

Supplementary material

Dimethylsulfoniopropionate in corals and its interrelations with bacterial assemblages in coral surface mucus

P. R. Frade,^{A,B,G} *V. Schwaninger*,^C *B. Glasl*,^A *E. Sintes*,^A *R. W. Hill*,^D *R. Simó*^E and *G. J. Herndl*^{A,F}

^AUniversity of Vienna, Department of Limnology and Bio-Oceanography, Althanstrasse 14, AT-1090 Vienna, Austria.

^BCaribbean Research and Management of Biodiversity (CARMABI) Foundation, Piscaderabaai z/n, PO Box 2090, Willemstad, Curaçao.

^CUniversity of Innsbruck, Institute of Ecology, Technikerstrasse 25, AT-6020 Innsbruck, Austria.

^DMichigan State University, Department of Zoology, 288 Farm Lane RM 203, East Lansing, MI 48824, USA.

^EInstitute of Marine Sciences (ICM-CSIC), Passeig Marítim de la Barceloneta 37-49, E-08003 Barcelona, Spain.

^FRoyal Netherlands Institute for Sea Research (NIOZ), Department of Biological Oceanography, 1790 AB Den Burg, Netherlands.

^GCorresponding author. Email: pedro.rodriques.frade@univie.ac.at

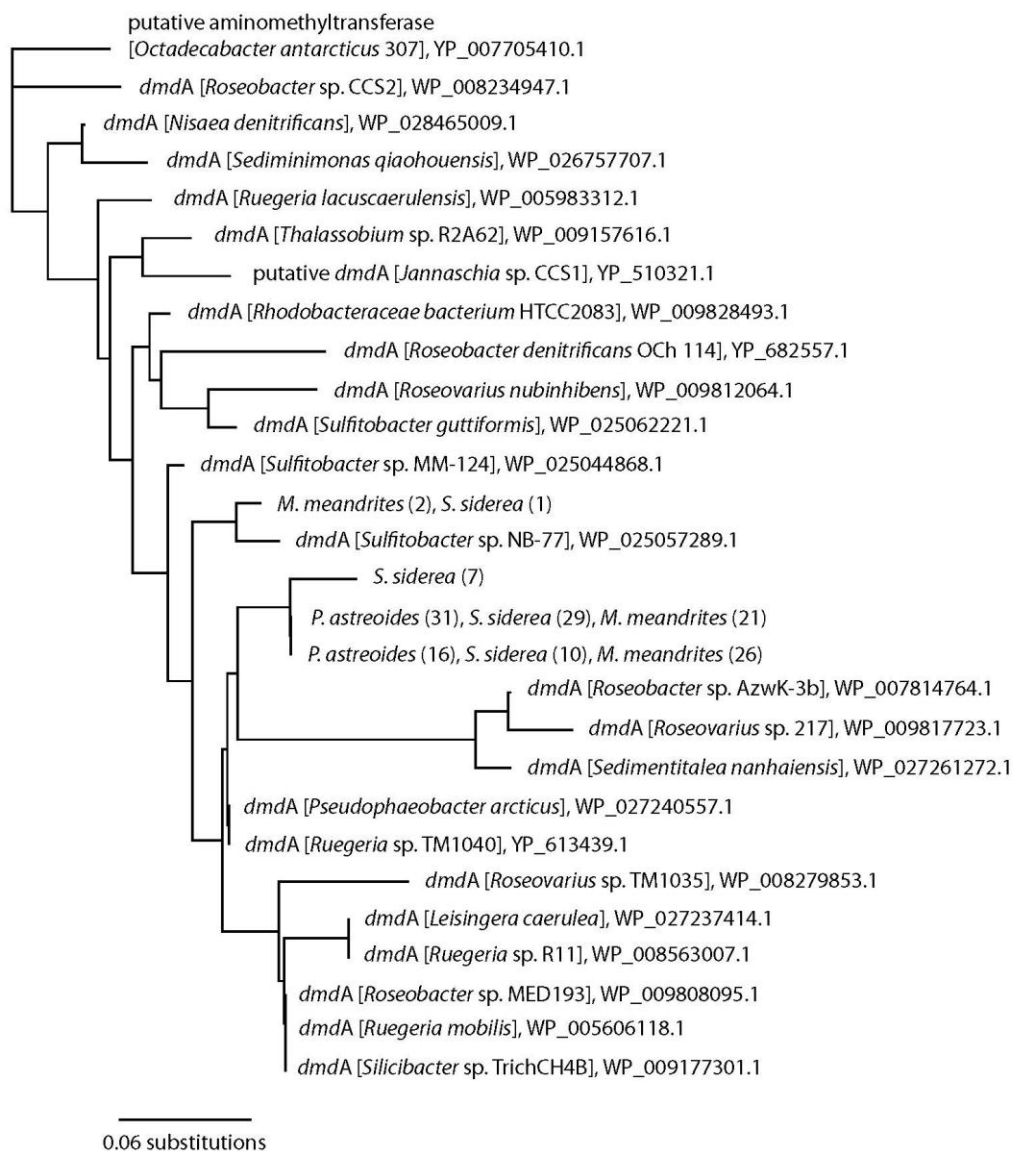


Fig. S1. *dmdA* gene subclade A/2: neighbour-joining amino acid tree representing the diversity and phylogenetic relationships of sequence homologues obtained from the clone libraries and including reference sequences retrieved from the NCBI database after BLAST searches. Entries obtained in the current study include the identity of coral host species and the number of sequences clustering in each branch (a clone code is shown in case of a single sequence). A related aminomethyltransferase sequence was used as outgroup.

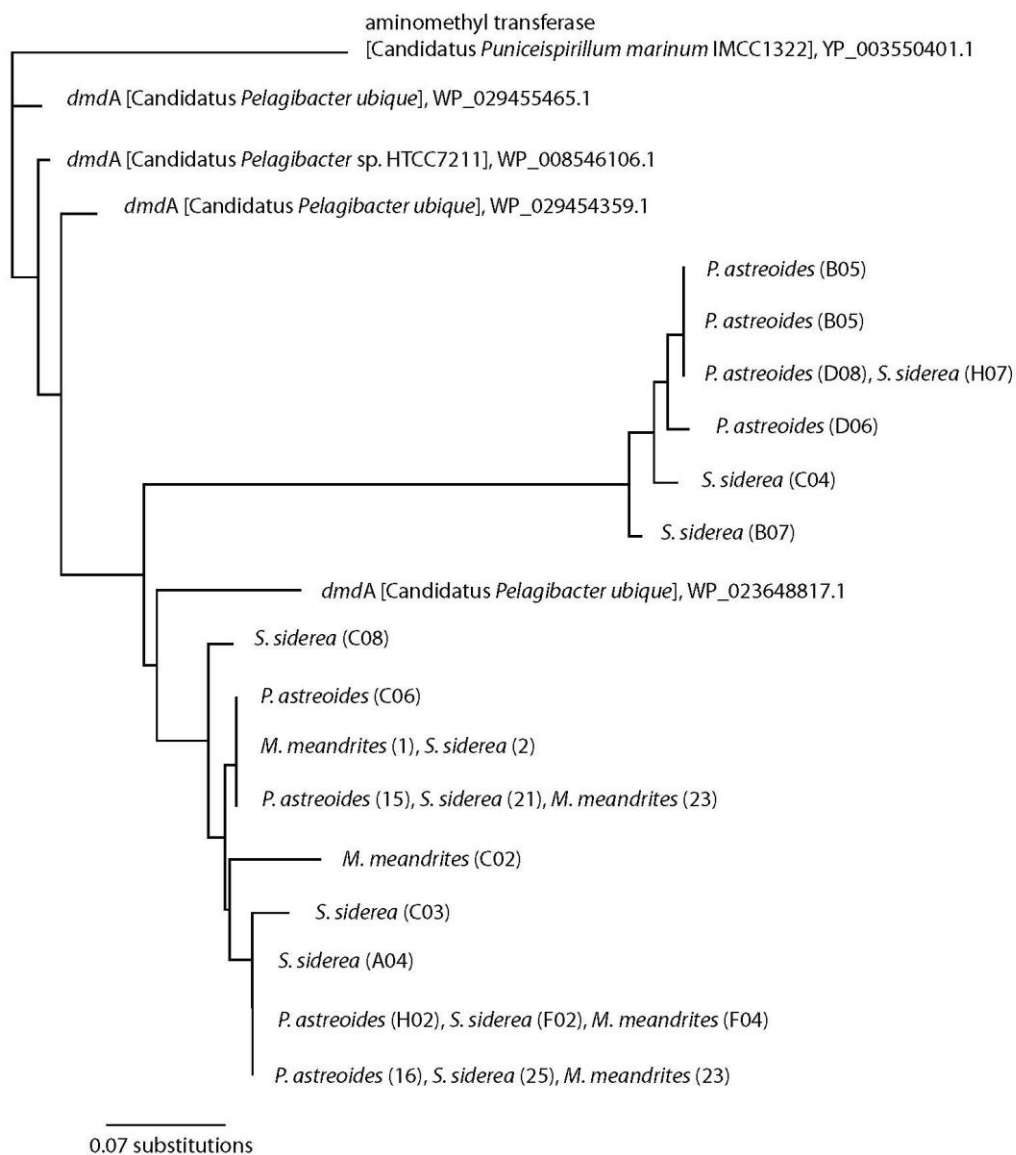


Fig. S2. *dmdA* gene subclade C/2: neighbour-joining amino acid tree representing the diversity and phylogenetic relationships of sequence homologues obtained from the clone libraries and including reference sequences retrieved from the NCBI database after BLAST searches. Entries obtained in the current study include the identity of coral host species and the number of sequences clustering in each branch (a clone code is shown in case of a single sequence). A related aminomethyltransferase sequence was used as outgroup.

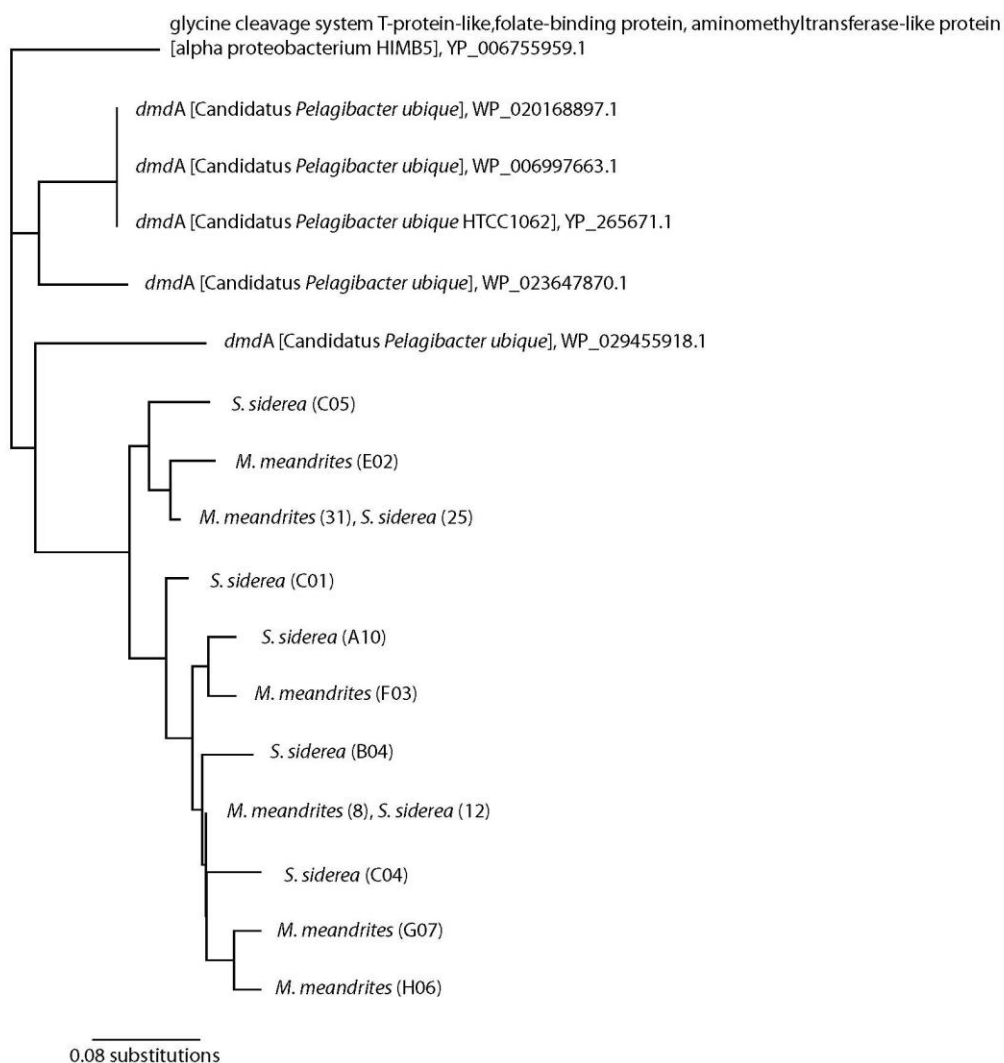


Fig. S3. *dmdA* gene subclade D/3: neighbour-joining amino acid tree representing the diversity and phylogenetic relationships of sequence homologues obtained from the clone libraries and including reference sequences retrieved from the NCBI database after BLAST searches. Entries obtained in the current study include the identity of coral host species and the number of sequences clustering in each branch (a clone code is shown in case of a single sequence). A related aminomethyltransferase sequence was used as outgroup.

Table S1. Statistical output of analysis of variation for the parameter ‘Symbiont cell abundance’ (log-transformed) using a GLM with Gaussian distribution

Level used as host species reference is ‘*M. meandrites*’. Probabilities are significant at: ***, $P < 0.001$; **, $0.001 < P < 0.01$; *, $0.05 < P < 0.1$

	Estimate	s.e.	t-value	Pr(> t)
(Intercept)	0.804	0.0529	15.2	$< 2 \times 10^{-16}$ ***
<i>P. astreoides</i>	-0.684	0.0739	-9.26	5.02×10^{-13} ***
<i>S. siderea</i>	-0.614	0.0748	-8.20	2.86×10^{-11} ***

Table S2. Statistical output of analysis of variation for the parameter ‘DMSP concentration per unit area’ (log-transformed) using a GLM with Gaussian distribution

Level used as treatment reference is ‘Control group’. Probabilities are significant at: ***, $P < 0.001$; **, $0.001 < P < 0.01$; *, $0.05 < P < 0.1$

	Estimate	s.e.	t-value	Pr(> t)
(Intercept)	1.23	0.0569	21.7	$< 2 \times 10^{-16}$ ***
(log) Symbiont cell abundance	0.665	0.0840	7.92	1.35×10^{-10} ***
Stressed group (air exposure)	0.293	0.0656	4.46	4.19×10^{-5} ***

Table S3. Statistical output of analysis of variation for the parameter ‘DMSP concentration per symbiont cell’ (log-transformed) using a GLM with Gaussian distribution

Level used as host species reference is ‘*M. meandrites*’. Level used as treatment reference is ‘Control group’. Probabilities are significant at: ***, $P < 0.001$; **, $0.001 < P < 0.01$; *, $0.05 < P < 0.1$

	Estimate	s.e.	t-value	Pr(> t)
(Intercept)	0.960	0.0635	15.1	$< 2 \times 10^{-16}$ ***
<i>P. astreoides</i>	0.199	0.0779	2.56	1.35×10^{-2} *
<i>S. siderea</i>	0.342	0.0797	4.29	7.7×10^{-5} ***
Stressed group (air exposure)	0.241	0.0656	3.68	5.47×10^{-4} ***

Table S4. Statistical output of analysis of variation for the parameter ‘*recA* abundance’ using a GLM with Quasipoisson distribution

Level used as sampling depth reference is ‘5-m depth’. Probabilities are significant at: ***, $P < 0.001$; **, $0.001 < P < 0.01$; *, $0.05 < P < 0.1$

	Estimate	s.e.	t-value	Pr(> t)
(Intercept)	9.48	0.137	69.2	$< 2 \times 10^{-16}$ ***
25-m depth	0.638	0.189	3.37	1.36×10^{-3} **

Table S5. Statistical output of analysis of variation for the parameter ‘subclade A/2 *dmdA* abundance’ using a GLM with Poisson distribution and the variable ‘*recA* abundance’ (log-transformed) as offset variable

Level used as host species reference is ‘*M. meandrites*’. Level used as time of the day reference is ‘Dawn’.
Level used as sampling depth reference is ‘5-m depth’. Probabilities are significant at: ***, $P < 0.001$; **, $0.001 < P < 0.01$; *, $0.05 < P < 0.1$

	Estimate	s.e.	z-value	Pr(> z)
(Intercept)	-1.12	0.112	-10.0	$< 2 \times 10^{-16}$ ***
(log) DMSP per unit area	1.07	0.0589	18.3	$< 2 \times 10^{-16}$ ***
<i>P. astreoides</i>	1.87	0.125	14.9	$< 2 \times 10^{-16}$ ***
<i>S. siderea</i>	4.86	0.429	11.3	$< 2 \times 10^{-16}$ ***
Noon	0.976	0.0301	32.4	$< 2 \times 10^{-16}$ ***
25-m depth	-0.172	0.0211	-8.17	3.01×10^{-16} ***
(log) DMSP per unit area: <i>P. astreoides</i>	-0.245	0.0782	-3.14	1.71×10^{-3} **
(log) DMSP per unit area: <i>S. siderea</i>	-3.03	0.290	-10.5	$< 2 \times 10^{-16}$ ***

Table S6. Statistical output of analysis of variation for the parameter ‘subclade C/2 *dmdA* abundance’ using a GLM with Poisson distribution and the variable ‘*recA* abundance’ (log-transformed) as offset variable

Level used as host species reference is ‘*M. meandrites*’. Level used as time of the day reference is ‘Dawn’.
Level used as sampling depth reference is ‘5-m depth’. Probabilities are significant at: ***, $P < 0.001$; **, $0.001 < P < 0.01$; *, $0.05 < P < 0.1$

	Estimate	s.e.	z-value	Pr(> z)
(Intercept)	0.693	0.116	5.96	2.51×10^{-9} ***
(log) DMSP per unit area	0.224	0.065	3.44	5.84×10^{-4} ***
<i>P. astreoides</i>	1.00	0.129	7.79	6.78×10^{-15} ***
<i>S. siderea</i>	-4.41	0.783	-5.63	1.76×10^{-8} ***
Noon	0.149	0.0296	5.02	5.06×10^{-7} ***
25-m depth	-0.445	0.0288	-15.5	$< 2 \times 10^{-16}$ ***
(log) DMSP per unit area: <i>P. astreoides</i>	0.299	0.0832	3.59	3.29×10^{-4} ***
(log) DMSP per unit area: <i>S. siderea</i>	3.17	0.528	6.01	1.83×10^{-9} ***

Table S7. Statistical output of analysis of variation for the parameter ‘subclade D/3 *dmdA* abundance’ using a GLM with Quasipoisson distribution and the variable ‘*recA* abundance’ (log-transformed) as offset variable

Level used as host species reference is ‘*M. meandrites*’. Level used as time of the day reference is ‘Dawn’.
Probabilities are significant at: ***, $P < 0.001$; **, $0.001 < P < 0.01$; *, $0.05 < P < 0.1$

	Estimate	s.e.	z-value	Pr(> z)
(Intercept)	2.91	0.293	9.93	9.92×10^{-9} ***
<i>P. astreoides</i>	1.06	0.256	4.15	6.06×10^{-4} ***
<i>S. siderea</i>	0.248	0.328	0.756	0.460
Noon	0.566	0.230	2.46	0.0244 *