

## Impacts of a reduction in seawater pH mimicking ocean acidification on the structure and diversity of mycoplankton communities

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**Table S1: Average pH values ( $\pm$  SD) in the microcosm at the four different incubation times.** The experiment included forty microcosms that differed only in their starter pH (8.26 or 7.67). Each week, five independent microcosms per starter pH type were harvested and the pH value was measured.

<b>Week</b>	<b>pH 8.26</b>	<b>pH 7.67</b>
1	8.21 $\pm$ 0.01	7.65 $\pm$ 0.02
2	8.18 $\pm$ 0.01	7.62 $\pm$ 0.01
3	8.16 $\pm$ 0.04	7.61 $\pm$ 0.02
4	8.14 $\pm$ 0.01	7.58 $\pm$ 0.01

**Table S2: Statistics of the downstream analysis process.** Sequence read number affected by the different steps. After quality control, ITS2 and 18S rDNA sequences were further analyzed with different approaches: ITS2 sequences were subjected to hierarchical clustering analyses while 18S rDNA sequences were further analyzed by a phylogenetic-based approach (no OTU forming).

<b>Downstream analysis step</b>	<b>ITS2</b>	<b>18S rDNA</b>
Total number of sequence reads	237,967	532,304
Sequences passing quality control	171,872	404,281
Final number of fungal sequences	116,056	126,051*
Fungal OTUs	387	

\*co-amplification of 18S rDNA primers mainly with the groups of Telonema, Alveolata and Stramenopiles

**Table S3: Fungal community composition of the positive control using the ITS2 as marker gene.**

<b>Phylum</b>	<b>Class</b>	<b>Rel. Abundances (%)</b>
Fungi (ambiguous)		2
Basidiomycota	Agaricomycetes	2
Ascomycota	Ambiguous	63
	Saccharomycetes	27
	Leotiomycetes	2
	Dothideomycetes	4

**Table S4: Fungal community composition of the positive control using 18S rDNA as marker gene.**

<b>Phylum</b>	<b>Class</b>	<b>Rel. Abundances (%)</b>
Cryptomycota		7
Basidiomycota	Microbotryomycetes	1
Ascomycota	Incertae Sedis	10
	Sordariomycetes	1
	Leotiomycetes	42
	Geoglossomycetes	1
	Eurotiomycetes	33
	Dothideomycetes	4

**Table S5: Diversity indices calculated for the different pH sample types and incubation times.** Sea water was filled in 1.6 l glass jars and incubated either at current *in situ* seawater pH (8.26) or adjusted to pH of 7.67. For each pH treatment, 20 replicates were set up. Every week, five independent microcosms for each pH type were harvested.

<b>Week</b>	<b>pH</b>	<b>Shannon Index</b>	<b>Simpson Index</b>	<b>Richness</b>
1	7.67	2.45	0.76	118
1	7.67	2.39	0.76	131
1	7.67	2.23	0.73	110
1	7.67	2.34	0.75	137
1	7.67	2.45	0.79	159
2	7.67	2.20	0.70	68
2	7.67	1.59	0.52	63
2	7.67	1.78	0.60	42
2	7.67	2.22	0.69	102
2	7.67	2.23	0.70	98
3	7.67	2.14	0.66	107
3	7.67	2.44	0.78	118
3	7.67	2.15	0.66	122
3	7.67	2.24	0.71	104
3	7.67	2.32	0.70	124
4	7.67	2.12	0.68	73
4	7.67	2.33	0.73	109
4	7.67	1.71	0.57	37
4	7.67	2.10	0.64	81
4	7.67	1.95	0.60	84
1	8.26	2.78	0.86	53
1	8.26	2.57	0.83	57
1	8.26	2.22	0.77	24
1	8.26	2.10	0.71	33
2	8.26	2.53	0.89	20
2	8.26	2.24	0.78	39
2	8.26	2.44	0.77	45
2	8.26	2.13	0.78	54
2	8.26	1.97	0.77	25
3	8.26	1.74	0.83	7
3	8.26	1.70	0.65	15
3	8.26	1.81	0.72	25
3	8.26	1.78	0.73	33
3	8.26	1.81	0.73	13
4	8.26	1.83	0.72	14
4	8.26	1.57	0.61	25
4	8.26	1.92	0.74	20
4	8.26	1.54	0.61	13
4	8.26	1.45	0.70	8