

Diversity and abundance of sulfate-reducing microorganisms in a Mediterranean lagoonal complex (Amvrakikos Gulf, Ionian Sea) derived from *dsrB* gene

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Supplement 1

Table S1: The results of the processing of the sequences during the noise removal. M: Mazoma lagoon, L: Logarou lagoon, S: Tsopeli lagoon, T: Tsoukalio lagoon, R: Rodia lagoon. 01: Station inside the lagoons. 02: Station in the channel connecting each lagoon to the gulf. A, B, C: replicate samples. a: number of raw sequences. b: number of sequences after the first filtering. c: number of sequences after the removal of sequencing errors. d: number of clustered sequences after the removal of the PCR errors. e: number of chimeras. f: number of clustered sequences after the removal of chimeras (high quality sequences). Sequencing of the sample M_01_A was considered to be faulty, resulting in a high number of errors, thus this sample was not included in the further analyses.

A/A	Sample libraries	a	b	c	d	e	f
1	M_01_B	6,622	4,802	4,363	998	9	989
2	M_01_C	5,798	3,960	3,633	1,005	7	998
3	M_02_A	1,752	1,229	1,020	391	0	391
4	M_02_B	3,617	2,476	2,222	667	4	663
5	M_02_C	8,104	5,264	4,104	914	2	912
6	L_01_A	13,913	6,698	5,689	1,082	217	865
7	L_01_B	5,411	3,120	2,439	850	131	719
8	L_01_C	3,602	2,533	2,242	749	1	748
9	L_02_A	5,191	3,568	3,142	858	1	857
10	L_02_B	4,559	3,083	2,891	967	1	966
11	L_02_C	6,504	4,755	4,179	1,152	3	1,149
12	S_01_A	5,763	4,248	3,012	520	7	513
13	S_01_B	4,057	2,738	2,083	513	5	508
14	S_01_C	1,502	1,067	883	246	1	245
15	S_02_A	6,959	4,546	3,447	995	1	994
16	S_02_B	1,079	691	596	241	1	240
17	S_02_C	3,881	2,868	2,636	846	9	837
18	R_01_A	5,470	3,939	3,442	950	234	716
19	R_01_B	3,311	2,133	1,934	475	1	474
20	R_01_C	2,378	1,794	1,400	339	1	338
21	R_02_A	7,540	5,831	3,276	522	4	518
22	R_02_B	5,802	4,488	3,226	560	2	558
23	R_02_C	9,134	6,747	4,350	676	7	669
24	T_01_A	5,064	3,299	2,896	705	2	703
25	T_01_B	1,310	910	761	260	0	260
26	T_01_C	8,200	5,965	3,641	655	7	648
27	T_02_A	3,112	2,121	1,402	388	1	387
28	T_02_B	5,501	4,171	3,089	465	3	462
29	T_02_C	3,490	2,368	1,597	329	1	328
Sum		148,626	101,412	79,595	19,318	663	18,655

Table S2: The classification of the OTUs from the present study based on the results of EPA and their comparison with those of Pelikan et al. (2016) (provided as an .xls file).

See Supplement 2 at www.int-res.com/articles/suppl/a079p209_supp2.xls

Table S3: Diversity indices of the samples, based on the 90% similarity cut-off. OTUs: total number of OTUs. N: total SRM relative abundance values. d: Margalef's species richness. J': Pielou's evenness. H': Shannon-Wiener. ACE: Abundance Coverage Estimator. M: Mazoma lagoon, L: Logarou lagoon, S: Tsopeli lagoon, T: Tsoukalio lagoon, R: Rodia lagoon. 01: Station inside the lagoons. 02: Station in the channel connecting each lagoon to the gulf. A, B, C: replicate samples.

	OTUs	N	d	J'	H'(log ₂)	Chao-1	ACE
M_01_B	469	3,628	57.1	0.8391	7.446	666,1667	656,9447
M_01_C	418	2,585	53.07	0.8249	7.182	608,987	639,5986
M_02_A	257	1,100	36.56	0.8362	6.694	380,0167	436,1893
M_02_B	398	2,054	52.05	0.8535	7.372	617,4925	634,6642
M_02_C	449	4,266	53.6	0.7756	6.834	588,0822	586,8483
L_01_A	383	5,148	44.7	0.8636	7.411	446,8936	441,4868
L_01_B	387	2,434	49.5	0.8561	7.359	576,4068	565,9593
L_01_C	408	2,016	53.49	0.862	7.476	621,1304	612,1865
L_02_A	397	2,595	50.37	0.8149	7.035	611,7619	608,364
L_02_B	422	1,877	55.85	0.8375	7.304	775,9516	731,6545
L_02_C	475	3,461	58.16	0.7638	6.791	698,875	723,8786
S_01_A	311	3,589	37.87	0.7736	6.406	466,1163	463,5426
S_01_B	238	2,153	30.88	0.7323	5.782	325,6923	367,0418
S_01_C	149	926	21.67	0.8404	6.067	195,1613	214,0853
S_02_A	411	3,403	50.42	0.705	6.121	541,679	557,0556
S_02_B	160	619	24.74	0.7355	5.386	277	317,8009
S_02_C	382	1,986	50.17	0.797	6.836	692,082	705,5519
R_01_A	381	3,192	47.1	0.8076	6.924	739,6829	637,4184
R_01_B	239	1,709	31.97	0.8167	6.452	346,8	374,3831
R_01_C	224	1,702	29.97	0.7763	6.061	339,1765	336,6552
R_02_A	312	5,518	36.1	0.676	5.601	430,1458	438,677
R_02_B	300	4,196	35.84	0.7313	6.018	386,8421	410,2137
R_02_C	351	6,194	40.09	0.7025	5.94	488,3077	481,892
T_01_A	311	2,404	39.82	0.7926	6.564	462,25	458,5118
T_01_B	171	812	25.38	0.8046	5.968	317,25	320,797
T_01_C	366	5,426	42.45	0.6938	5.908	491,5091	490,3717
T_02_A	223	1,943	29.32	0.7609	5.935	338,1613	311,9816
T_02_B	292	3,948	35.14	0.7944	6.506	410,825	410,6931
T_02_C	226	2,204	29.23	0.7205	5.634	313,1277	356,1822

Table S4: The Chi-Square values of the Kruskal-Wallis tests for the diversity indices between the salinity categories and the lagoons. OTUs: total number of OTUs. N: total SRM relative abundance values. d: Margalef's species richness. J': Pielou's evenness. H': Shannon-Wiener. ACE: Abundance Coverage Estimator. *: p < 0.05. **: p < 0.01. n.s.: not significant.

	OTUs	N	d	J'	H'(log ₂)	Chao-1	ACE
Salinity categories	9.099 *	n.s.	9.814 **	6.423 *	8.363 *	7.351 *	8.630 *
Lagoon	14.697 **	n.s.	15.326 **	11.913 *	17.694 **	10.128 *	11.103 *

Table S5: The values of the Mann-Whitney U tests used for the *post-hoc* pairwise significant comparisons, after the Bonferroni correction. OTUs: total number of OTUs. N: total SRM relative abundance values. d: Margalef's species richness. J': Pielou's evenness. H': Shannon-Wiener. ACE: Abundance Coverage Estimator. *: $p < 0.17$ in the case of the salinity categories. *: $p < 0.01$ in the case of the lagoons. n.s.: not significant.

		OTUs	N	d	J'	H'(log₂)	Chao-1	ACE
Salinity categories	(Mixo-) a-mesohaline vs (Mixo-) b-mesohaline	n.s.	n.s.	n.s.	n.s.	37.000 *	n.s.	n.s.
	(Mixo-) a-mesohaline vs (Mixo-) polyhaline	0 *	n.s.	0 *	n.s.	1 *	n.s.	1 *
Lagoons	Mazoma vs Tsoukalio	n.s.	n.s.	n.s.	n.s.	0 *	n.s.	n.s.
	Tsopeli vs Logarou	n.s.	n.s.	n.s.	n.s.	1 *	n.s.	n.s.
	Rodia vs Logarou	0 *	n.s.	1 *	n.s.	1 *	n.s.	n.s.
	Tsoukalio vs Logarou	0 *	n.s.	0 *	n.s.	0 *	2 *	2 *

Table S6: The values of the Mann-Whitney U tests for the diversity indices between the locations. OTUs: total number of OTUs. N: total SRM relative abundance values. d: Margalef's species richness. J': Pielou's evenness. H': Shannon-Wiener. ACE: Abundance Coverage Estimator. *: $p < 0.05$. n.s.: not significant.

	OTUs	N	d	J'	H'(log₂)	Chao-1	ACE
Location	n.s.	n.s.	n.s.	59.000 *	n.s.	n.s.	n.s.

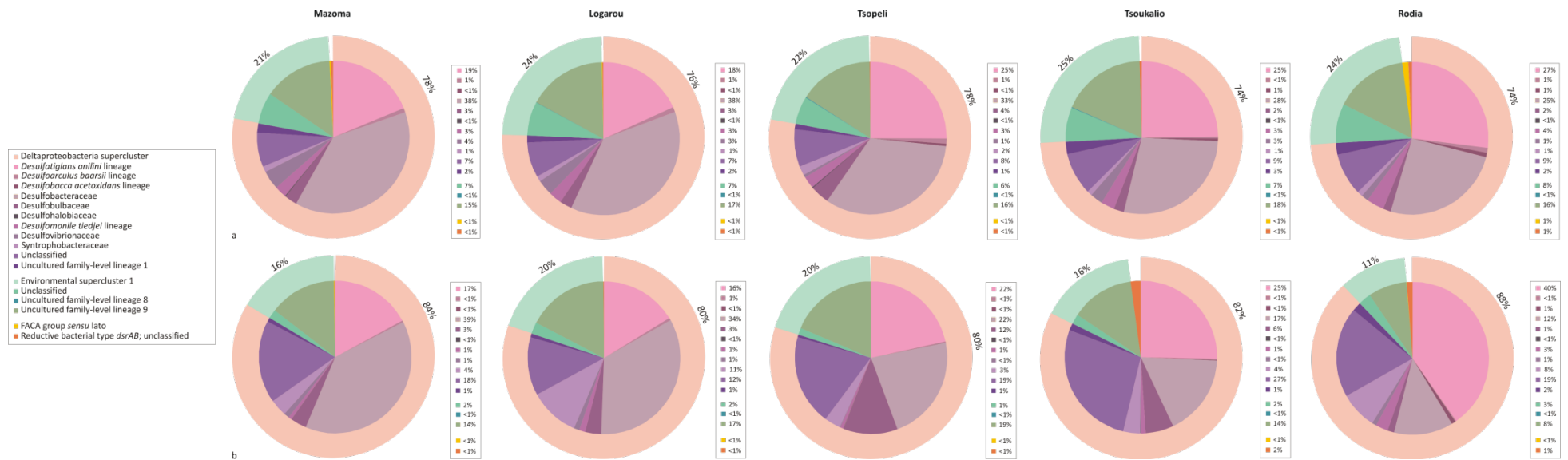


Figure S1: Taxonomic classification of the SRM OTUs of the different lagoons: a) based on the presence/absence of OTUs, b) based on the abundance of OTUs.

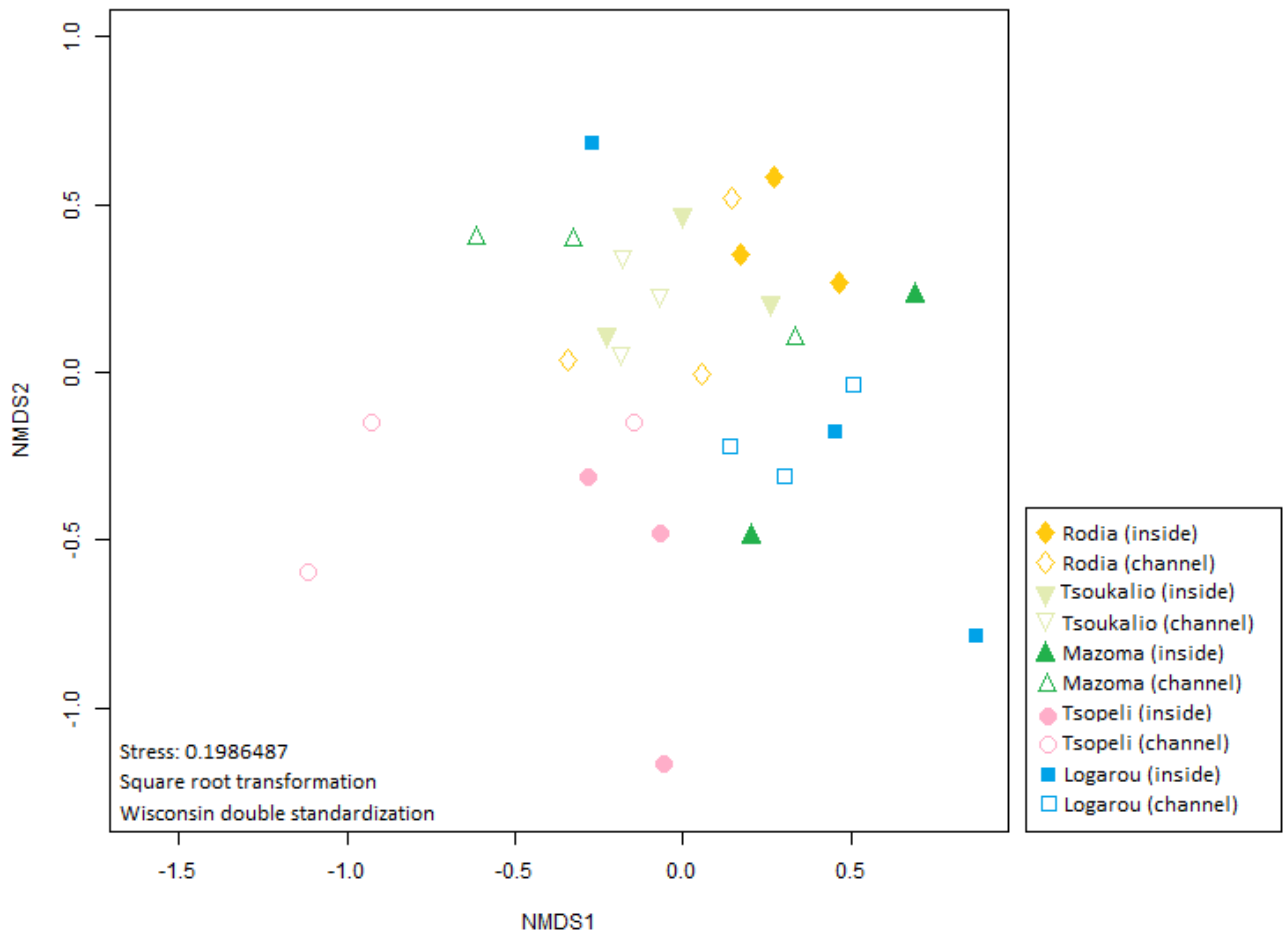


Figure S2: Multidimensional scaling of the SRM OTUs (90% similarity cut-off), based on the abundance of the environmental terms that they have been associated with. Data labels according to the location of the sampling station, as in Figure 4.