Supplementary Material

Aldaulactone – an original phytotoxic secondary metabolite involved in the aggressiveness of *Alternaria dauci* on carrot

Julia Courtial, Latifa Hamama, Jean-Jacques Helesbeux, Mickaël Lecomte, Yann Renaux, Esteban Guichard, Linda Voisine, Claire Yovanopoulos, Bruno Hamon, Laurent Ogé, Pascal Richomme, Mathilde Briard, Tristan Boureau, Séverine Gagné, Pascal Poupard and Romain Berruyer\*

**\* Correspondence:** [romain.berruyer@univ-angers.fr](mailto:romain.berruyer@univ-angers.fr)

**Supplementary Table 1. List of characterized genes corresponding to quantitative disease resistance loci.** This table sums up literature presented previously (French et al., 2016; Lecomte et al., 2014; Poland et al., 2009) or not (for *At5g22540*, *qPLSr5a*, and *pan1*). Mixed-up references presented in (French et al., 2016) have been sorted out.

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| --- | --- | --- | --- | --- | --- |
| gene | type | pathogen | plant | Reference | Categorya |
| *ZmWAK* | wall-associated kinase, non-RD | *Sporisorium reilianum* | maize | (Zuo et al., 2015) | 2, 5b |
| *Htn1* | wall-associated kinase, non-RD | *Exserohilum turcicum* | maize | (Hurni et al., 2015) | 2, 5 |
| *Yr36* | kinase with START domain | *Puccinia striiformis* | wheat | (Fu et al., 2009) | 6 |
| *RFO1 / WAKL22* | wall associated kinase-like | *Fusarium oxysporum* f. sp. *matthioli* | *Arabidopsis* | (Diener and Ausubel, 2005) | 2, 5 |
| *RKS1* | atypical kinase | *Xanthomonas campestris* pv *campestris* | *Arabidopsis* | (Huard-Chauveau et al., 2013) | 6 |
| *Lr34* | putative ABC transporter | *P. striiformis, Puccinia triticina, Blumeria graminis* | wheat | (Chauhan et al., 2015) | 6 |
| *pi21* | proline containing protein | *Magnaporthe oryzae* | rice | (Fukuoka et al., 2009) | 6 |
| *Rhg4* | serine hydroxy-methyl transferase | *Heterodera glycines* | soybean | (Liu et al., 2012) | 6 |
| *Rhg1* | three ORF, an aa transporter, an alpha SNAP protein and a wound inducible protein | *H. glycines* | soybean | (Cook et al., 2012) | 6 |
| *Pi34* | unknown | *M. oryzae* | rice | (Zenbayashi-Sawata et al., 2007) | 6 |
| *Pi35* | NBS-LRR | *M. oryzae* | rice | (Fukuoka et al., 2014) | 5 |
| *RPS4* | gene pair: NBS-LRR and NBS-LRR-WRKY | *Xanthomonas campestris* pv *campestris* | *Arabidopsis* | (Debieu et al., 2016) | 5 |
| *At5g22540* | unknown | *X.campestris* pv *campestris* | *Arabidopsis* | (Debieu et al., 2016) | 6 |
| *Chr8 QTL* | complex locus, Os-GLP cluster, germin-like proteins | *M.oryzae* | rice | (Manosalva et al., 2009) | 6c |
| *qBlsr5a(1)* | recessive resistance gene xa5 | *Xanthomonas oryzae* pv *oryzicola* | rice | (Xie et al., 2014) | 5 |
| *qBlsr5a(2)* | polygalacturonase-inhibiting protein | *X. oryzae* pv *oryzicola* | rice | (Feng et al., 2016) | 2 |
| *BSR1* | receptor-like cytoplasmic kinase | *Pseudomonas syringae* | *Arabidopsis* | (Dubouzet et al., 2011) | 2, 5 |
| *Pm-21* | serine/threonine kinase | *Blumeria grazminis* f. sp. *tritici* | wheat | (Cao et al., 2011) | 6 |
| *pan1* | receptor-like kinase | *E. turcicum*, *Pantoea stewartii* | maize | (Jamann et al., 2014) | 2, 5 |

aCategories are numbered according to the mechanisms proposed in ([Poland et al., 2009](#_ENREF_35)).1: morphological variation, 2: involvement of microbial triggered immunity, 3: involvement of chemical warfare, 4: involvement of signal transduction pathways involved in effector triggered immunity, 5: QRLs as weak version of the resistance genes, and 6: new mechanisms. b*ZmWAK, Htn,1 RFO1 / WAKL22, BSR1and pan1* show homologies with both resistance genes and pathogen reconnaissance protein genes involved in microbial triggered immunity. cGLPs are known plant defense proteins. Although not new, this mechanism was not classified by Poland et al. (2009).