistic	Value
Sample skewness	-1.944
Sample excess kurtosis	4.179
Passed Shapiro Wilk normality test	No (p-value = 8.774E-06 < 0.05)



Analysis ratio movement to detection duration (H4 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_detection_duration_H4_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4462	0.3083	0.6457	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_detection_duration_H4_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 69.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.3925	-0.2011	0.3861	0.6667	1.0638

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0790	0.2811
Residual		0.5169	0.7189

Number of obs: 30, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

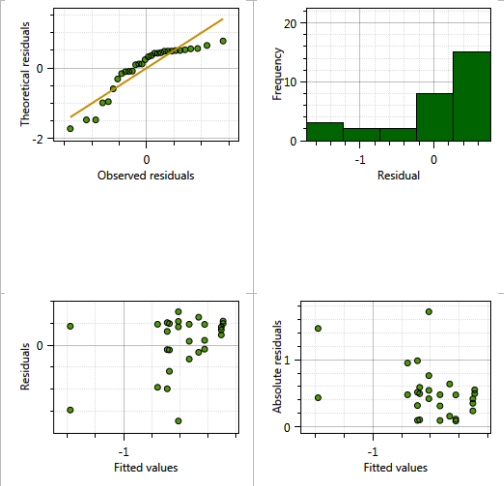
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.8070	0.1597	7.8349	-5.054	0.00105 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

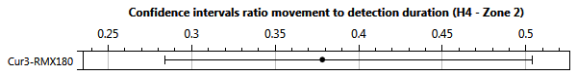
Model residuals

Statistic	Value
Sample skewness	-1.322
Sample excess kurtosis	0.7704
Passed Shapiro Wilk normality test	No (p-value = 0.0001739 < 0.05)



Analysis ratio movement to detection duration (H4 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_detection_duration_H4_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.3782	0.2838	0.504	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_detection_duration_H4_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) +
(1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 74.3

Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.9975 -0.0326  0.2569  0.5125  1.2086

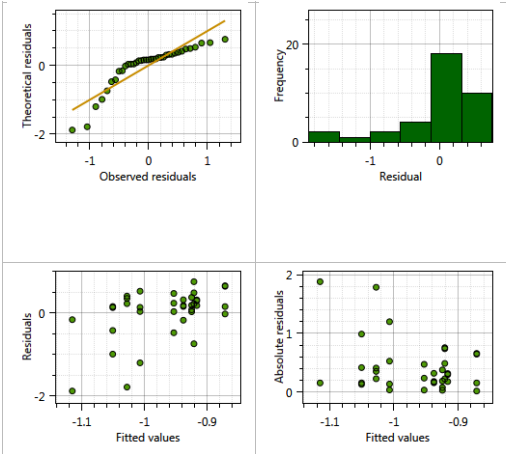
Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.00000  0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.02756  0.1660
Residual                      0.39365  0.6274

Number of obs: 37, groups:  Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   -0.9724     0.1160  5.7327  -8.379   2e-04 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

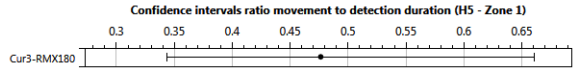
Model residuals

Statistic	Value
Sample skewness	-1.792
Sample excess kurtosis	3.104
Passed Shapiro Wilk normality test	No (p-value = 1.287E-05 < 0.05)



Analysis ratio movement to detection duration (H5 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_detection_duration_H5_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio movement to detection duration (H5 - Zone 1)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4763	0.3433	0.661	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_detection_duration_H5_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) +
(1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 62.6

Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.4473 -0.4980  0.1956  0.6349  1.1829

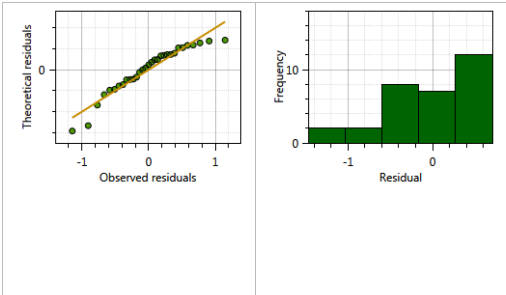
Random effects:
Groups              Name              Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.080838  0.28432
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.003602  0.06001
Residual                      0.356889  0.59740

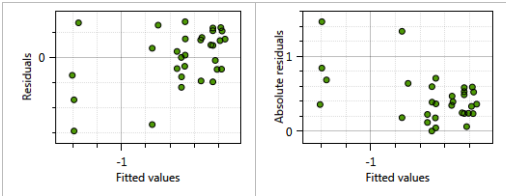
Number of obs: 31, groups:  Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   -0.7416     0.1426  8.1829  -5.201 0.000765 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model residuals

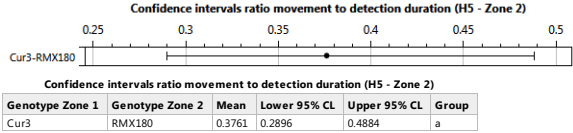
Statistic	Value
Sample skewness	-0.9809
Sample excess kurtosis	0.7264
Passed Shapiro Wilk normality test	No (p-value = 0.02248 < 0.05)





Analysis ratio movement to detection duration (H5 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_detection_duration_H5_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_detection_duration_H5_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 76

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.3769	-0.4693	0.2427	0.6612	1.3713

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.04202	0.2050
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.00000	0.0000
Residual		0.35971	0.5998

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

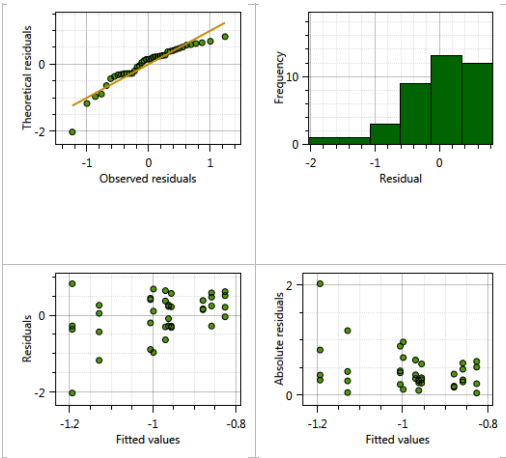
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.9779	0.1159	9.2385	-8.434	1.23e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

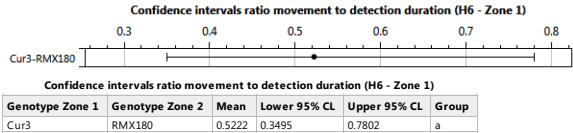
Model residuals

Statistic	Value
Sample skewness	-1.404
Sample excess kurtosis	2.846
Passed Shapiro Wilk normality test	No (p-value = 0.002086 < 0.05)



Analysis ratio movement to detection duration (H6 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_detection_duration_H6_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_detection_duration_H6_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 58

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.4588	-0.2706	0.2866	0.4878	1.4006

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.1608	0.4010
Residual		0.3712	0.6093

Number of obs: 27, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

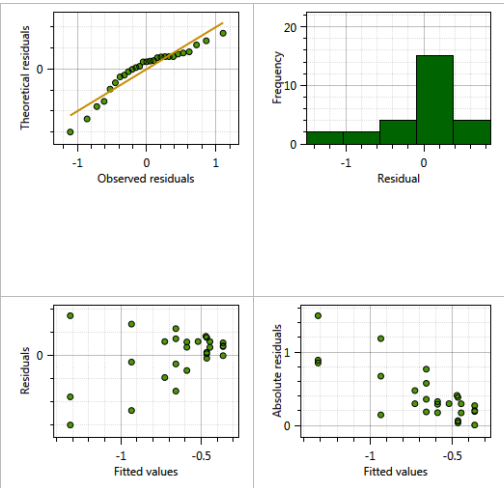
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.6497	0.1770	8.8496	-3.67	0.00531 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

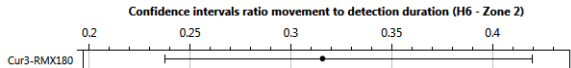
Model residuals

Statistic	Value
Sample skewness	-1.207
Sample excess kurtosis	1.294
Passed Shapiro Wilk normality test	No (p-value = 0.009886 < 0.05)



Analysis ratio movement to detection duration (H6 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_detection_duration_H6_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.3156	0.2373	0.4198	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_detection_duration_H6_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 86.5

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.6731	-0.5087	0.2754	0.6331	1.1694

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	1.826e-02	1.351e-01
Genotype_Zone_2:Plant_Zone_2	(Intercept)	1.558e-15	3.948e-08
Residual		5.342e-01	7.309e-01

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

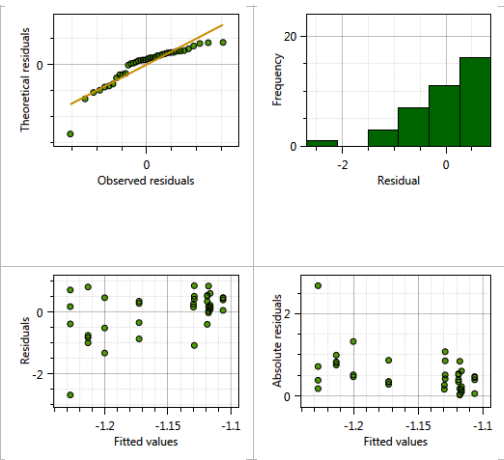
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-1.1532	0.1261	8.9886	-9.145	7.56e-06 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

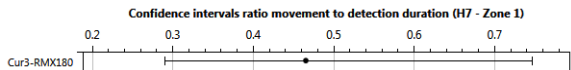
Model residuals

Statistic	Value
Sample skewness	-1.713
Sample excess kurtosis	3.954
Passed Shapiro Wilk normality test	No (p-value = 0.0001193 < 0.05)



Analysis ratio movement to detection duration (H7 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_detection_duration_H7_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio movement to detection duration (H7 - Zone 1)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4652	0.2897	0.747	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_detection_duration_H7_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) +
(1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 64.2

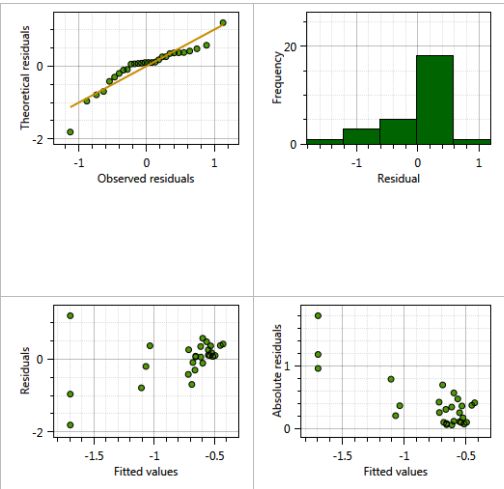
Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.8498 -0.2151  0.1491  0.5453  1.8688

Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.03593  0.1896
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.19424  0.4407
Residual                                0.40307  0.6349
Number of obs: 28, groups:  Genotype_Zone_2:Plant_Zone_2, 10; Genotype_Zone_1:Plant_Zone_1, 9

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -0.7653      0.2015  7.2132  -3.798  0.00636 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

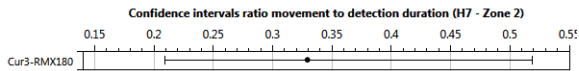
Model residuals

Statistic	Value
Sample skewness	-1.244
Sample excess kurtosis	3.41
Passed Shapiro Wilk normality test	No (p-value = 0.005849 < 0.05)



Analysis ratio movement to detection duration (H7 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_detection_duration_H7_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio movement to detection duration (H7 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.3293	0.2089	0.5191	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_detection_duration_H7_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) +
(1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 85.1

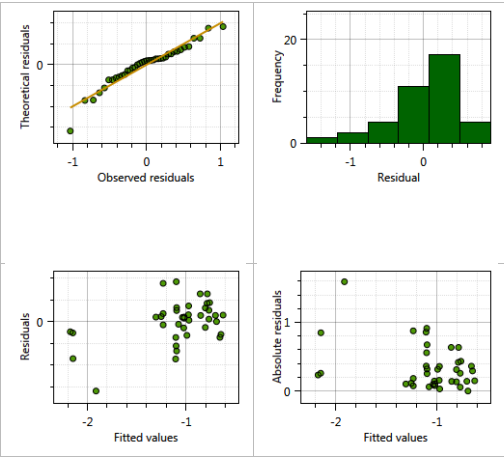
Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.8301 -0.4385  0.1720  0.4554  1.6247

Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.22447  0.4738
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.08578  0.2929
Residual                                0.31687  0.5629
Number of obs: 39, groups:  Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -1.1107      0.1981  8.1834  -5.608  0.000466 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

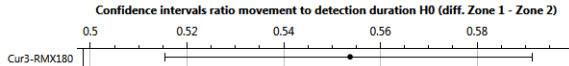
Model residuals

Statistic	Value
Sample skewness	-0.9166
Sample excess kurtosis	2.269
Passed Shapiro Wilk normality test	No (p-value = 0.04354 < 0.05)



Analysis ratio movement to detection duration H0 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_movement_to_detection_duration_H0_Zone_1,Ratio_movement_to_detection_duration_H0_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals ratio movement to detection duration H0 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5537	0.5153	0.5915	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 45.9

Scaled residuals:
Min IQ Median 3Q Max
-3.13650 -0.35537 0.08674 0.67271 1.79103

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0000 0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.0000 0.0000
Residual 0.0618 0.2486
Number of obs: 34, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

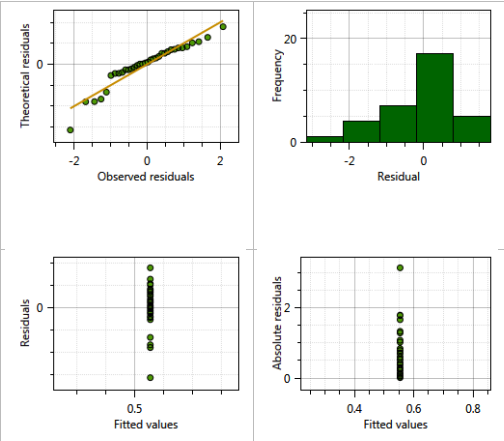
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 0.21569 0.07585 33.00000 2.844 0.0076 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.2486

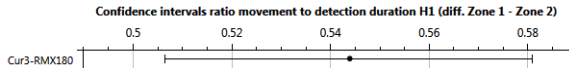
Model residuals

Statistic	Value
Sample skewness	-1.137
Sample excess kurtosis	1.93
Passed Shapiro Wilk normality test	No (p-value = 0.01647 < 0.05)



Analysis ratio movement to detection duration H1 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_movement_to_detection_duration_H1_Zone_1,Ratio_movement_to_detection_duration_H1_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals ratio movement to detection duration H1 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5439	0.5063	0.5809	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data

Weights: wi

REML criterion at convergence: 48.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.8795	-0.4899	0.1180	0.6690	1.7095

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.00000	0.0000
Residual		0.06037	0.2457

Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

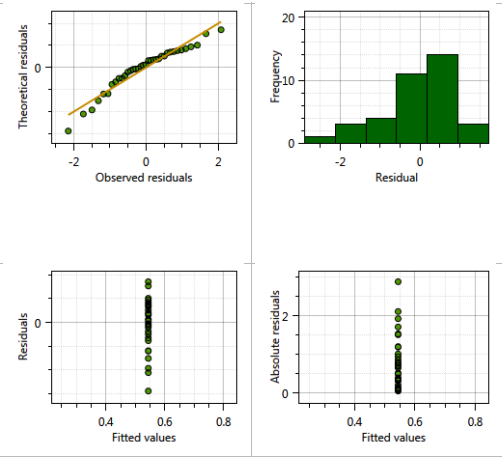
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.1760	0.0742	35.0000	2.372	0.0233 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.2457

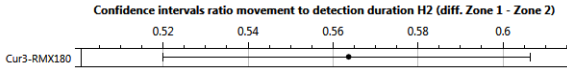
Model residuals

Statistic	Value
Sample skewness	-0.9303
Sample excess kurtosis	0.9799
Passed Shapiro Wilk normality test	Yes (p-value = 0.05516 > 0.05)



Analysis ratio movement to detection duration H2 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_movement_to_detection_duration_H2_Zone_1,Ratio_movement_to_detection_duration_H2_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals ratio movement to detection duration H2 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5637	0.5199	0.6065	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: ziFormula

Data: data

Weights: wi

REML criterion at convergence: 65.1

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.2391	-0.5352	0.2299	0.6642	2.1968

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000e+00	0.000e+00
Genotype_Zone_2:Plant_Zone_2	(Intercept)	7.077e-18	2.660e-09
Residual		7.539e-02	2.746e-01

Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

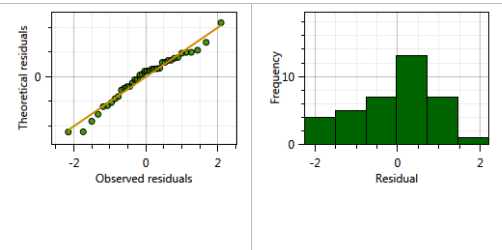
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.25602	0.08705	36.00000	2.941	0.00569 **

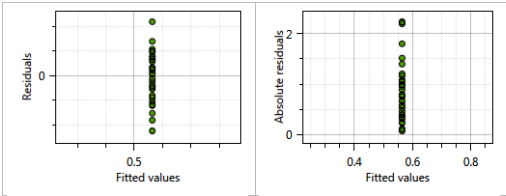
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.2746

Model residuals

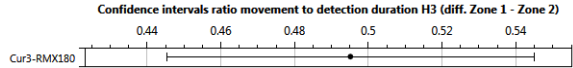
Statistic	Value
Sample skewness	-0.4267
Sample excess kurtosis	0.1046
Passed Shapiro Wilk normality test	Yes (p-value = 0.3861 > 0.05)





Analysis ratio movement to detection duration H3 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_movement_to_detection_duration_H3_Zone_1,Ratio_movement_to_detection_duration_H3_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals ratio movement to detection duration H3 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.4951	0.4453	0.5451	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 66

Scaled residuals:
Min 1Q Median 3Q Max
-2.21290 -0.63333 0.06631 0.56370 2.13322

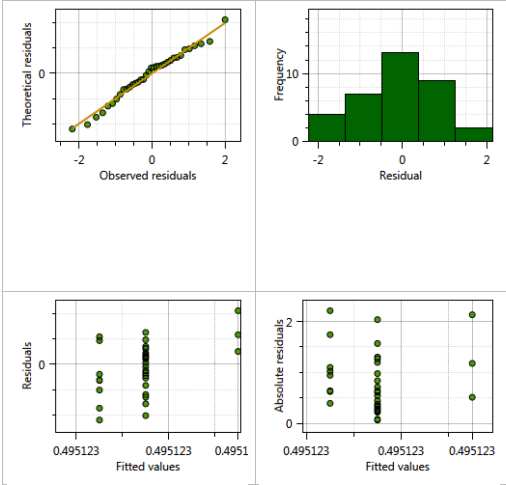
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.000e+00 0.000e+00
Genotype_Zone_2:Plant_Zone_2 (Intercept) 1.043e-16 1.021e-08
Residual 9.212e-02 3.035e-01
Number of obs: 35, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) -0.01951 0.09857 34.00000 -0.198 0.844

Dispersion: 0.3035

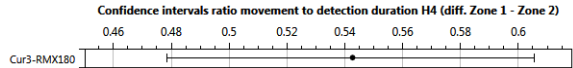
Model residuals

Statistic	Value
Sample skewness	-0.2515
Sample excess kurtosis	-0.141
Passed Shapiro Wilk normality test	Yes (p-value = 0.8446 > 0.05)



Analysis ratio movement to detection duration H4 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_movement_to_detection_duration_H4_Zone_1,Ratio_movement_to_detection_duration_H4_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals ratio movement to detection duration H4 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5427	0.4784	0.6056	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 52.2

Scaled residuals:
Min 1Q Median 3Q Max
-2.6762 -0.6641 0.1961 0.6195 1.3471

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.00000 0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.04440 0.2107
Residual 0.05852 0.2419
Number of obs: 30, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

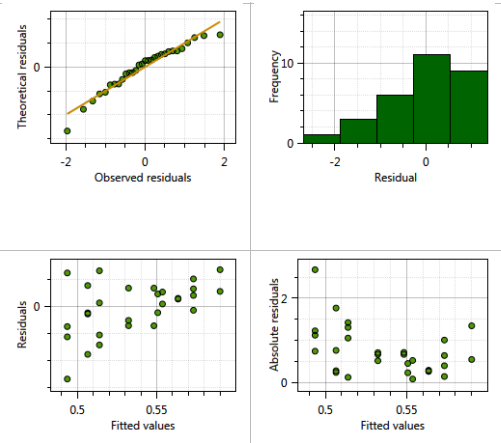
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)

(Intercept) 0.1711 0.1129 8.5218 1.515 0.166

Dispersion: 0.2419

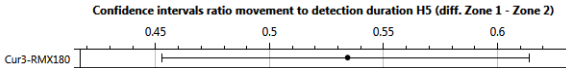
Model residuals

Statistic	Value
Sample skewness	-0.8523
Sample excess kurtosis	0.7578
Passed Shapiro Wilk normality test	Yes (p-value = 0.1599 > 0.05)



Analysis ratio movement to detection duration H5 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_movement_to_detection_duration_H5_Zone_1,Ratio_movement_to_detection_duration_H5_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5342	0.4526	0.6141	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 71.6

Scaled residuals:
Min IQ Median 3Q Max
-1.82641 -0.86450 -0.05246 0.57713 1.98275

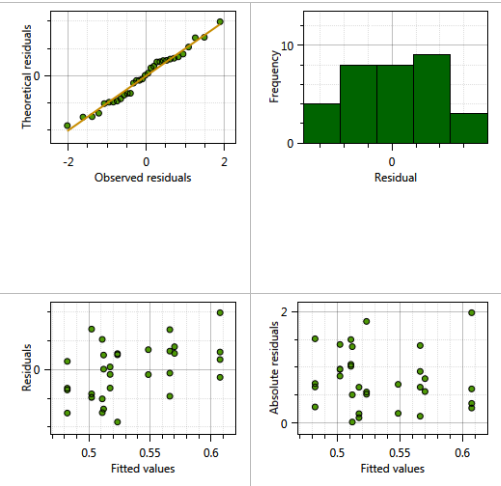
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.07043 0.2654
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.00000 0.0000
Residual 0.10684 0.3269
Number of obs: 32, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 0.1371 0.1443 8.8611 0.95 0.367

Dispersion: 0.3269

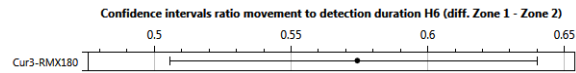
Model residuals

Statistic	Value
Sample skewness	0.06061
Sample excess kurtosis	-0.6387
Passed Shapiro Wilk normality test	Yes (p-value = 0.6971 > 0.05)



Analysis ratio movement to detection duration H6 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_movement_to_detection_duration_H6_Zone_1,Ratio_movement_to_detection_duration_H6_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5742	0.5055	0.6402	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 63.7

Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.22084 -0.67060 -0.02399  0.63923  1.71038

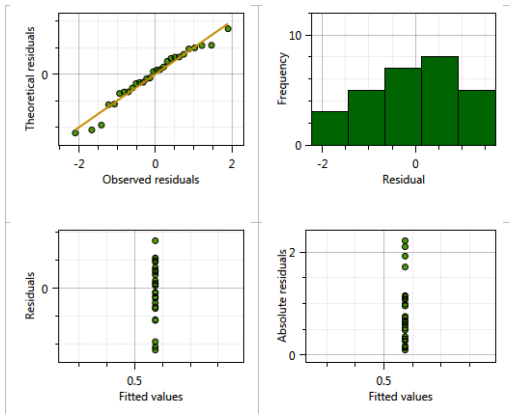
Random effects:
Groups              Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0000  0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.0000  0.0000
Residual                                0.1278  0.3576
Number of obs: 28, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    0.2991     0.1350 27.0000   2.216   0.0353 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.3576
```

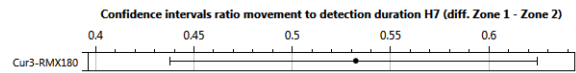
Model residuals

Statistic	Value
Sample skewness	-0.5219
Sample excess kurtosis	-0.1067
Passed Shapiro Wilk normality test	Yes (p-value = 0.3846 > 0.05)



Analysis ratio movement to detection duration H7 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_movement_to_detection_duration_H7_Zone_1,Ratio_movement_to_detection_duration_H7_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.5323	0.4376	0.6247	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 66.4

Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.28017 -0.54709 -0.07411  0.78402  1.24263

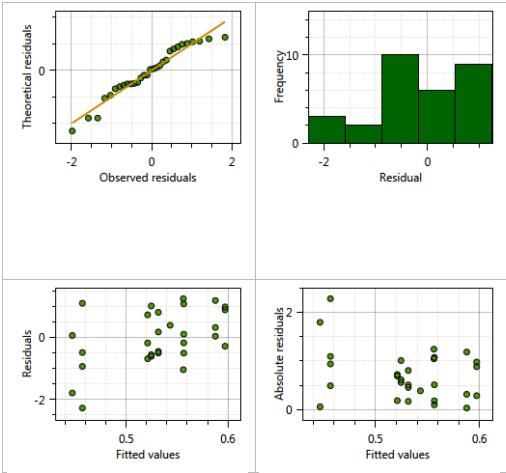
Random effects:
Groups              Name                Variance Std.Dev.
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.0991  0.3148
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.0000  0.0000
Residual                                0.0977  0.3126
Number of obs: 30, groups: Genotype_Zone_2:Plant_Zone_2, 10; Genotype_Zone_1:Plant_Zone_1, 9

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    0.1293     0.1571  6.2792   0.823   0.441

Dispersion: 0.3126
```

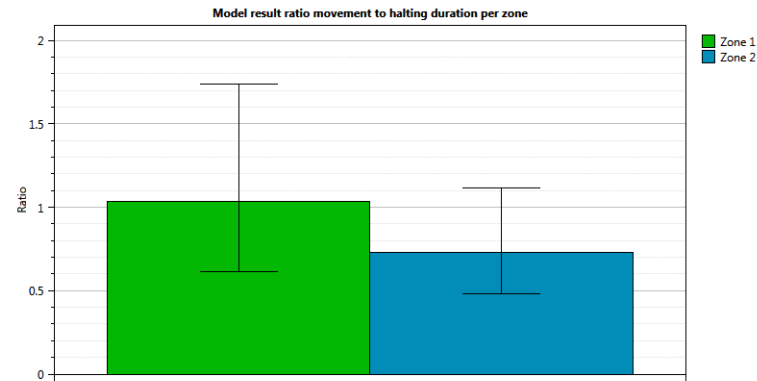
Model residuals

Statistic	Value
Sample skewness	-0.5043
Sample excess kurtosis	-0.1685
Passed Shapiro Wilk normality test	Yes (p-value = 0.1371 > 0.05)



Ratio movement to halting duration per zone

Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



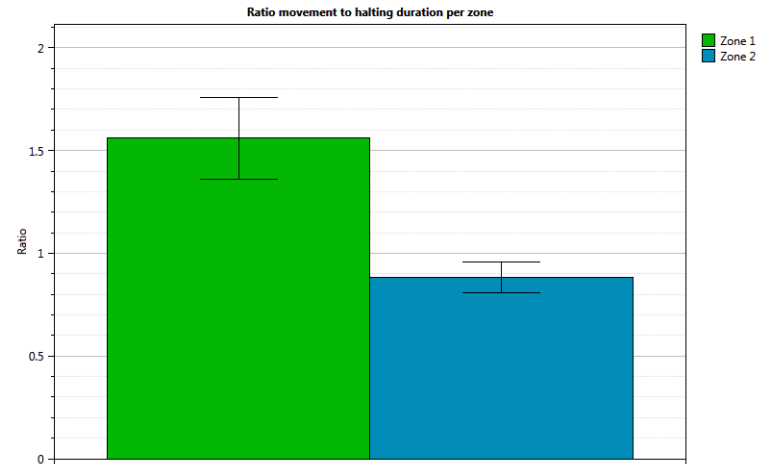
Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.

Behaviour statistic	Cur3-RMX180
Ratio movement to halting duration (diff. Zone 1 - Zone 2)	p=0.00183** [0.274, 0.846]

Statistic	Cur3-RMX180	Remark
Ratio movement to halting duration (Zone 1)	1.03 [0.614, 1.74]	CR
Ratio movement to halting duration (Zone 2)	0.73 [0.479, 1.11]	CR

CR = Check residuals

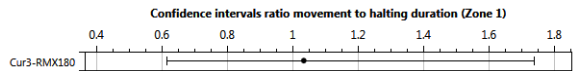
Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean Zone 1	StdErr Zone 1	Mean Zone 2	StdErr Zone 2
Cur3	RMX180	Neutral	1.56	0.2	0.88	0.08

Analysis ratio movement to halting duration (Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_halting_duration_Zone_1 ~ 1 + (1 Genotype_Zone_1.Plant_Zone_1) + (1 Genotype_Zone_2.Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	1.034	0.6144	1.74	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_halting_duration_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 122.1

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.9030	-0.3888	0.2385	0.5130	1.4739

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.07718	0.2778
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.07456	0.2731
Residual		1.19307	1.0923

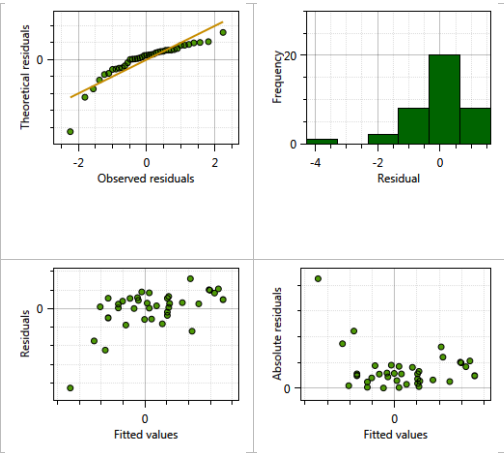
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.03325	0.21411	6.17021	0.155	0.882

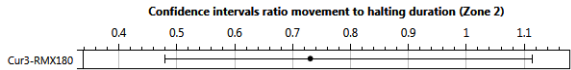
Model residuals

Statistic	Value
Sample skewness	-2.12
Sample excess kurtosis	6.667
Passed Shapiro Wilk normality test	No (p-value = 3.045E-05 < 0.05)



Analysis ratio movement to halting duration (Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_halting_duration_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.7305	0.4789	1.114	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_halting_duration_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 88.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.3551	-0.2150	0.2033	0.5003	1.6114

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0009767	0.03125
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0105675	0.10280
Residual		0.5332202	0.73022

Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

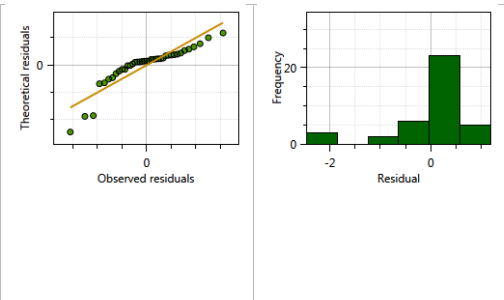
Fixed effects:

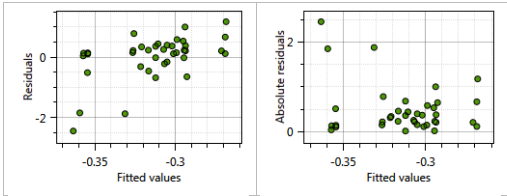
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.3140	0.1218	2.6119	-2.578	0.0942 .

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

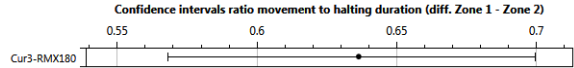
Statistic	Value
Sample skewness	-1.78
Sample excess kurtosis	4.001
Passed Shapiro Wilk normality test	No (p-value = 2.426E-05 < 0.05)





Analysis ratio movement to halting duration (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_movement_to_halting_duration_Zone_1,Ratio_movement_to_halting_duration_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals ratio movement to halting duration (diff. Zone 1 - Zone 2)					
Genotype_Zone_1	Genotype_Zone_2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.6364	0.568	0.6997	a

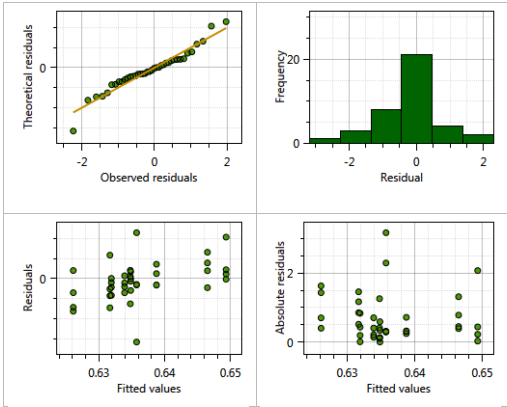
Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1
REML criterion at convergence: 98.9
Scaled residuals:
Min 1Q Median 3Q Max
-3.1693 -0.5568 -0.1979 0.3677 2.2929
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.00000 0.0000
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.01201 0.1096
Residual 0.31357 0.5600
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 0.5596 0.1251 8.4151 4.474 0.00183 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Dispersion: 0.56

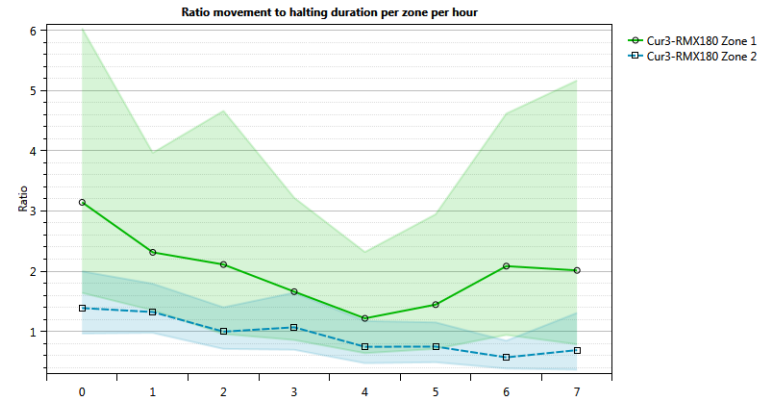
Model residuals

Statistic	Value
Sample skewness	-0.1781
Sample excess kurtosis	2.245
Passed Shapiro Wilk normality test	Yes (p-value = 0.1022 > 0.05)



Ratio movement to halting duration per zone per hour

Selected hours	0, 1, 2, 3, 4, 5, 6, 7
Selected zones	Zone 1, Zone 2
Data transformation	Natural logarithm
Analysis	Zone difference analysis



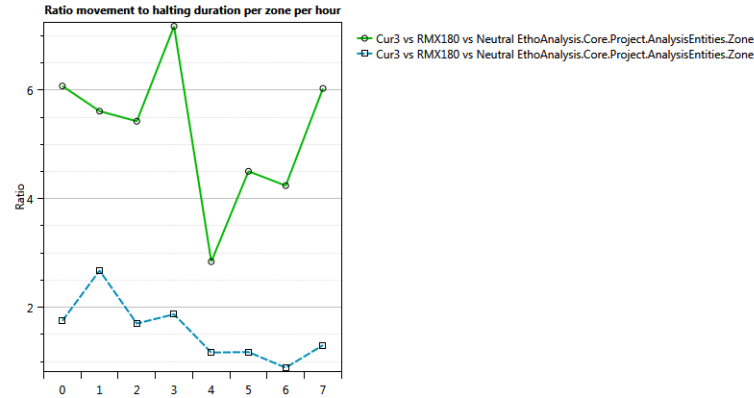
Results difference tests Zone 1 - Zone 2: p values and 95% confidence intervals of the difference on the transformed scale for each statistic.	
Behaviour statistic	Cur3-RMX180

Behaviour statistic	Cur3-RMX180
Ratio movement to halting duration H0 (diff. Zone 1 - Zone 2)	p=0.0143* [0.253, 1.85]
Ratio movement to halting duration H1 (diff. Zone 1 - Zone 2)	p=0.142 [-0.311, 1.83]
Ratio movement to halting duration H2 (diff. Zone 1 - Zone 2)	p=0.0535 [-0.0158, 1.67]
Ratio movement to halting duration H3 (diff. Zone 1 - Zone 2)	p=0.196 [-0.389, 1.71]
Ratio movement to halting duration H4 (diff. Zone 1 - Zone 2)	p=0.204 [-0.397, 1.62]
Ratio movement to halting duration H5 (diff. Zone 1 - Zone 2)	p=0.0525 [-0.0149, 1.93]
Ratio movement to halting duration H6 (diff. Zone 1 - Zone 2)	p=1.31E-05*** [0.861, 1.92]
Ratio movement to halting duration H7 (diff. Zone 1 - Zone 2)	p=0.087 [-0.174, 1.98]

The model predictions and 95% confidence intervals for each statistic.		
Statistic	Cur3-RMX180	Remark
Ratio movement to halting duration (H0 - Zone 1)	3.15 [1.64, 6.04]	CR
Ratio movement to halting duration (H0 - Zone 2)	1.39 [0.963, 2]	
Ratio movement to halting duration (H1 - Zone 1)	2.31 [1.35, 3.97]	CR
Ratio movement to halting duration (H1 - Zone 2)	1.32 [0.975, 1.79]	
Ratio movement to halting duration (H2 - Zone 1)	2.11 [0.956, 4.66]	CR
Ratio movement to halting duration (H2 - Zone 2)	0.996 [0.708, 1.4]	
Ratio movement to halting duration (H3 - Zone 1)	1.66 [0.856, 3.22]	CR
Ratio movement to halting duration (H3 - Zone 2)	1.07 [0.694, 1.64]	
Ratio movement to halting duration (H4 - Zone 1)	1.22 [0.638, 2.32]	CR
Ratio movement to halting duration (H4 - Zone 2)	0.743 [0.471, 1.17]	
Ratio movement to halting duration (H5 - Zone 1)	1.44 [0.708, 2.95]	
Ratio movement to halting duration (H5 - Zone 2)	0.747 [0.486, 1.15]	
Ratio movement to halting duration (H6 - Zone 1)	2.08 [0.94, 4.62]	
Ratio movement to halting duration (H6 - Zone 2)	0.568 [0.381, 0.845]	
Ratio movement to halting duration (H7 - Zone 1)	2.01 [0.784, 5.17]	
Ratio movement to halting duration (H7 - Zone 2)	0.689 [0.363, 1.31]	

CR = Check residuals

Data summary



Genotype Zone 1	Genotype Zone 2	Genotype Zone 3	Mean H0 - Zone 1	StdErr H0 - Zone 1	Mean H0 - Zone 2	StdErr H0 - Zone 2	Mean H1 - Zone 1	StdErr H1 - Zone 1	Mean H1 - Zone 2	StdErr H1 - Zone 2	Mean H2 - Zone 1	StdErr H2 - Zone 1	Mean H2 - Zone 2	StdErr H2 - Zone 2	Mean H3 - Zone 1	StdErr H3 - Zone 1	Mean H3 - Zone 2	StdErr H3 - Zone 2	Mean H4 - Zone 1	StdErr H4 - Zone 1	Mean H4 - Zone 2	StdErr H4 - Zone 2	Mean H5 - Zone 1	StdErr H5 - Zone 1	Mean H5 - Zone 2	StdErr H5 - Zone 2	Mean H6 - Zone 1	StdErr H6 - Zone 1	Mean H6 - Zone 2	StdErr H6 - Zone 2
Cur3	RMX180	Neutral	6.08	1.44	1.75	0.41	5.61	2.39	2.68	1.39	5.43	1.58	1.7	0.42	7.18	3.73	1.87	0.42	2.84	0.87	1.17	0.21	4.51	1.43	1.17	0.18	4.24	0.9	0.89	0.13

Analysis ratio movement to halting duration (H0 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_halting_duration_H0_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	3.145	1.639	6.037	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_halting_duration_H0_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 101.7

Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.45882 -0.59111 -0.09918  0.69006  1.68965

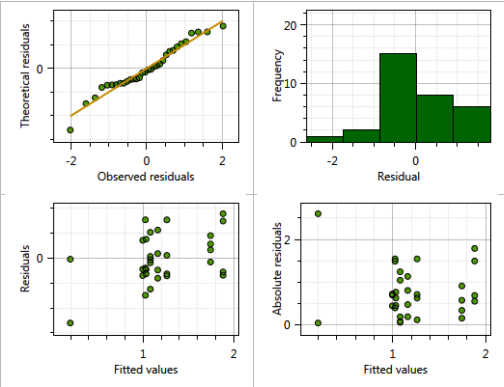
Random effects:
Groups             Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.403    0.6349
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.000    0.0000
Residual              1.122    1.0591

Number of obs: 32, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    1.1459     0.2787  7.3961  4.111  0.00401 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

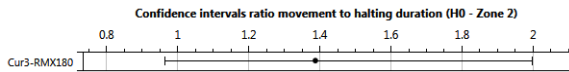
Model residuals

Statistic	Value
Sample skewness	-0.1699
Sample excess kurtosis	0.381
Passed Shapiro Wilk normality test	Yes (p-value = 0.3485 > 0.05)



Analysis ratio movement to halting duration (H0 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_halting_duration_H0_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	1.387	0.963	1.998	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_halting_duration_H0_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 73.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.67968	-0.42498	-0.03249	0.24118	2.86815

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	1.860e-16	1.364e-08
Genotype_Zone_2:Plant_Zone_2	(Intercept)	1.483e-01	3.851e-01
Residual		3.644e-01	6.037e-01

Number of obs: 35, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

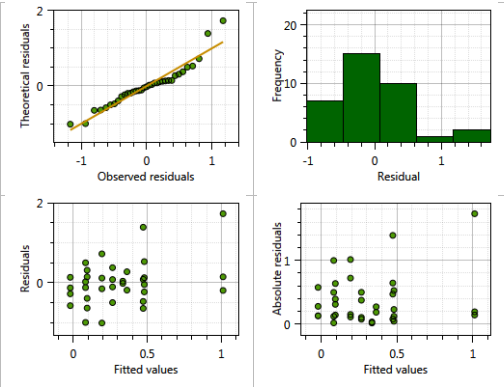
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.3273	0.1601	8.5753	2.044	0.0729

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

Statistic	Value
Sample skewness	1.008
Sample excess kurtosis	2.551
Passed Shapiro Wilk normality test	No (p-value = 0.01716 < 0.05)

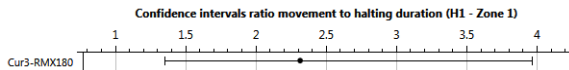


Data points with high residuals

Trial	Arena
Trial 3	37

Analysis ratio movement to halting duration (H1 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_halting_duration_H1_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	2.314	1.349	3.967	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: Ratio_movement_to_halting_duration_H1_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 115.7

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.47146	-0.48181	0.05113	0.57796	2.72888

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.1318	0.363
Residual		1.4745	1.214

Number of obs: 35, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

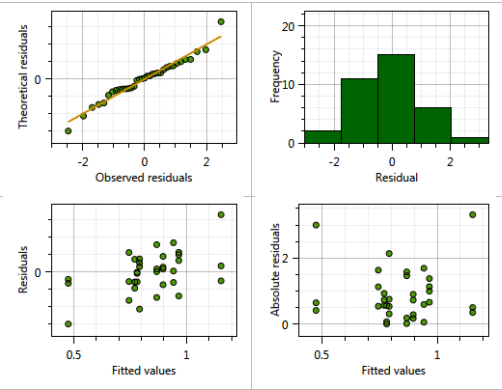
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.8388	0.2356	8.3533	3.56	0.0069 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

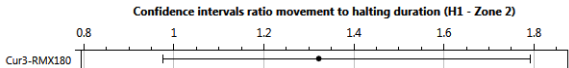
Model residuals

Statistic	Value
Sample skewness	0.03686
Sample excess kurtosis	1.498
Passed Shapiro Wilk normality test	Yes (p-value = 0.5835 > 0.05)



Analysis ratio movement to halting duration (H1 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_halting_duration_H1_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	1.322	0.9747	1.792	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_halting_duration_H1_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 95.5

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.2644	-0.3188	-0.0314	0.3779	4.1197

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.0000	0.0000
Residual		0.8101	0.9001

Number of obs: 36, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

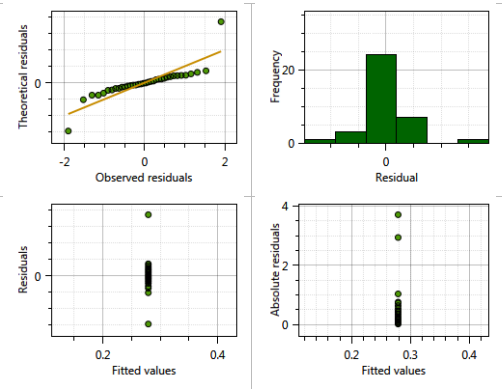
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.2789	0.1500	35.0000	1.859	0.0714 .

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

Statistic	Value
Sample skewness	1.008
Sample excess kurtosis	10.49
Passed Shapiro Wilk normality test	No (p-value = 2.146E-06 < 0.05)

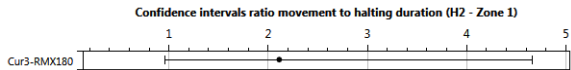


Data points with high residuals

Trial	Arena
Trial 3	14

Analysis ratio movement to halting duration (H2 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_halting_duration_H2_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio movement to halting duration (H2 - Zone 1)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	2.111	0.9556	4.664	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_halting_duration_H2_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 126.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.9784	-0.8379	0.2246	0.6729	1.6448

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.005956	0.07717
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.634259	0.79640
Residual		1.774460	1.33209

Number of obs: 35, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

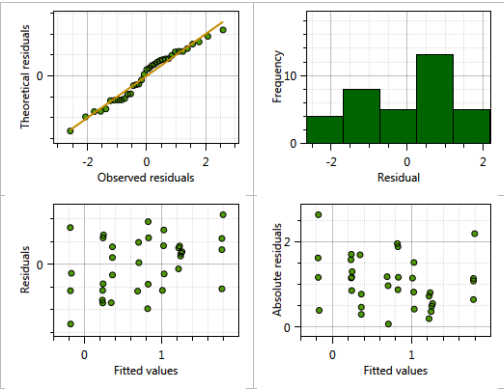
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.7472	0.3396	7.4801	2.2	0.0613

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

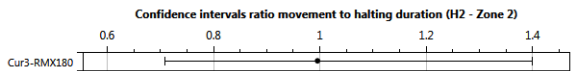
Model residuals

Statistic	Value
Sample skewness	-0.2247
Sample excess kurtosis	-0.9037
Passed Shapiro Wilk normality test	Yes (p-value = 0.3448 > 0.05)



Analysis ratio movement to halting duration (H2 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_halting_duration_H2_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio movement to halting duration (H2 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.9955	0.7079	1.4	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_halting_duration_H2_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 107.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.59637	-0.56268	-0.04578	0.31938	2.41403

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.000	0.000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.000	0.000
Residual		1.045	1.022

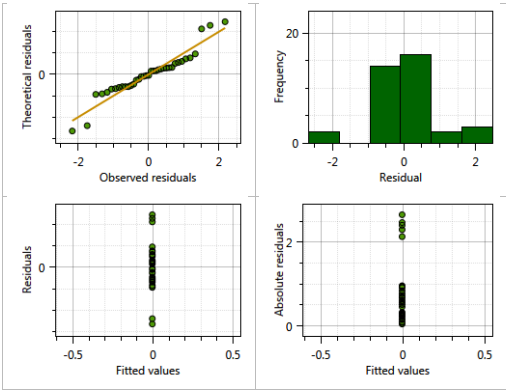
Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.00448	0.16810	36.00000	-0.027	0.979

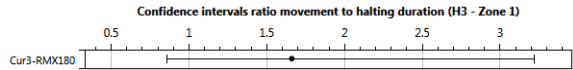
Model residuals

Statistic	Value
Sample skewness	0.07732
Sample excess kurtosis	1.942
Passed Shapiro Wilk normality test	No (p-value = 0.01317 < 0.05)



Analysis ratio movement to halting duration (H3 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_halting_duration_H3_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	1.66	0.8556	3.221	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_halting_duration_H3_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 116.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.53588	-0.63676	-0.04659	0.37418	2.66943

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.1698	0.4121
Residual		2.1080	1.4519

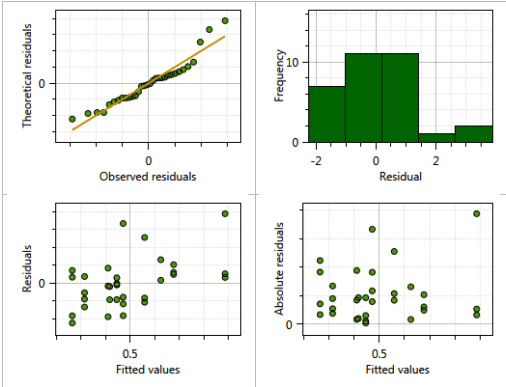
Number of obs: 32, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.5069	0.2892	8.2862	1.753	0.116

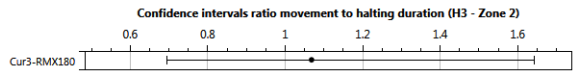
Model residuals

Statistic	Value
Sample skewness	0.9606
Sample excess kurtosis	1.304
Passed Shapiro Wilk normality test	No (p-value = 0.036 < 0.05)



Analysis ratio movement to halting duration (H3 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_halting_duration_H3_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	1.068	0.6937	1.644	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_halting_duration_H3_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 118.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.64838	-0.42157	0.03559	0.52667	2.32545

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.06999	0.2646
Residual		1.15496	1.0747

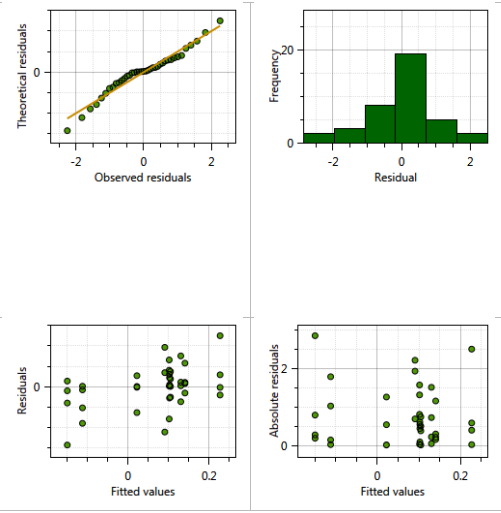
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.06562	0.19144	9.25215	0.343	0.739

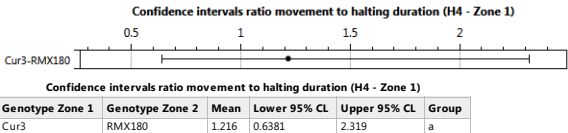
Model residuals

Statistic	Value
Sample skewness	-0.3751
Sample excess kurtosis	1.171
Passed Shapiro Wilk normality test	Yes (p-value = 0.2917 > 0.05)



Analysis ratio movement to halting duration (H4 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_halting_duration_H4_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: Ratio_movement_to_halting_duration_H4_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)

Data: data

REML criterion at convergence: 102.5

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.88135	-0.44860	0.05438	0.63338	2.09220

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.00000	0.000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.04794	0.219
Residual		1.97950	1.407

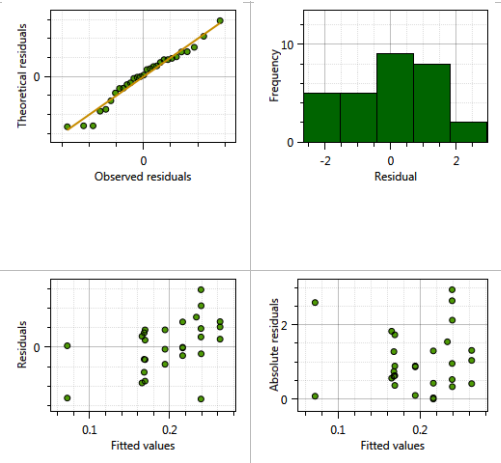
Number of obs: 29, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.1959	0.2712	6.7997	0.722	0.494

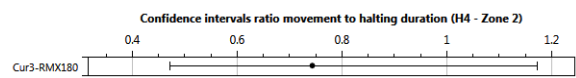
Model residuals

Statistic	Value
Sample skewness	-0.2951
Sample excess kurtosis	-0.118
Passed Shapiro Wilk normality test	Yes (p-value = 0.487 > 0.05)



Analysis ratio movement to halting duration (H4 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_halting_duration_H4_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio movement to halting duration (H4 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.7433	0.4709	1.173	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_halting_duration_H4_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 106

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.3500	-0.2924	0.1325	0.4705	2.0109

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.0000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.1262	0.3552
Residual		0.9083	0.9530

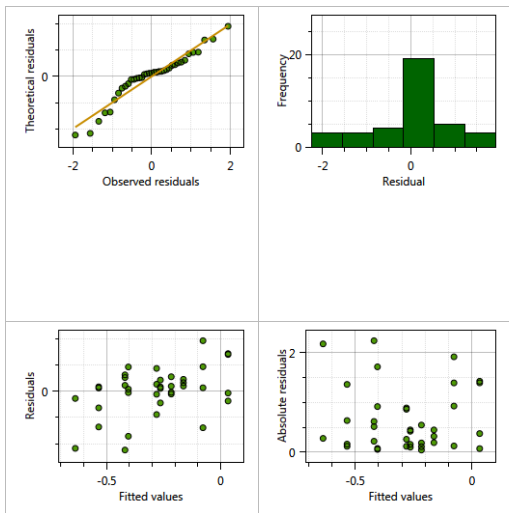
Number of obs: 37, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.2967	0.1935	7.0931	-1.533	0.169

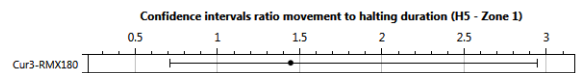
Model residuals

Statistic	Value
Sample skewness	-0.6693
Sample excess kurtosis	0.9096
Passed Shapiro Wilk normality test	No (p-value = 0.03411 < 0.05)



Analysis ratio movement to halting duration (H5 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_halting_duration_H5_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio movement to halting duration (H5 - Zone 1)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	1.444	0.7082	2.946	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_halting_duration_H5_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 111.1

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.8358	-0.6601	-0.1754	0.5099	1.9986

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.02601	0.1613
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.01011	0.1006
Residual		2.36754	1.5387

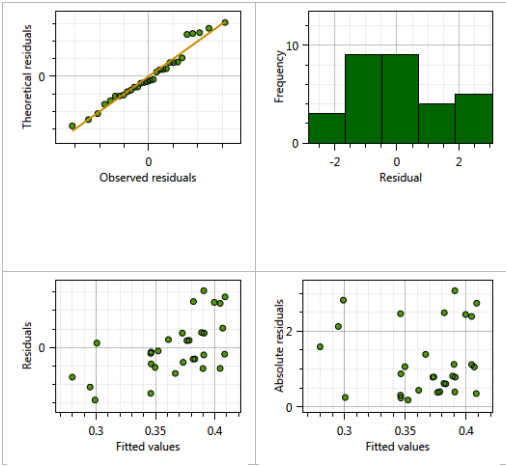
Number of obs: 30, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.3677	0.2877	5.7100	1.278	0.251

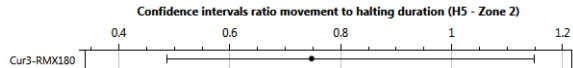
Model residuals

Statistic	Value
Sample skewness	0.3805
Sample excess kurtosis	-0.2836
Passed Shapiro Wilk normality test	Yes (p-value = 0.3021 > 0.05)



Analysis ratio movement to halting duration (H5 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_halting_duration_H5_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio movement to halting duration (H5 - Zone 2)					
Genotype_Zone_1	Genotype_Zone_2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.7474	0.486	1.149	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_halting_duration_H5_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 113.6

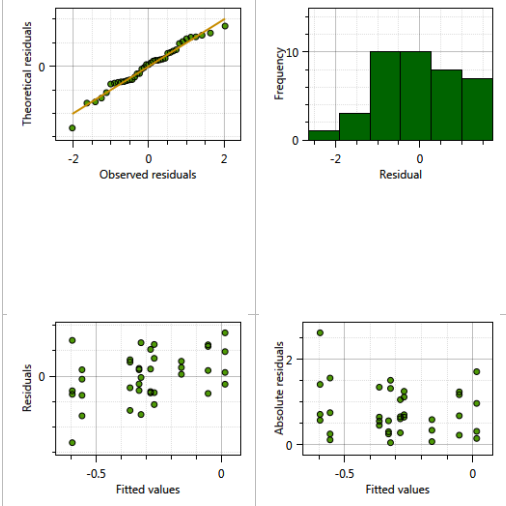
Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.6723 -0.6405  0.0773  0.6319  1.7448

Random effects:
Groups                Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept)  0.1173   0.3424
Genotype_Zone_2:Plant_Zone_2 (Intercept)  0.0000   0.0000
Residual                                0.9639   0.9818
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)  -0.2912     0.1910   9.2404  -1.524   0.161
```

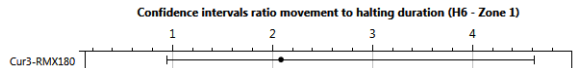
Model residuals

Statistic	Value
Sample skewness	-0.4197
Sample excess kurtosis	0.2561
Passed Shapiro Wilk normality test	Yes (p-value = 0.5416 > 0.05)



Analysis ratio movement to halting duration (H6 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_halting_duration_H6_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio movement to halting duration (H6 - Zone 1)					
Genotype_Zone_1	Genotype_Zone_2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	2.084	0.9403	4.62	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_halting_duration_H6_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data
```

REML criterion at convergence: 95.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.8271	-0.5980	0.2741	0.6134	1.6214

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.0000	0.000
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.5112	0.715
Residual		1.6849	1.298

Number of obs: 27, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

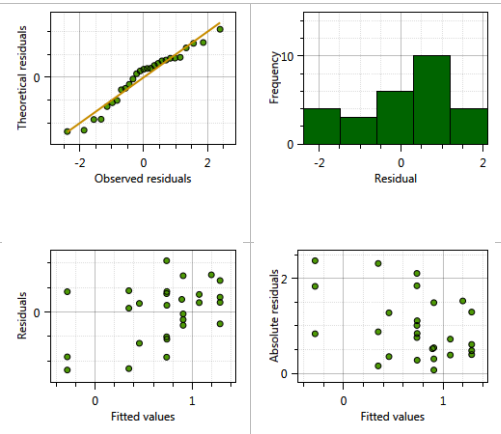
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.7344	0.3450	7.9792	2.129	0.066

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

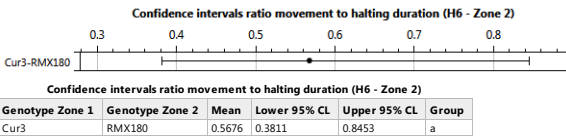
Model residuals

Statistic	Value
Sample skewness	-0.5154
Sample excess kurtosis	-0.4743
Passed Shapiro Wilk normality test	Yes (p-value = 0.2069 > 0.05)



Analysis ratio movement to halting duration (H6 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_halting_duration_H6_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_halting_duration_H6_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 114.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.0905	-0.6249	0.2019	0.5668	1.7192

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	3.749e-03	6.123e-02
Genotype_Zone_2:Plant_Zone_2	(Intercept)	7.444e-17	8.628e-09
Residual		1.165e+00	1.079e+00

Number of obs: 38, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

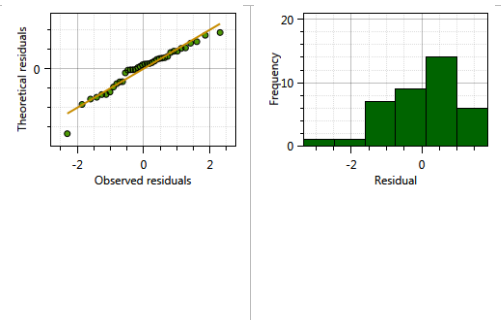
Fixed effects:

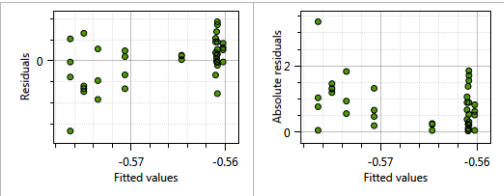
	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.5664	0.1762	9.0210	-3.215	0.0105 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Model residuals

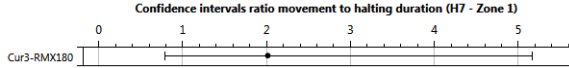
Statistic	Value
Sample skewness	-0.8394
Sample excess kurtosis	1.153
Passed Shapiro Wilk normality test	Yes (p-value = 0.1056 > 0.05)





Analysis ratio movement to halting duration (H7 - Zone 1)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_halting_duration_H7_Zone_1 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio movement to halting duration (H7 - Zone 1)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	2.014	0.7844	5.17	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_halting_duration_H7_Zone_1 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 98.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.99007	-0.49441	-0.09405	0.51653	1.74936

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.8425	0.9179
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.1879	0.4335
Residual		1.5661	1.2514

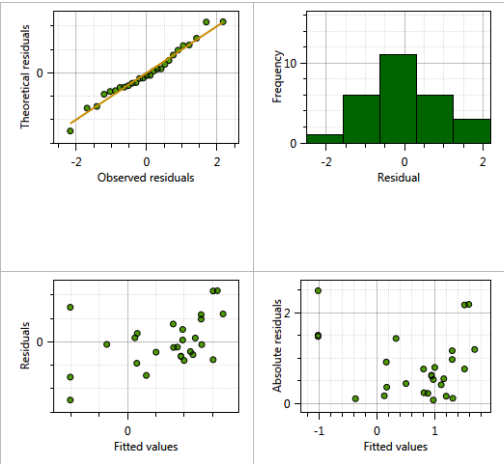
Number of obs: 27, groups: Genotype_Zone_2:Plant_Zone_2, 10; Genotype_Zone_1:Plant_Zone_1, 9

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.7000	0.4166	8.9663	1.68	0.127

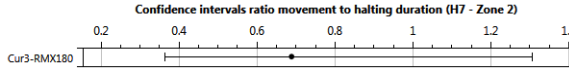
Model residuals

Statistic	Value
Sample skewness	0.1457
Sample excess kurtosis	0.2823
Passed Shapiro Wilk normality test	Yes (p-value = 0.7807 > 0.05)



Analysis ratio movement to halting duration (H7 - Zone 2)

Analysis model	Linear mixed model fit by REML: Ratio_movement_to_halting_duration_H7_Zone_2 ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Natural logarithm



Confidence intervals ratio movement to halting duration (H7 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.6886	0.3628	1.307	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: Ratio_movement_to_halting_duration_H7_Zone_2 ~ 1 + (1 | Genotype_Zone_1:Plant_Zone_1) + (1 | Genotype_Zone_2:Plant_Zone_2)
Data: data

REML criterion at convergence: 125.7

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.32854	-0.53379	0.02204	0.57527	1.68287

Random effects:

Groups	Name	Variance	Std.Dev.
Genotype_Zone_1:Plant_Zone_1	(Intercept)	0.27859	0.5278
Genotype_Zone_2:Plant_Zone_2	(Intercept)	0.09625	0.3102
Residual		1.17487	1.0839

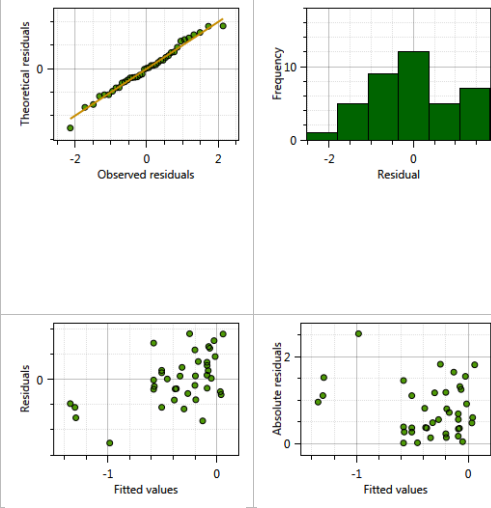
Number of obs: 39, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	-0.3731	0.2603	5.8514	-1.433	0.203

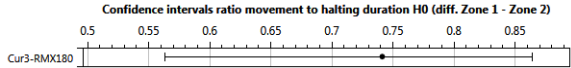
Model residuals

Statistic	Value
Sample skewness	-0.1273
Sample excess kurtosis	-0.0672
Passed Shapiro Wilk normality test	Yes (p-value = 0.879 > 0.05)



Analysis ratio movement to halting duration H0 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_movement_to_halting_duration_H0_Zone_1,Ratio_movement_to_halting_duration_H0_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.7412	0.563	0.8643	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 120.1

Scaled residuals:
Min IQ Median 3Q Max
-1.90613 -0.80783 0.01609 0.64147 1.04786

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.2901 0.5386
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.5697 0.7548
Residual 1.5142 1.2305
Number of obs: 32, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

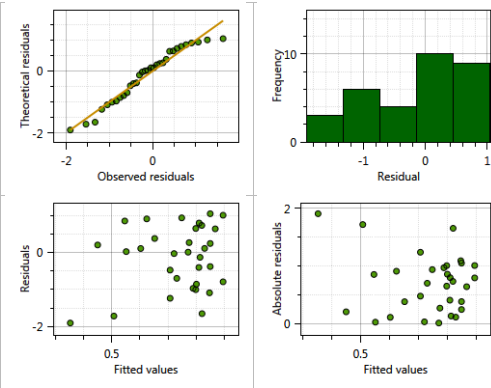
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 1.0522 0.3645 11.3777 2.887 0.0143 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 1.231

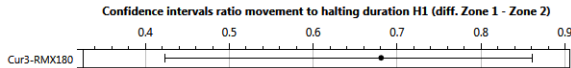
Model residuals

Statistic	Value
Sample skewness	-0.437
Sample excess kurtosis	-0.7788
Passed Shapiro Wilk normality test	Yes (p-value = 0.117 > 0.05)



Analysis ratio movement to halting duration H1 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_movement_to_halting_duration_H1_Zone_1,Ratio_movement_to_halting_duration_H1_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.6808	0.4228	0.8614	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 147

Scaled residuals:
Min 1Q Median 3Q Max
-2.2876 -0.4480 -0.1675 0.5199 1.9181

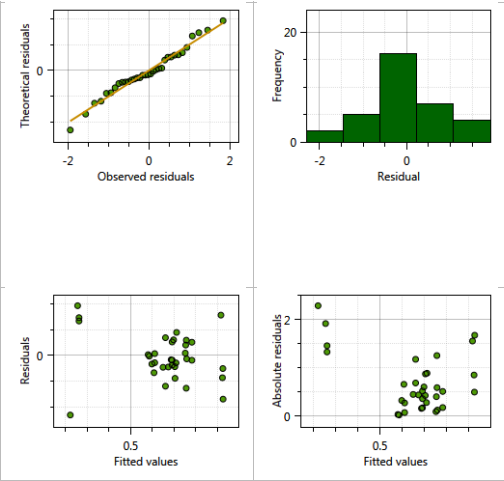
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.06116 0.2473
Genotype_Zone_2:Plant_Zone_2 (Intercept) 1.33008 1.1533
Residual 2.81030 1.6764
Number of obs: 34, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 0.7576 0.4689 8.5641 1.616 0.142

Dispersion: 1.676

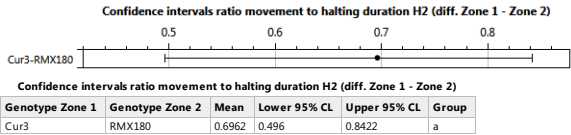
Model residuals

Statistic	Value
Sample skewness	0.001798
Sample excess kurtosis	0.4979
Passed Shapiro Wilk normality test	Yes (p-value = 0.7137 > 0.05)



Analysis ratio movement to halting duration H2 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_movement_to_halting_duration_H2_Zone_1,Ratio_movement_to_halting_duration_H2_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 128.4

Scaled residuals:
Min 1Q Median 3Q Max
-1.2775 -0.7335 -0.2226 0.4879 1.6820

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.5991 0.7740
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.4913 0.7009
Residual 0.8185 0.9047
Number of obs: 35, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

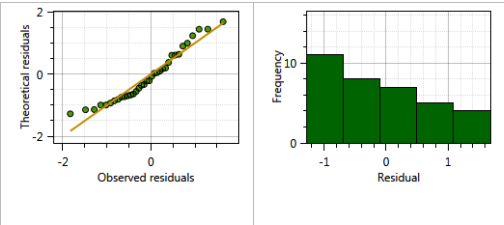
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 0.8293 0.3710 8.6024 2.236 0.0535 .

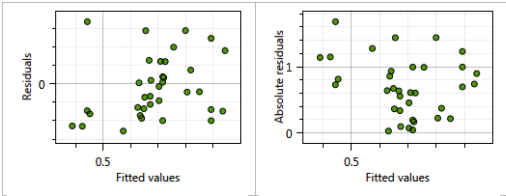
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 0.9047

Model residuals

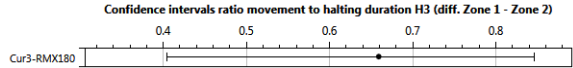
Statistic	Value
Sample skewness	0.6003
Sample excess kurtosis	-0.6196
Passed Shapiro Wilk normality test	Yes (p-value = 0.05333 > 0.05)





Analysis ratio movement to halting duration H3 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_movement_to_halting_duration_H3_Zone_1:Ratio_movement_to_halting_duration_H3_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals ratio movement to halting duration H3 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.6591	0.404	0.8464	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 150.6

Scaled residuals:
Min 1Q Median 3Q Max
-2.8093 -0.7079 -0.2808 0.1691 1.6285

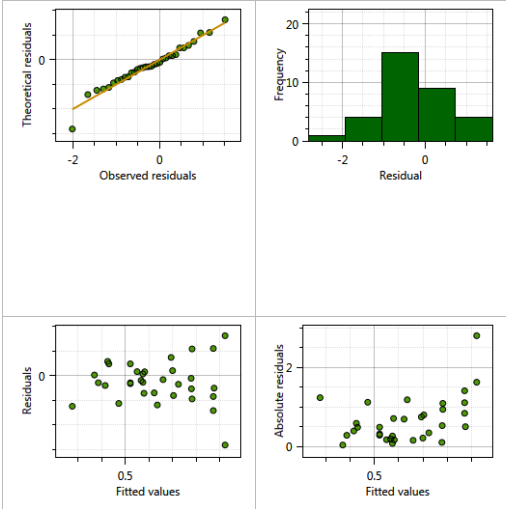
Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 1.0063 1.0032
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.4718 0.6869
Residual 2.9240 1.7100
Number of obs: 33, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 0.6591 0.4826 12.3970 1.366 0.196

Dispersion: 1.71

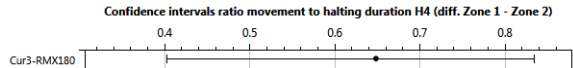
Model residuals

Statistic	Value
Sample skewness	-0.4035
Sample excess kurtosis	1.746
Passed Shapiro Wilk normality test	Yes (p-value = 0.4531 > 0.05)



Analysis ratio movement to halting duration H4 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_movement_to_halting_duration_H4_Zone_1:Ratio_movement_to_halting_duration_H4_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals ratio movement to halting duration H4 (diff. Zone 1 - Zone 2)

Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.6482	0.4021	0.8347	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: w1

REML criterion at convergence: 93.9

Scaled residuals:
Min 1Q Median 3Q Max
-1.57495 -0.52408 0.00396 0.42340 1.71245

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.7898 0.8887
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.8249 0.9083
Residual 0.4623 0.6799
Number of obs: 27, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

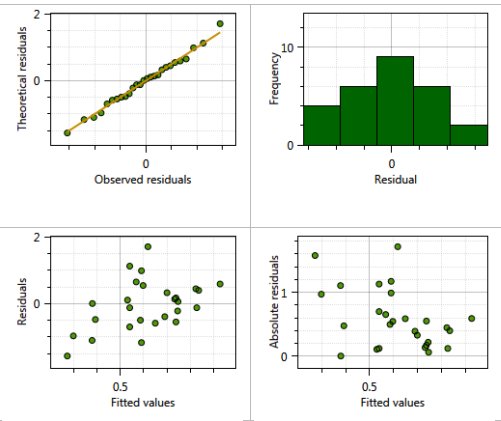
Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)
(Intercept)	0.6113	0.4470	9.1903	1.367	0.204

Dispersion: 0.6799

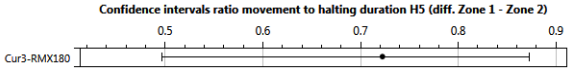
Model residuals

Statistic	Value
Sample skewness	0.1422
Sample excess kurtosis	0.1176
Passed Shapiro Wilk normality test	Yes (p-value = 0.9993 > 0.05)



Analysis ratio movement to halting duration H5 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_movement_to_halting_duration_H5_Zone_1,Ratio_movement_to_halting_duration_H5_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.7223	0.4963	0.8729	a

Model summary

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 135.3

Scaled residuals:
Min 1Q Median 3Q Max
-2.5722 -0.6894 -0.3691 0.1739 1.7732

Random effects:
Groups Name Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.1973 0.4442
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.3120 0.5585
Residual 2.3371 1.5287
Number of obs: 31, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

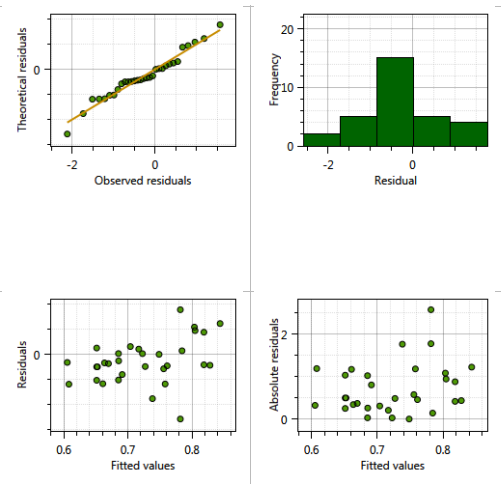
Fixed effects:
Estimate Std. Error df t value Pr(>|t|)
(Intercept) 0.9561 0.3803 5.1143 2.514 0.0525 .

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 1.529

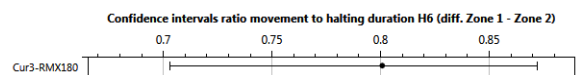
Model residuals

Statistic	Value
Sample skewness	-0.01542
Sample excess kurtosis	0.8422
Passed Shapiro Wilk normality test	Yes (p-value = 0.5659 > 0.05)



Analysis ratio movement to halting duration H6 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_movement_to_halting_duration_H6_Zone_1,Ratio_movement_to_halting_duration_H6_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals ratio movement to halting duration H6 (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.8007	0.7029	0.8722	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 96.8

Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.0794 -0.7852 -0.1556  0.3049  1.6056

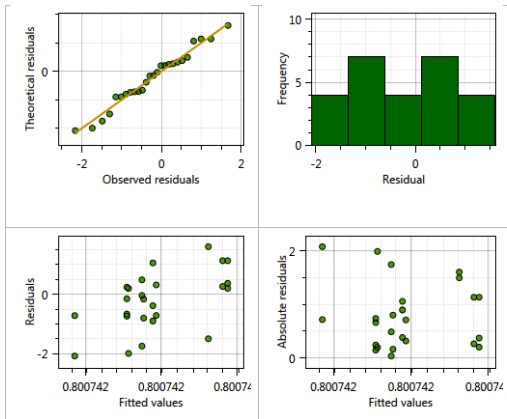
Random effects:
Groups              Name                Variance Std.Dev.
Genotype_Zone_1:Plant_Zone_1 (Intercept) 3.317e-14 1.821e-07
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.000e+00 0.000e+00
Residual                      1.509e+00 1.228e+00
Number of obs: 26, groups: Genotype_Zone_1:Plant_Zone_1, 10; Genotype_Zone_2:Plant_Zone_2, 10

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   1.3909      0.2573 25.0000   5.405 1.31e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 1.228
```

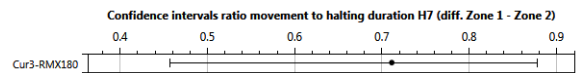
Model residuals

Statistic	Value
Sample skewness	-0.1296
Sample excess kurtosis	-0.413
Passed Shapiro Wilk normality test	Yes (p-value = 0.6303 > 0.05)



Analysis ratio movement to halting duration H7 (diff. Zone 1 - Zone 2)

Analysis model	Generalized linear mixed model with dispersion factor, formula=cbind(Ratio_movement_to_halting_duration_H7_Zone_1:Ratio_movement_to_halting_duration_H7_Zone_2) ~ 1 + (1 Genotype_Zone_1:Plant_Zone_1) + (1 Genotype_Zone_2:Plant_Zone_2)
Transformation	Logit



Confidence intervals ratio movement to halting duration H7 (diff. Zone 1 - Zone 2)					
Genotype Zone 1	Genotype Zone 2	Mean	Lower 95% CL	Upper 95% CL	Group
Cur3	RMX180	0.7112	0.4566	0.8783	a

Model summary

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: ziFormula
Data: data
Weights: wi

REML criterion at convergence: 112.1

Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.0089 -0.5616 -0.1922  0.3123  1.5092

Random effects:
Groups              Name                Variance Std.Dev.
Genotype_Zone_2:Plant_Zone_2 (Intercept) 0.1438  0.3793
Genotype_Zone_1:Plant_Zone_1 (Intercept) 0.8932  0.9451
Residual                      2.0676  1.4379
Number of obs: 27, groups: Genotype_Zone_2:Plant_Zone_2, 10; Genotype_Zone_1:Plant_Zone_1, 9

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)   0.9012      0.4469  6.4527   2.017  0.087 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Dispersion: 1.438
```

Model residuals

Statistic	Value
Sample skewness	-0.2606
Sample excess kurtosis	0.0009445
Passed Shapiro Wilk normality test	Yes (p-value = 0.8588 > 0.05)

