

The following supplement accompanies the article

Prokaryotic and diazotrophic population dynamics within a large oligotrophic inverse estuary

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Supplementary Figures

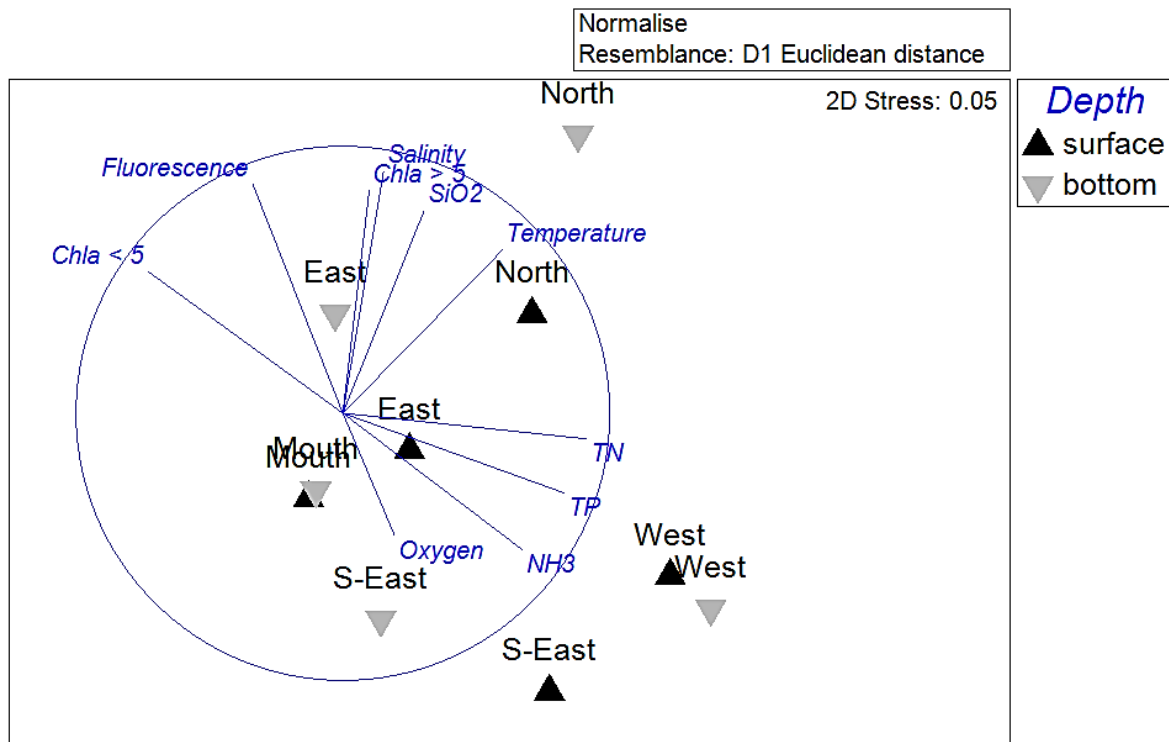


Figure S1. Non-metric multidimensional scaling showing normalised measured biotic and abiotic variables, overlaid with Pearson correlations of the environmental parameters, at five sampling locations within Spencer Gulf. TN = total nitrogen, TP = total phosphorous, Chla > 5 = Chlorophyll α > 5 μm fraction, Chla < 5 = Chlorophyll α < 5 μm fraction.

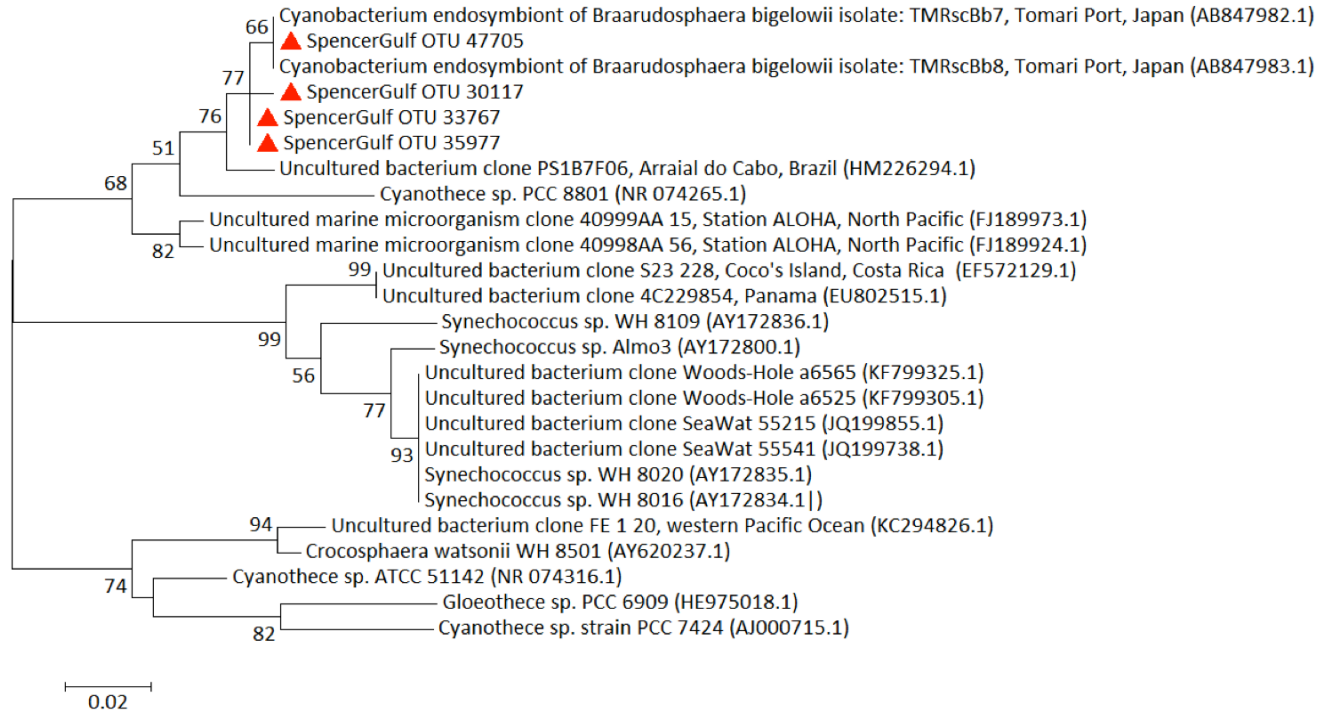


Figure S2. Maximum likelihood phylogenetic tree (including the Jukes-Cantor correction) of UCYN-A 16S rRNA gene sequences recovered during this study (red triangles) and other representative unicellular cyanobacteria. Bootstraps over 50 % for 1000 permutations, and a scale bar of 0.02 base pair substitutions, are shown.

Table S1. Marginal test results from distance based linear modelling (distLM) of bacterioplankton taxonomic (16S rRNA gene) and diazotroph (nifH gene) composition in relation to available predictor variables. Variables in bold displayed significant ($p < 0.05$) explanatory power and were subsequently used in distance based redundancy analysis (dbRDA).

	16S rRNA assemblage		NifH assemblage	
	Pseudo-F	P	Pseudo-F	P
Temperature	1.7171	0.028	1.6482	0.035
Salinity	1.6069	0.036	1.9789	0.004
Fluorescence	1.5634	0.055	1.0184	0.425
Oxygen	1.3236	0.131	1.1327	0.21
Total Nitrogen (TN)	2.0117	0.006	1.0921	0.315
Total Phosphorous (TP)	2.3434	0.008	0.9816	0.502
Ammonia (NH ₃)	1.2614	0.208	0.8899	0.562
Silicate (SiO ₂)	1.2476	0.147	1.5123	0.049
Chlorophyll $\alpha > 5 \mu\text{m}$ fraction (Chla > 5)	1.2265	0.171	1.3824	0.052
Chlorophyll $\alpha < 5 \mu\text{m}$ fraction (Chla < 5)	1.8272	0.01	0.9860	0.463

Table S2. Samples collected as part of Australia's Ocean Microbiome Project, totalling 101 samples that were collected from surface and chlorophyll maximum depths (determined via fluorescence depth profiles) from the Kimberley region in north-western Australia (2010), the East Australian Current (EAC, 2010) and the Tasman Sea including the Port Hacking and Maria Island (2009-2011) National Reference Stations, (Seymour, Brown et al. Unpublished data) and this study, containing UCYN-A 16S sequences identified as Bacteria; __Cyanobacteria; __Cyanobacteria; __SubsectionI; __FamilyI; __marine_group in the Silva database, and clustered with UCYN-A 16S sequences in arb. The abundance of the 4 UCYN-A OTUs are represented as raw sequence hits. Only samples with UCYN-A 16S hits are shown.

OTU ID	EAC	Mouth(S)	North(B)	North(S)	East(B)	East(S)	S-East(B)	S-East(S)
30117	0	0	0	1	0	0	0	0
33767	0	0	2	1	1	0	0	0
35977	0	0	9	1	1	0	0	1
47705	2	2	38	44	19	6	4	1
Total	2	2	49	47	21	6	4	2