

Supplementary Material

The Microbiome of *Posidonia oceanica* Seagrass Leaves Can Be Dominated by Planctomycetes

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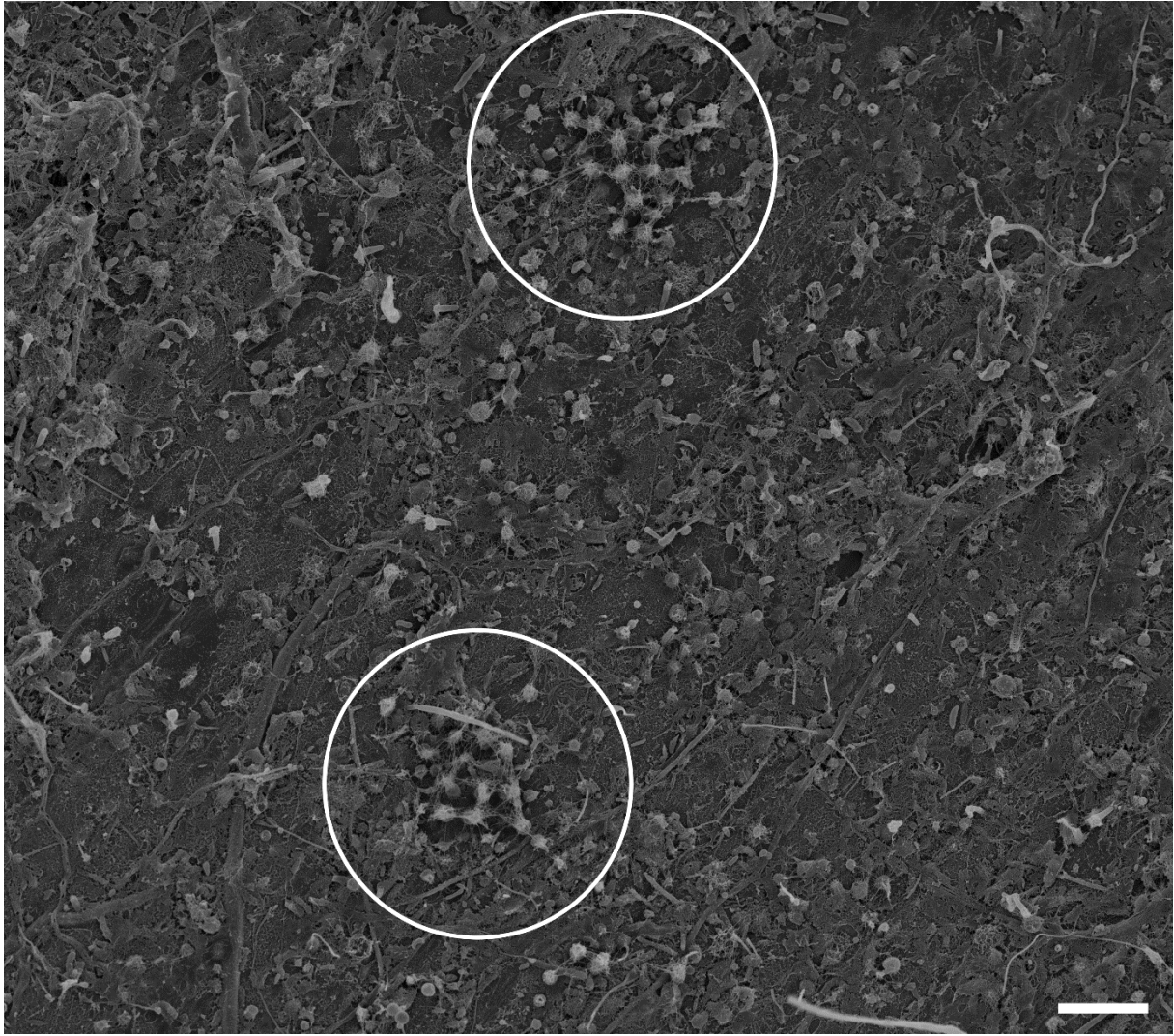


Figure S1. Scanning electron micrograph of a young *P. oceanica* leaf biofilm.

Microcolonies of cells with planctomycetal morphology (white circles) are spread over the biofilm. Scale bar is 6 μm .

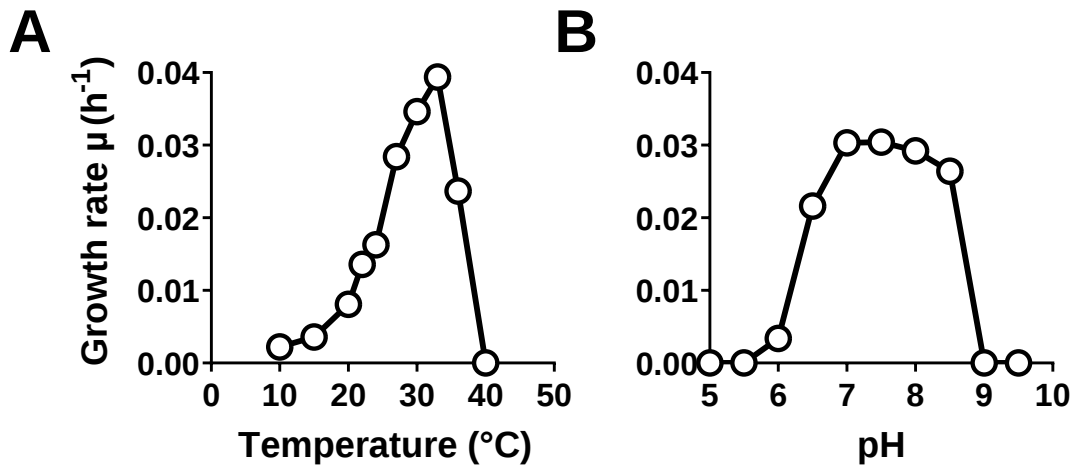


Figure S2. Temperature (A) and pH optimum (B) of strain KOR34^T.

The optical density was measured at 600 nm and growth rates were calculated and plotted against the corresponding pH or temperature. Data represent average values from three biological replicates.

A) Temperature (°C)

15 20 22 24 27 30 33 36 40



B) pH

5.0 5.5 6.0 6.5 7.0 7.5 8.0 8.5 9.0 9.5

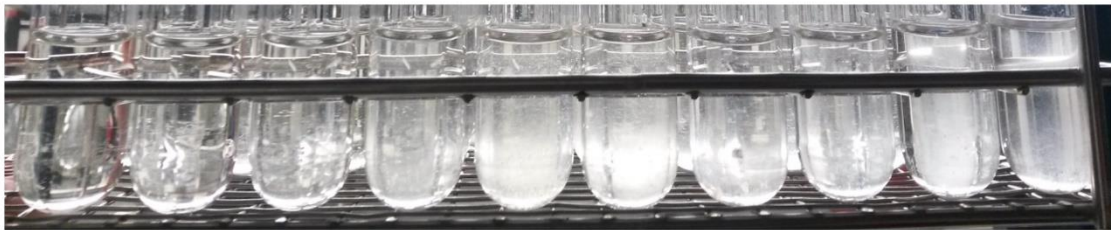


Figure S3. Temperature (A) and pH optimum (B) of strain KOR42^T.

Measurement of the optical density was not possible due to extreme aggregate formation of the strain. Instead, growth was analyzed visually.

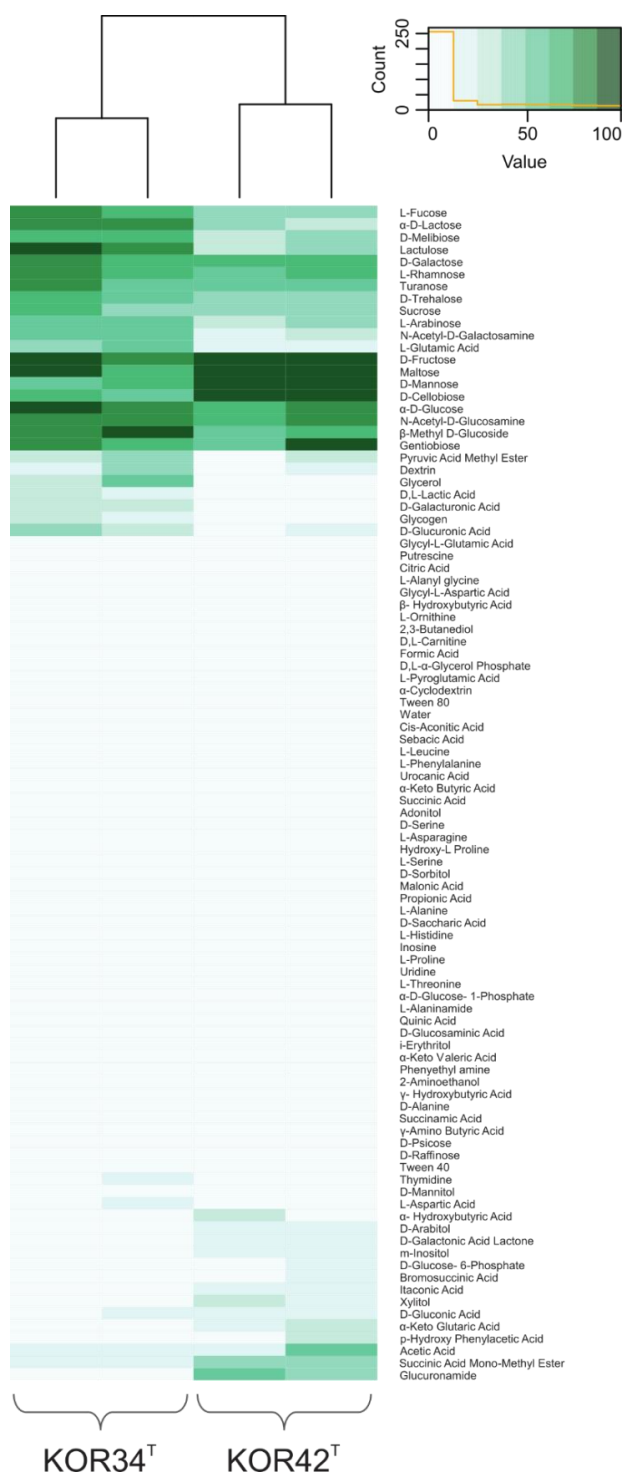


Figure S4. Substrate utilization patterns of KOR34^T and KOR42^T

Heat map of substrate utilization patterns of strains KOR34^T and KOR42^T. Two biological replicates were performed using the MicroLog GN2 substrate plates. Both strains utilized a variety of sugar substrates and KOR34^T utilized a few sugar acids not converted by KOR42^T. Color scale shows substrate usage in percent utilization. Values <25% were below threshold and evaluated as negative.

Table S1. Number of sequences, operating taxonomic units (OTUs) and diversity indices (Chao1, Shannon and Simpson) of V3 16S rRNA gene amplicons.

Sample	Sequences	OTUs	chao1	Shannon	Simpson	Planctomycetes
Biofilm (young leaves)	22,887	551	583.56	5.9	0.95	85.4 %
Biofilm (old leaves)	26,429	611	645.61	6.45	0.97	83.2 %
Water sample	28,118	489	508	5.36	0.94	1.3 %

Table S2. Similarity values for the novel isolates KOR34^T and KOR42^T compared to closely related species. The similarity values are given for each strain compared to the novel isolates. All values are given in %.

Strain	16S rRNA gene	<i>rpoB</i>	AAI	POCP
KOR34 ^T	100	100	100	100
<i>Bythopirellula goksoyri</i> Pr1d ^T	91.6	75.5	55.4	45.9
<i>Lacipirellula parvula</i> PX69 ^T	91.6	82.3	54.4	43.2
<i>Blastopirellula marina</i> DSM 3645 ^T	88.1	71.3	50.2	35.6
<i>Stieleria maiorica</i> Mal15 ^T	87	74.0	48.2	31.0
<i>Mariniblastus fucicola</i> FC18 ^T	86.2	71.6	47.3	29.5
<i>Rhodopirellula baltica</i> SH1 ^T	86.1	69.5	48.2	31.8
<i>Roseimaritima ulvae</i> UC8 ^T	86	71.8	48.9	34.1
<i>Rhodopirellula rosea</i> LHWP3 ^T	85.9	not available	not available	not available
<i>Rubripirellula obstinata</i> LF1 ^T	84.9	67.6	47.7	27.4
<i>Pirellula staleyi</i> DSM 6068 ^T	84.3	73.7	49.8	34.3
KOR42 ^T	100	100	100	100
<i>Planctomicrobium piriforme</i> P3 ^T	92.2	76.4	57.8	47.1
<i>Rubinisphaera brasiliensis</i> DSM 5305 ^T	88.7	71.5	52.2	42.3
<i>Gimesia maris</i> DSM 8797 ^T	87.4	68.9	51.8	41.1
<i>Fuerstiella marisgermanici</i> NH11 ^T	84.9	68.1	51.3	38.1
<i>Planctopirus limnophila</i> DSM 3776 ^T	84.5	69.6	49.4	36.1
<i>Schlesneria paludicola</i> DSM 18645 ^T	83.7	69.8	49.9	34.3
<i>Alienimonas californiensis</i> CA12 ^T	81.8	67.7	49.0	34.9

Table S3. Gene clusters putatively involved in the biosynthesis of secondary metabolites in KOR34^T and KOR42^T predicted by antiSMASH.

Locus tag	Putative annotation
KOR34^T	
<i>cluster 1 - polyketide</i>	
KOR34_06730	type III polyketide synthase
<i>cluster 2 - terpenoid</i>	
KOR34_14530	ferredoxin family protein
KOR34_14540	radical SAM protein
KOR34_14550	polyprenyl synthetase
KOR34_14560	prenyltransferase and squalene oxidase repeat protein
KOR34_14570	squalene--hopene cyclase
<i>cluster 3 - terpenoid</i>	
KOR34_18720	pentalenene oxygenase
<i>cluster 4 - mixed polyketide/ nonribosomal peptide</i>	
KOR34_27310	nonribosomal peptide synthetase
KOR34_27320	oxidoreductase
KOR34_27330	nonribosomal peptide synthetase
<i>cluster 5 - amino acid-derived compound</i>	
KOR34_39200	aminotransferase class I/II
<i>cluster 6 - terpenoid</i>	
KOR34_50450	oxidoreductase
KOR34_50460	hypothetical protein
KOR34_50470	squalene--hopene cyclase
KOR42^T	
<i>cluster 1 - terpenoid</i>	
KOR42_04850	squalene synthase
<i>cluster 2 - terpenoid</i>	
KOR42_08130	squalene--hopene cyclase
<i>cluster 3 - terpenoid</i>	
KOR42_18540	squalene--hopene cyclase
KOR42_18550	polyprenyl synthetase
<i>cluster 4 - polyketide</i>	
KOR42_21030	type III polyketide synthase
<i>cluster 5 - terpenoid</i>	
KOR42_26350	squalene/phytoene synthase family protein