

Station		T (°C)	pH _T	pCO ₂ μatm	CO ₂ μmol kg ⁻¹	HCO ₃ ⁻ μmol kg ⁻¹	CO ₃ ²⁻ μmol kg ⁻¹	Ω _{calc}	Ω _{arag}
Ambient	Mean	30.37	8.009	412	10	1629	214	5.25	3.52
	SD	0.12	0.035	43	1	33	13	0.32	0.22
	Min	29.84	7.917	347	9	1575	181	4.44	2.97
	Max	30.93	8.066	532	13	1712	235	5.78	3.87
High St 1	Mean	30.35	7.782	781	20	1809	141	3.47	2.32
	SD	0.08	0.069	151	4	46	19	0.45	0.30
	Min	30.24	7.586	584	14	1721	95	2.33	1.56
	Max	30.51	7.906	1280	32	1924	177	4.34	2.90
High St 2	Mean	30.35	7.766	834	21	1832	132	3.25	2.17
	SD	0.09	0.075	169	4	48	19	0.47	0.32
	Min	30.18	7.569	529	13	1711	92	2.26	1.51
	Max	30.51	7.919	1337	33	1932	181	4.44	2.97
High St 3	Mean	30.36	7.731	725	18	1797	146	3.59	2.40
	SD	0.08	0.070	164	4	43	17	0.43	0.29
	Min	30.05	7.560	595	15	1744	89	2.19	1.46
	Max	30.52	7.877	1369	34	1938	167	4.11	2.75
High St 4	Mean	30.25	7.783	777	19	1809	141	3.47	2.32
	SD	0.06	0.066	142	3	44	17	0.43	0.29
	Min	30.13	7.588	513	13	1702	95	2.35	1.57
	Max	30.45	7.930	1276	32	1923	184	4.53	3.03

Supplementary Table 1. Seawater temperature and pH_T measured in 2018. Carbonate chemistry parameters were calculated with CO₂sys using the temperature, pH_T data collected by the SeaFETs at 10-min logging interval (n is in brackets), the mean total alkalinity (A_T = 2158.5 and 2182.6 μmol kg⁻¹, for Ambient and High CO₂ stations respectively; n = 28 and 95, respectively), and salinity (34) (see Pichler et al., (2019) for details of the methods).

Feeding experiment				
	C (ng C cell⁻¹)	Reference	C assimilation (ng C cm⁻² h⁻¹)	
			Ambient CO₂ site	High CO₂ site
<i>Pocillopora damicornis</i>				
<i>Prochlorococcus</i> sp.	3.6 10 ⁻⁵ (a)	Buitenhuis <i>et al.</i> , 2012	0.000	0.015 ± 0.033
<i>Synechococcus</i> sp.	2.5 10 ⁻⁴ (a)	Buitenhuis <i>et al.</i> , 2012	10.212 ± 6.753	29.299 ± 17.902
picoeukaryotes	2.6 10 ⁻³ (a)	Buitenhuis <i>et al.</i> , 2012	6.038 ± 2.152	6.851 ± 0.153
	N (ng N cell⁻¹)	Reference	N assimilation (ng C cm⁻² h⁻¹)	
			Ambient CO₂ site	High CO₂ site
<i>Pocillopora damicornis</i>				
<i>Prochlorococcus</i> sp.	9.6 ± 0.9 10 ⁻⁶ (b)	Bertilsson <i>et al.</i> , 2003	0.000	0.002 ± 0.005
<i>Synechococcus</i> sp.	3.79 10 ⁻⁵ (c)	Redfield (1958)	1.547 ± 1.023	4.439 ± 2.712
picoeukaryotes	3.94 10 ⁻⁴ (c)	Redfield 1958; Mulholland 2007	0.914 ± 0.326	0.010 ± 0.023
Endosymbiotic diazotroph activity experiment				
			DDN assimilation (ng N cm⁻² h⁻¹)	
			Ambient CO₂ site	High CO₂ site
<i>Pocillopora damicornis</i>				
Tissue: Symbiodiniaceae			0.032 ± 0.023	0.140 ± 0.116
Total N (ng N cm⁻² h⁻¹)			Ambient CO₂ site	High CO₂ site
<i>Pocillopora damicornis</i>			2.495	5.620

(a) Average, direct, from cultures

(b) In axenic cultures (*Prochlorococcus* MED4) in P-limited conditions (mean ± SD)

(c) According to the Redfield ratio

Supplementary Table 2: Carbon and nitrogen cell content (ng cell⁻¹) and related assimilation rates (µg cm⁻² h⁻¹) calculated for *Prochlorococcus*, *Synechococcus* and picoeukaryotes using literature conversion factors and the results of the present study (mean ± SE)

DDN assimilation rates	diff	adj. <i>p</i> -value
Ambient CO₂ site		
Symbiodiniaceae: Tissue	< 0.001	0.982
High CO₂ site		
Symbiodiniaceae: Tissue	< 0.001	0.01
Symbiodiniaceae		
High CO ₂ site: Ambient CO ₂ site	< 0.001	0.02
Tissue		
High CO ₂ site: Ambient CO ₂ site	- 0.000	1

Supplementary Table 4: Summary of statistical analyses of DDN assimilation rates performed with the two-way factorial ANOVA. Significant value (adj. *p*-value < 0.05) are indicated in bold