

Average Growth Rate (day ⁻¹) of Different <i>Prochlorococcus</i> Strains as a Function of Temperature								
HL or LL Clade Identification is Based on rDNA ITS Sequences [§]								
Temperature (°C)	MED4ax [†] HL(I)	MIT9515 [†] HL(I)	MIT9215 [†] HL(II)	MIT9312 [†] HL(II)	MIT9321 [‡] HL(II)	AS9601 [‡] HL(II)	NATL2A [‡] LL(I)	MIT9313 [‡] LL(IV)
11	0.09 ± 0.02	0.10 ± 0.03	–	–	–	–	–	–
13	0.20 ± 0.01	0.19 ± 0.01	–	–	–	–	0.00 ± 0.00	–
14	0.24 ± 0.04	0.21 ± 0.03	–	–	–	–	0.18 ± 0.01	–
15	0.23 ± 0.03	0.24 ± 0.02	0.00 ± 0.00	0.00 ± 0.00	–	–	–	–
17	0.30 ± 0.02	–	0.16 ± 0.03	0.28 ± 0.06	–	–	0.27 ± 0.01	–
18	0.30 ± 0.03	0.27 ± 0.03	0.17 ± 0.03	0.29 ± 0.06	–	0.00 ± 0.00	–	–
19	0.32 ± 0.07	0.33 ± 0.05	0.22 ± 0.02	0.32 ± 0.02	–	0.25 ± 0.02	0.31 ± 0.03	–
21	–	–	–	0.36 ± 0.12	–	0.30 ± 0.03	–	–
22	0.37 ± 0.02	–	0.36 ± 0.03	0.49 ± 0.01	–	–	0.43 ± 0.01	0.37 ± 0.05
23	0.40 ± 0.02	–	0.40 ± 0.02	0.54 ± 0.02	–	–	0.47 ± 0.02	0.39 ± 0.05
24	0.39 ± 0.02	0.46 ± 0.03	0.44 ± 0.02	0.58 ± 0.03	–	–	0.48 ± 0.01	0.43 ± 0.02
25	0.40 ± 0.01	0.47 ± 0.01	0.50 ± 0.01	0.62 ± 0.03	–	–	0.47 ± 0.03	0.44 ± 0.02
26	0.38 ± 0.01	0.43 ± 0.03	0.43 ± 0.01	0.58 ± 0.03	–	–	0.42 ± 0.02	0.45 ± 0.04
27	0.34 ± 0.02	–	0.47 ± 0.03	0.61 ± 0.01	–	–	0.36 ± 0.01	0.47 ± 0.04
28	0.00 ± 0.02	0.28 ± 0.04	0.43 ± 0.01	0.47 ± 0.08	0.47 ± 0.47	–	0.00 ±	0.38 ± 0.04
29	–	0.00 ±	0.43 ± 0.01	0.33 ± 0.04	0.44 ± 0.44	0.43 ± 0.02	–	0.00 ± 0.05
30	–	–	0.45 ± 0.01	0.00 ±	0.37 ± 0.37	0.42 ± 0.04	–	–
31	–	–	0.43 ± 0.01	–	–	0.39 ± 0.01	–	–
33	–	–	0.00 ±	–	0.00 ± 0.00	0.00 ±	–	–

0.40 ± 0.02 = Highest Observed Growth Rate

– No data available

Average growth rates (day⁻¹) of *Prochlorococcus* strains and associated clades at different temperatures. All replicate cell cultures were grown in a 14:10 light:dark cycle at 66 ± 1 μmol Q m⁻² s⁻¹. Data for MED4ax, MIT 91515, MIT9215, and MIT9312, denoted with [†], from Johnson et al. 2006; data for MIT9321, ASS9601, NATL2A, and MIT9313, denoted with [‡], from Zinser et al. 2007. *Prochlorococcus* clades are defined by the evolutionary relationships determined from the 16S-23S rDNA spacer, also called the internal transcribed spacer (ITS) sequence[§].

References

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