

Proteomics analysis of the response of the marine bacterium *Marinobacter adhaerens* HP15 to the diatom *Thalassiosira weissflogii*

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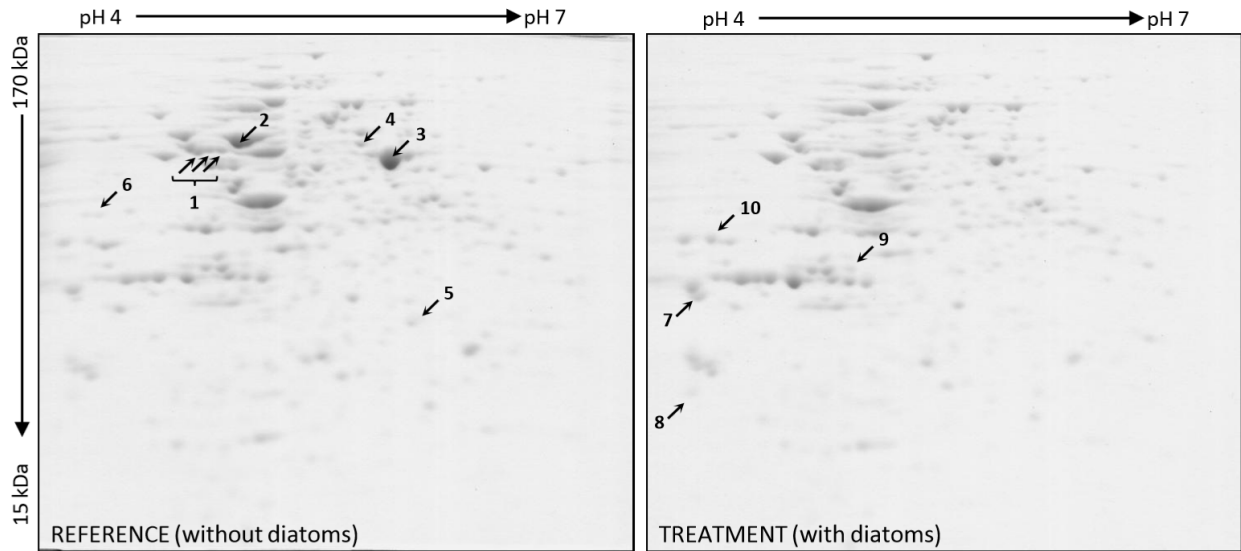


Fig. S1. 2D-SDS-PAGE of cytoplasmic proteins obtained from *M. adhaerens* HP15 in the REFERENCE treatment (left) and in co-cultivation with the diatom *T. weissflogii* (right). Proteins significantly up- or down-regulated are assigned with an arrow. Protein names are given below. **1.** quinorotein alcohol dehydrogenase **2.** low quality protein: quinoprotein alcohol dehydrogenase. **3.** NAD-dependent aldehyde dehydrogenase **4.** isocitrate lyase **5.** 3-hydroxyisobutyrate dehydrogenase **6.** urea short chain amide or branched amino acid uptake ABC transporter, periplasmic solute binding protein (UrtA) **7.** phosphonate ABC transporter, periplasmic phosphonate-binding protein (PhnD) **8.** extracellular solute-binding protein (AotJ) **9.** TRAP dicarboxylate family transporter, DctP subunit **10.** amino acid binding protein (LivK).

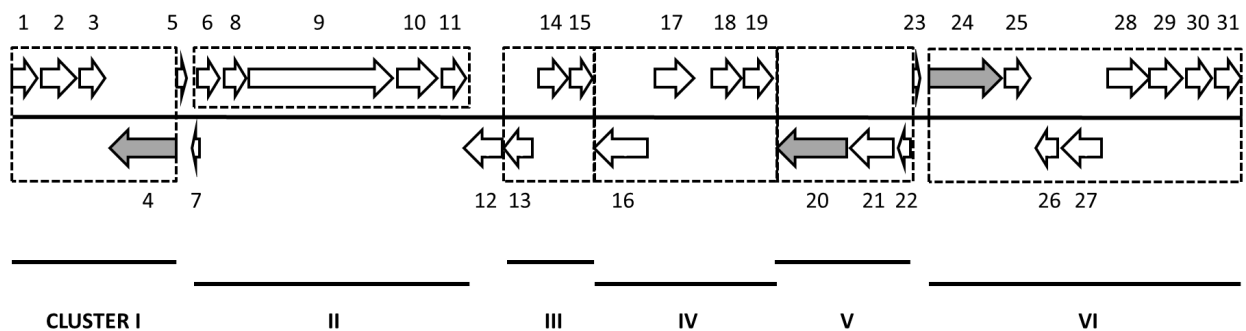


Fig. S2. Cluster Analysis of genomic region encoding down-regulated alcohol and aldehyde dehydrogenases. Dashed boxes frame the identified cluster. Grey gene products were found to be down-regulated in *M. adhaerens* P15 during co-cultivation with diatom *T. weissflogii*: **4:** aldehyde dehydrogenase gene (ADP98908.1) **20** and **24:** alcohol dehydrogenases (ADP98924.1 and ADP98928.1). See details on further genes in Table S2.

Table S1. Raw data of fold-changes and *p*-values of significantly altered bacterial proteins of *M. adhaerens* HP15 during co-cultivation with the diatom *T. weissflogii* (as obtained from Delta2D software).

Identified protein (annotation according to NCBI)	Accession	Gene Locus	Fold-Change]0.5..2[<i>p</i> -Value (<0.05)
Down-regulated during co-cultivation with the diatom:				
quinoprotein alcohol dehydrogenase ^{*1}	ADP98924.1	HP15_3160	0.327 0.338 0.392	0.0111 0.0032 0.0470
low quality protein: quinoprotein alcohol dehydrogenase	ADP98928.1	HP15_3164	0.136	0.0273
NAD-dependent aldehyde dehydrogenase ^{*1}	ADP98908.1	HP15_3144	0.241 0.361 0.324	0.0469 0.0090 0.0446
isocitrate lyase	ADP98998.1	HP15_3234	0.355	0.0032
3-hydroxyisobutyrate dehydrogenase	ADP96674.1	HP15_910	0.361	0.0248
urea short-chain amide or branched-chain amino acid uptake ABC transporter, periplasmic solute-binding protein	ADP98645.1	HP15_2881	0.371	0.0056
Up-regulated during co-cultivation with the diatom				
phosphonate ABC transporter, periplasmic phosphonate-binding protein	ADP97492.1	HP15_1728	2.272	0.0126
extracellular solute-binding protein, family 3	ADP98795.1	HP15_3031	2.007	0.0429
TRAP dicarboxylate family transporter, DctP subunit	ADP98792.1	HP15_3028	2.241	0.0365
amino acids binding protein	ADP99862.1	HP15_4098	3.345	0.0148

^{*1} Proteins 'quinoprotein alcohol dehydrogenase' and 'NAD-dependent aldehyde dehydrogenase' were represented by three protein spots on the corresponding gels

Table S2. Genes and gene clusters in close proximity of the down-regulated alcohol and aldehyde dehydrogenases. Down regulated gene products are shown in grey (see also Fig. S2)

Gene number	Gene annotation	Accession	Cluster
1	transcriptional regulator, TetR family	ADP98905.1	I
2	quinone oxidoreductase, YhdH/YhfP family	ADP98906.1	I
3	uncharacterized peroxidase-related protein	ADP98907.1	I
4	NAD-dependent aldehyde dehydrogenase	ADP98908.1	I
5	hypothetical protein	ADP98909.1	-
6	urea carboxylase-associated protein 2	ADP98910.1	II
7	urea carboxylase-associated protein 1	ADP98911.1	II
8	hypothetical protein	ADP98912.1	-
9	urea amidolyase-like protein/ urea carboxylase	ADP98913.1	II
10	ABC transporter, periplasmic substrate-binding protein / NifT/TauT family transport system substrate-binding protein	ADP98914.1	II
11	transcriptional regulator, TetR family	ADP98915.1	II
12	regulatory protein ada	ADP98916.1	-
13	protein containing cyclic nucleotide-binding domain	ADP98917.1	III
14	class II aldolase/adducin family protein	ADP98918.1	III
15	metal dependent phosphohydrolase	ADP98919.1	III
16	glutamate-ammonia ligase/ glutamine synthetase	ADP98920.1	IV
17	metX, homoserine O-acetyltransferase	ADP98921.1	IV
18	binding-protein-dependent transport systems inner membrane component	ADP98922.1	IV
19	spermidine/putrescine ABC transporter ATPase	ADP98923.1	IV
20	quinoprotein alcohol dehydrogenase	ADP98924.1	V
21	extracellular solute-binding protein, family 3	ADP98925.1	V
22	cytochrome c550	ADP98926.1	V
23	hypothetical protein	ADP98927.1	-
24	LOW QUALITY PROTEIN: quinoprotein alcohol dehydrogenase	ADP98928.1	VI
25	pentapeptide repeat family protein	ADP98929.1	VI
26	two component transcriptional regulator, LuxR family	ADP98930.1	VI
27	integral membrane sensor signal transduction histidine kinase	ADP98931.1	VI
28	conserved hypothetical protein, secreted	ADP98932.1	VI
29	40-residue YVTN family beta-propeller repeat-containing protein	ADP98933.1	VI
30	ABC efflux transporter, ATP-binding protein	ADP98934.1	VI
31	ABC efflux transporter, permease protein	ADP98935.1	VI

Table S3. Known oligosaccharide and polyol transporters [section ABC transporter, mad02010] (KEGG, November 2015). Those uptake systems identified in *M. adhaerens* HP15 according to KEGG algorithms are shown in **bold**.

Substrate	Corresponding proteins involved in substrate uptake
Maltose/ Maltodextrin	MalE, MalF, MalG, MalK
Galactose oligomer/ Maltooligosaccharide	GanO, GanP, GanQ, MsmX
Raffinose/ Stachyose/ Melibiose	MsmE, MsmF, MsmG, MsmK
Lactose/ L-arabinose	LacE, LacF, LacG, LacK
Sorbitol/ Mannitol	SmoE, SmoF, SmoG, SmoK
α -Glucoside	AglE, AglF, AglG, AglK
Oligogalacturonide	TogB, TogM, TogN, TogA
α -1,4-Digalacturonate	AguE, AguF, AguG
Aldouronate	LplA, LplB, LplC
Trehalose/ Maltose	ThuE, ThuF, ThuG, ThuK
Trehalose	TreS, TreT, TreU, TreV
N-Acetylglucosamine	NgcE, NgcF, NgcG
Cellobiose	CebE, VebF, CebG, MsiK
Chitobiose	DasA, DasB, DasC, MsiK
Chitobiose	ChiE, ChiF, ChiG
Arabinoooligosaccharide	AraN, AraP, AraQ, MsmX
Xylobiose	BxlE, BxlF, BxlG
Multibel Sugar?	ChvE, GguB, GguA
Phospholipid	MlaC, MlaD, MlaE, MlaB, MlaF

Table S4. Known monosaccharide transporters [section ABC transporter, mad02010] (KEGG, November 2015). Transporters identified in *M. adhaerens* HP15 according to KEGG algorithms are shown in **bold**.

Substrate	Corresponding proteins involved in substrate uptake
Glucose/ Arabinose	GlcS, GlcU, GlcT, GlcV
Glucose/ Mannose	GtsA, GtsB, GtsC, MalK
Ribose/ Autoinducer 2/ D-Xylose	RbsB, RbsC, RbsD, RbsA
L-Arabinose	AraF, AraH, AraG
Methyl-galactoside	MglB, MglC, MglA
D-Xylose	XylF, XylH, XylG
D-Allose	AlsB, AlsC, AlsA
Fructose	FrcB, FrcC, FrcA
Autoinducer 2	LsrB, LsrC, LsrD, LsrA
Rhamnose	RhaS, RhaP, RhaQ, RhaT
Erythritol	EryG, EryF, EryE
Xylitol	XltC, XltB, XltA
myo-Inositol	IbpA, IatP, IatA
Glycerol	GlpV, GlpP, GlpQ, GlpS, GlpT,
Sn-Glycerol 3-phosphate	UgpB, UgpA, UgpE, UgpC,

Table S5. Known phosphotransferase systems (PTS, mad02060) (KEGG, November 2015). Those systems identified in *M. adhaerens* HP15 according to KEGG algorithms are in **bold**.

Substrate	Corresponding proteins involved in substrate utilization
Glc family	
Glucose → Glucose 6-phosphate	PtsG, Crr
N-Acetyl-D-glucosamine → N-Acetyl-D-glucosamine 6-phosphate	NagE
Maltose → Maltose 6-phosphate	MalX, Crr
D-Glucosamine → D-Glucosamine 6-phosphate	GamP
Sucrose → Sucrose-6-phosphate	ScrA
β-Glucosides → Phospho-β-glucosides	BglF
Arbutin/ Salicin → Arbutin/ Salicin 6-phosphate	AscF, Crr
Trehalose → Trehalose 6-phosphate	TreB, TreP/Crr
N-Acetyl-muramic acid → N-Acetyl-muramic acid 6-phosphate	MurP, Crr
Arbutin → Arbutin 6-phosphate	GlvC, Crr, GlvB
Lac family	
Lactose → Lactose 6-phosphate	LacE, LacF
Cellobiose → [...]	CelB, CelC, CelA
Fru family	
Mannitol → Mannitol 1-phosphate	MtlA
2-O-α-Mannosyl-D-glycerate → 2-O-(6-Phosphate-α-mannosyl)-D-Glycerate	MngA
Fructose → Fructose 1-phosphate	FruA, FruB
Man family	
Mannose → Mannose 6-phosphate	ManY, ManZ, ManX
Fructose-/Glucoselysine → Fructose-/Glucoselysine 6-phosphate	GfrC, GfrD, GfrA, GfrB
Fructose → Fructose 1-phosphate	LevF, LevG, LevD, LevE
Sorbose → Sorbose 1-phosphate	SorA, SorM, SorF, SorB
N-Acetyl-galactosamine → N-Acetyl-galactosamine 6-phosphate	AgaW, AgaE, AgaF, AgaV
Galactosamine → Galactosamin 6-phosphate	AgaC, AgaE, AgaF, AgaB
D-Glucosamine → D-Glucosamine 6-phosphate	DgaC, DgaD, DgaA, DgaB
Other family	
Sorbitol → Sorbitol 6-phosphate	SrlA/SrlE, SrlB, SrlE
Galactitol → Galactitol 1-phosphate	GatC, GatA, GatB
L-Ascorbate → L-Ascorbate 6-phosphate	UlaA, UlaC, UlaB
Nitrogen regulation	
Nitrogen → [...]	[...], PtsN
Phosphoenol-pyruvate → pyruvate	PtsP, PstI