

## Effects of bacterial communities on the sensitivity of the phytoplankton *Stephanodiscus minutulus* and *Desmodesmus armatus* to tannic acid

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### Supplement. Data on detailed phylogenetic analysis

Table S1. Phylogenetic affiliation of sequenced DGGE bands (indicated with “DGGE” in community label and accession number) of attached (att.) and free living (f.l.) bacteria with no (C), low (L) and high (H) tannic acid (TA) treatment in Expt 1, and with (1 mg TA l<sup>-1</sup> d<sup>-1</sup>) and without further TA addition in Expt 2 (C<sub>TA</sub>, L<sub>TA</sub>, H<sub>TA</sub> or C, L, H), and isolated bacteria in Expt 3 (indicated with “Iso” in the community label) to closest relative in NCBI GenBank. For phylogenetic relationship of representatives of DGGE and isolates see phylogenetic tree based on 16S rDNA (Fig. 3)

DGGE / Iso bands with community labels & accession No.	att. / f.l. bac-teria	TA-treatment C L H	Phylum or group	Family	Next cultivated relative	Accession No.	Similarity [%]	Closest relative in GenBank	Accession No.	Max. ident [%]	Band-No. (Fig. 7)
KLnbDGGE_1 GQ332384	att.	C (Expt 1)	Proteobacteria; Betaproteobacteria; Burkholderiales;	Comamonadaceae; Acidovorax.	<i>Acidovorax avenae</i> subsp. <i>citrulli</i> AAC00-1, complete genome	NC 008752	97	Uncultured bacterium clone 655935 16S ribosomal RNA gene, partial sequence	DQ404721.1	97	1
DGGE 3		L (Expt 1)	Proteobacteria; Alphaproteobacteria; Rickettsiales;	Rickettsiaceae; Rickettsiae; Rickettsia; typhus group	<i>Rickettsia canadensis</i> str. McKiel, complete genome	AACY020 000000	86	Uncultured bacterium clone 1P-2-L11 16S ribosomal RNA gene, partial sequence	FJ562174.1	89	3
DGGE 4		L (Expt 1)	Proteobacteria; Betaproteobacteria; Burkholderiales;	Burkholderiaceae; Limnobacter	<i>Limnobacter</i> sp. MED105 1103186003328, whole genome shotgun sequence.	NZ ABCT010 00008.1	96	Limnobacter sp. Cy2 16S ribosomal RNA gene, partial sequence.	FJ377408.1	96	4

KLnbDGGE 5 GQ332385	L (Expt 1)	Proteobacteria; Alphaproteobacteria; Rhodobacterales;	Rhodobacteraceae; Rhodobacter	<i>Rhodobacter sphaeroides</i> ATCC 17025 plasmid pRSPA02, complete sequence	ATCC 17025	95	Uncultured Rhodobacteraceae bacterium clone Gap-2-91 16S ribosomal	EU642175. 1	98	5
KLnbDGGE 6 GQ332386	H (Expt 1)	Actinobacteria; Actinobacteridae; Actinomycetales;	Streptomycineae; Streptomycetaceae; Streptomyces	<i>Streptomyces avermitilis</i> MA-4680, complete genome	NC 003155.4	91	Uncultured bacterium partial 16S rRNA gene, clone L50Sp-17.	AJ966223. 1	99	6
KLnbDGGE 7 GQ332393	C (Expt 2)	Proteobacteria; Betaproteobacteria; Burkholderiales;	Comamonadaceae; Rhodoferrax.	<i>Rhodoferrax</i> <i>ferrireducens</i> T118, complete genome	NC 007908.1	96	Uncultured Comamonadaceae bacterium clone LW18m- 1-58 16S rRNA gene, partial sequence.	EU642288. 1	98	7
DGGE 8	C <sub>TA</sub> (Expt 2)	Proteobacteria; Betaproteobacteria; Burkholderiales;	Comamonadaceae; Delftia	<i>Delftia acidovorans</i> SPH-1, complete genome	NC 010002	94	Comamonadaceae bacterium IK1_39 gene for 16S rRNA, partial sequence, strain: IK1_39	AB461020 .1	92	8
KLnbDGGE 10	L <sub>TA</sub> (Expt 2)	Proteobacteria; Alphaproteobacteria; Sphingomonadales;	Erythrobacteraceae; Erythrobacter	<i>Erythrobacter litoralis</i> HTCC2594, complete genome	NZ AAMW010 00002.1	88	Uncultured bacterium partial 16S rRNA gene, clone MBR-8_LF_BF90.	FM201099 .1	91	10
KLnbDGGE 13 GQ332395	H <sub>TA</sub> (Expt 2)	Actinobacteria; Actinobacteridae; Actinomycetales;	Streptomycineae; Streptomycetaceae; Streptomyces	<i>Streptomyces avermitilis</i> MA-4680, complete genome.	NC 003155.1	91	Uncultured bacterium partial 16S rRNA gene, clone L50Sp-17.	AJ966223	99	13
DGGE 14	H <sub>TA</sub> (Expt 2)	Proteobacteria; Betaproteobacteria; Burkholderiales;	Comamonadaceae; Rhodoferrax	<i>Rhodoferrax</i> <i>ferrireducens</i> T118, complete genome	NC 007908.1	83	Uncultured Comamonadaceae bacterium clone GC1m-2- 16 16S ribosomal RNA gene, partial sequence	EU640750. 1	85	14
KLnbDGGE 15 GQ332396	f. l. C (Expt 1)	Proteobacteria; Gammaproteobacteri a; Legionellales	Legionellaceae; Legionella	<i>Legionella pneumophila</i> str. Paris, complete genome	NC 006368.1	95	<i>Legionella pneumophila</i> isolate DGGE band 4 16S ribosomal RNA gene, partial sequence	DQ408661 .1	95	15
KLnbDGGE 16 GQ332397	C (Expt 1)	Proteobacteria; Gammaproteobacteri a; Legionellales;	Legionellaceae; Legionella.	<i>Legionella pneumophila</i> str. Corby, complete genome	NC 009494.1	90	<i>Legionella beliardensis</i> strain Montbeliard A1 16S ribosomal RNA gene, partial sequence	AF122884. 2	91	16
KLnbIso3 GQ332384		Proteobacteria; Gammaproteobacteri a; Pseudomonadales;	Pseudomonadaceae; Pseudomonas	<i>Pseudomonas libanensis</i> strain a105 partial sequence .	EU434380	99	<i>Pseudomonas libanensis</i> strain a105 16S ribosomal RNA gene, partial sequence	EU434380	99	

KLnbIso5 GQ332385		Proteobacteria; Gammaproteobacteria; Pseudomonadales;	Pseudomonadaceae; Pseudomonas	<i>Pseudomonas sp.</i> 104 16S ribosomal RNA gene, partial sequence.	FJ013262	99	Uncultured bacterium clone nbt27f08 16S ribosomal RNA gene, partial sequence	EU535591	100
KLnbIso6 GQ332386		Proteobacteria; Gammaproteobacteria; Pseudomonadales;	Pseudomonadaceae; Pseudomonas	<i>Pseudomonas sp.</i> 104 16S ribosomal RNA gene, partial sequence.	FJ013262 GI:219551 897	99	<i>Pseudomonas sp.</i> 104 16S ribosomal RNA gene, partial sequence.	FJ013262 GI:219551 897	99
KLnbIso7 GQ332387, KLnbIso8 GQ332388	Expt 3	Proteobacteria; Gammaproteobacteria; Pseudomonadales;	Pseudomonadaceae; Pseudomonas	<i>Pseudomonas sp.</i> NJ-61 16S rRNA gene, strain NJ-61	AM42198 2	99	Uncultured soil bacterium clone T7_7 16S ribosomal RNA gene, partial sequence	FJ184352. 1 GI:208341 952	99
KLnbIso11 GQ332389	Expt 3	Proteobacteria; Gammaproteobacteria; Pseudomonadales;	Pseudomonadaceae; Pseudomonas	<i>Pseudomonas putida</i> strain KT-ql-116 16S ribosomal RNA gene, partial sequence.	FJ611926	100	<i>Pseudomonas putida</i> strain KT-ql-116 16S ribosomal RNA gene, partial sequence	FJ611926. 1	100
KLnbIso12 GQ332390	Expt 3	Proteobacteria; Gammaproteobacteria; Pseudomonadales;	Pseudomonadaceae; Pseudomonas	<i>Pseudomonas sp.</i> Pi 3-8 gene for 16S rRNA, partial sequence	AB365065	94	Uncultured bacterium clone E4 16S ribosomal RNA gene, partial sequence	FJ347716	98

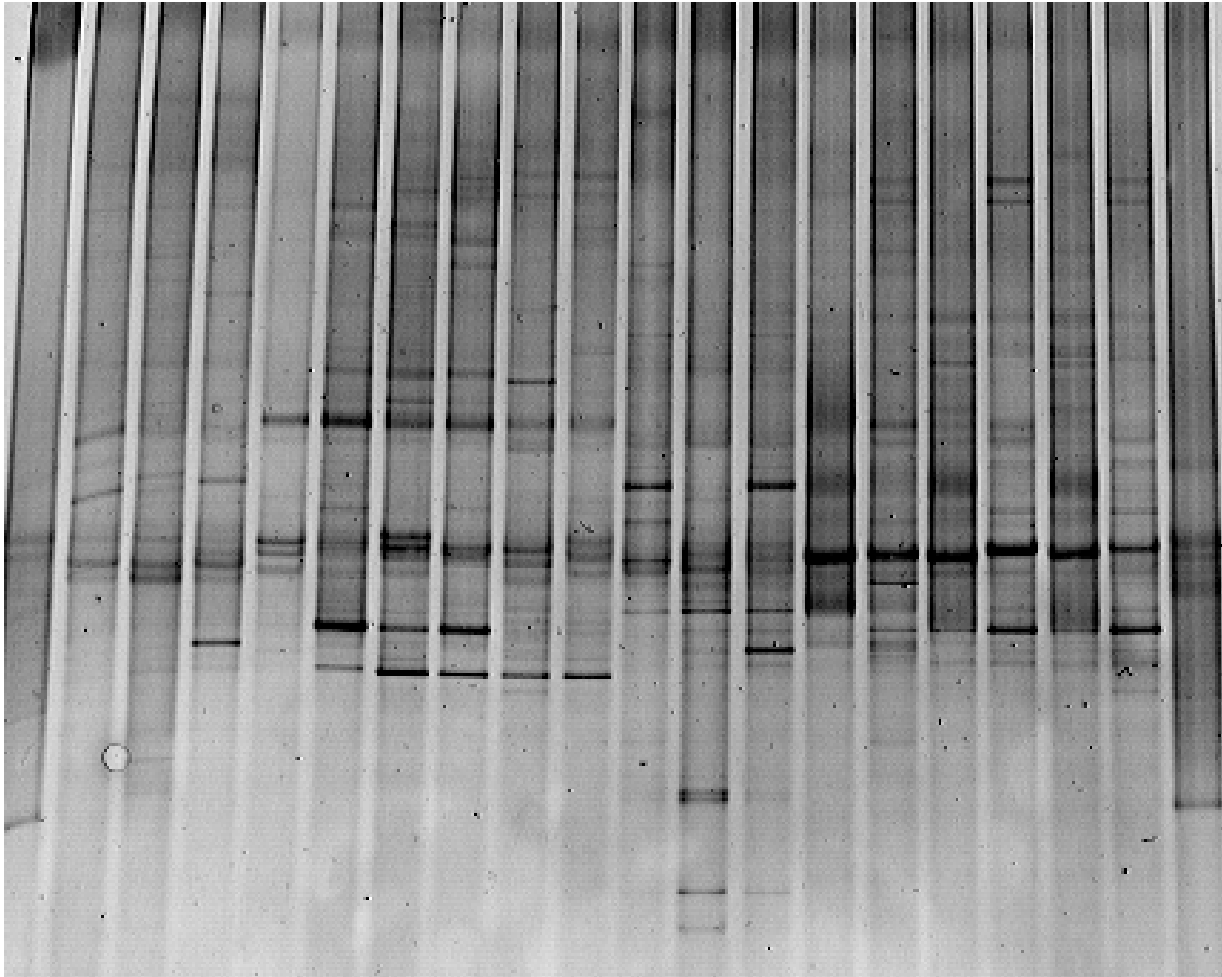
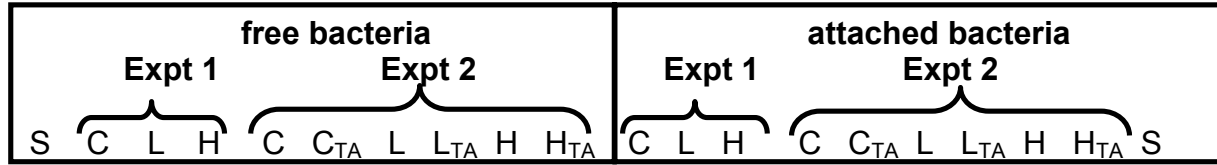


Fig. S1. *Stephanodiscus minutulus*. DGGE banding pattern of all treatments visualized by DGGE of PCR-amplified partial 16S rRNA genes of free-living and attached bacteria. S: standard. In Expt 1, pre-treated bacterial community with no (control) = C, low (0.05%) = L, and high (0.5%) = H tannic acid (TA) concentration at the end of pre-treatment and at the start of the incubation with *S. minutulus*. In Expt 2, C<sub>TA</sub>, L<sub>TA</sub>, H<sub>TA</sub>: respective bacterial communities treated with daily addition of TA (1 mg l<sup>-1</sup>); C, L, H: respective bacterial communities without further TA addition