Supplementary Data

Rapid establishment of the non-indigenous ascidian Styela plicata and its associated bacteria in marinas and fishing harbors along the Mediterranean coast of Israel

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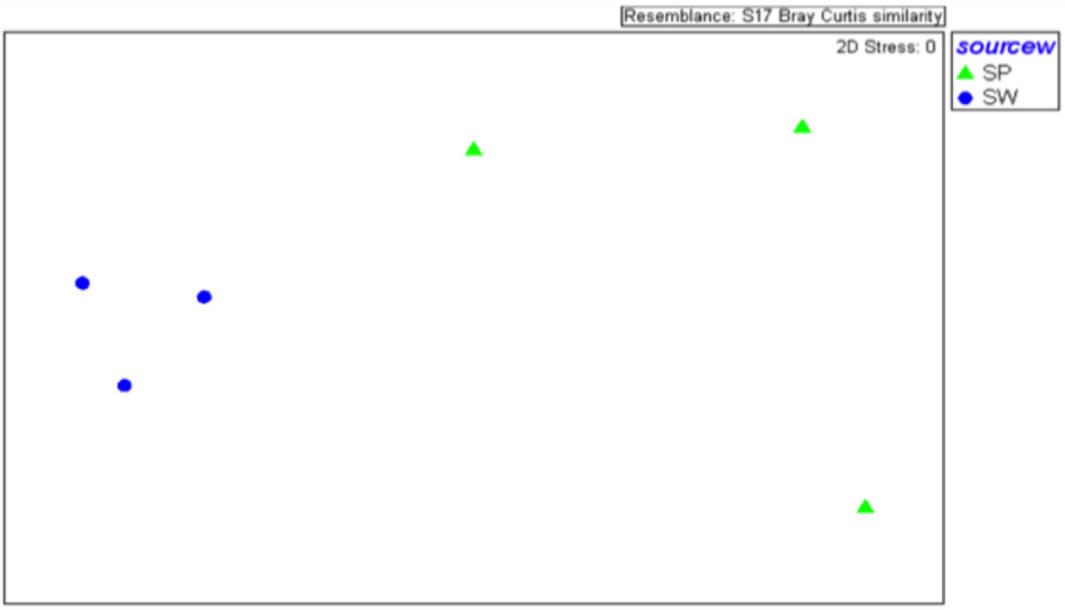

Fig. S1: Multidimensional scaling (MDS) plot for the microbial community of *S. plicata* (SP) and seawater (SW).

Table S1. Taxonomic composition and relative abundance (%) of three *S. plicata* individuals (SP) and three seawater samples (SW), based on a 97% cut-off sequence similarity to known OTUs and compared to *S. plicata* from Spain (shown only phyla present in all three samples) (Erwin *et al.,* 2013).

Bacterial phyla	SP1	SP2	SP3	SP Avg.	SW1	SW2	SW3	SW Avg.	Spain
Acidobacteria	0	0.055	1.691	0.582	0.640	0.901	0.553	0.698	
Actinobacteria	0.205	0	0.245	0.150	0.585	0.411	0.490	0.495	< 8
Bacteroidetes	3.500	1.564	12.658	5.908	31.542	35.248	32.759	33.183	19.5–32.7
Chloroflexi	0	0	0.032	0.011	0.016	0.008	0.008	0.011	< 8
Cyanobacteria	0.047	0.032	0.435	0.171	1.335	1.075	1.493	1.301	< 8
Fibrobacteres	0	0	0.008	0.003	0	0	0	0.000	
Firmicutes	0.119	0.190	2.062	0.790	0.111	0.150	0.158	0.140	< 8
Nitrospirae	0.032	0	0.016	0.016	0.008	0	0	0.003	
OP3	0	0	0.032	0.011	0	0	0	0.000	
Planctomycetes	0.229	0.111	1.114	0.485	0.419	0.205	0.292	0.306	9.8–12.8
Proteobacteria	92.723	8.1461	53.650	51.507	60.596	56.740	59.355	58.897	25.4–50.0
SAR406	0	0	0	0.000	0	0.016	0	0.005	
Thermi	0	0.008	0.032	0.013	0.300	0.316	0.593	0.403	
Verrucomicrobia	0.111	0.047	0.403	0.187	0.063	0.032	0.079	0.058	
WS3	0	0	0.008	0.003	0	0	0	0.000	
unclassified	3.034	89.847	27.615	40.165	4.385	4.899	4.219	4.501	

Table S2. BLASTn matches of top OTUs in *S. plicata* samples (SP) versus seawater samples (SW).

OTU	READS						Phylum	Lowest taxonomic rank	Top BLAST match (% Identity, accession number)	Ref.
	SP1	SP2	SP3	SW1	SW2	SW3				
0001	244	11284	280	2	1	2	*Chloroflexi*	Uncultured *Chloroflexi*	Sponge associated (88%, EF076231)	Taylor 2007
0003	10233	78	2	0	0	0	Unclassified	Uncultured environmental samples	Seawater (100%, JQ198505)	Bik 2011 unpublished
0006	41	33	703	331	245	321	*Proteobacteria* (α)	Family *Rhodobacteraceae*	[1]Salt marsh plant (100%, KT324750)	Fidalgo 2016
0009	8	9	1971	1	0	2	Unclassified	Uncultured environmental samples	Seawater (89%, FR875936)	Grünke 2012
0013	46	47	501	24	8	9	*Proteobacteria* (α)	Family *Pelagibacteraceae*	Seawater (100%, KX588323)	Bandekar 2016
0017	203	67	483	1	0	0	*Bacteroidetes*	Family *Saprospiraceae*	Seawater (100%, KT764025)	Zhao 2015 unpublished
0022	18	77	409	0	2	0	*Proteobacteria* (γ)	Uncultured environmental samples	Seawater (100%, KR077407)	Liu 2015 unpublished
0033	161	199	1	0	1	0	*Proteobacteria* (γ)	[2]uncultured SAR86 (pipeline: *Chromatium okenii*)	Seawater (100%, KX371459)	Mayali 2016 unpublished
0034	8	3	298	1	0	2	*Proteobacteria* (γ)	*Vibrio* sp.	[1]Salt marsh plant (100%, KT325172)	Fidalgo 2016
0057	230	89	0	0	0	0	*Proteobacteria* (α)	Family *Rhodobacteraceae*	[3]Sponge associated (100%, EU919124)	Wang 2008 unpublished

[1]Influence of metal(loid) contamination
[2] Purple sulfur bacteria; stagnant water
[3] Invasive sponge