

Supplementary information for

Is the distribution of *Prochlorococcus* and *Synechococcus* ecotypes in the Mediterranean Sea affected by global warming?

Daniella Mella-Flores^{1,2†}, Sophie Mazard^{3†}, Florian Humily^{1,2}, Frédéric Partensky^{1,2}, Frédéric Mahé^{1,2}, Laëtitia Bariat⁴, Claude Courties⁴, Dominique Marie^{1,2}, Joséphine Ras⁵, Romain Mauriac⁶, Christian Jeanthon^{1,2}, El Mahdi Bendif^{1,2}, Martin Ostrowski³, David J. Scanlan³ and Laurence Garczarek^{1,2}

¹CNRS/INSU, Observatoire Océanologique de Roscoff, UMR 7144, Groupe Plancton Océanique, 29680 Roscoff, France; ²UPMC-Université Paris 06, Station Biologique, Place Georges Teissier, 29680 Roscoff, France; ³School of Life Sciences, University of Warwick, Coventry CV4 7AL, UK; ⁴CNRS/INSU and UPMC-Université Paris 06, Laboratoire Arago, UMS 2348, Observatoire Océanologique, 66651 Banyuls-sur-mer, France; ⁵CNRS/INSU and Université Paris 06, UMR 7093, Laboratoire d'Océanographie de Villefranche, 06234 Villefranche-sur-mer, France; ⁶Laboratoire d'océanographie physique et biogéochimique, Centre d'océanologie de Marseille, case 901, campus de Luminy, 13288 Marseille cedex 09, France

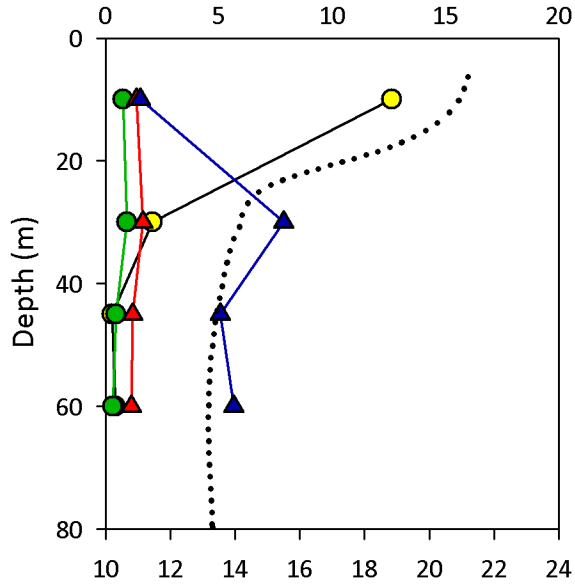
This file includes:

Figure S1 Depth profiles of the dominant *Prochlorococcus* and *Synechococcus* lineages at stations BOUSSOLE (left panels) and DYF (right panels) analyzed by dot blot hybridization using 16S rRNA gene ecotype-specific oligonucleotides probes. Percent relative hybridizations represent the signal of the ecotype-specific probe relative to the hybridization signal for the eubacterial probe EUB338, as a proportion of all products amplified by the OXY107F-OXY1313R primer pair. In the upper panels, *Prochlorococcus* ecotypes are indicated by colors as follows: HLI (high light type I or eMED4), yellow; HLII (high light type II or eMIT9312), green; LLI/LLIV (low light ecotypes I or eNATL and IV or eMIT9313), red and LLII (low light ecotype II or eSS120), blue. In the lower panels, *Synechococcus* lineages are indicated as follows: clade I, yellow; clade III, green; clade IV, red and clades V/VI/VII, blue. The dashed line represents temperature in °C.

Figure S2 Placement of environmental sequences from the BOUM cruise on a reference Maximum Likelihood tree (based on a full-length ITS sequence alignment) using Pplacer. The position of the different *Synechococcus* and *Prochlorococcus* sequences are indicated by additional branches of different colors, depending on the clade/ecotype to which they belong. For each clone library, the size of circles at the end of branches is proportional to the number of environmental sequences.

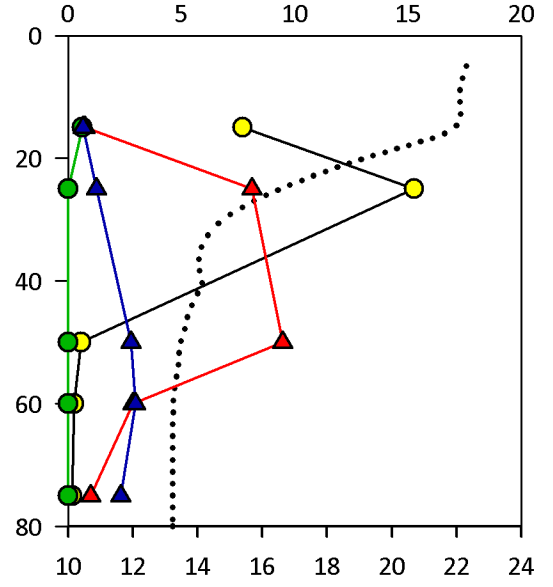
BOUSSOLE

% Relative Hybridization



DYF

% Relative Hybridization

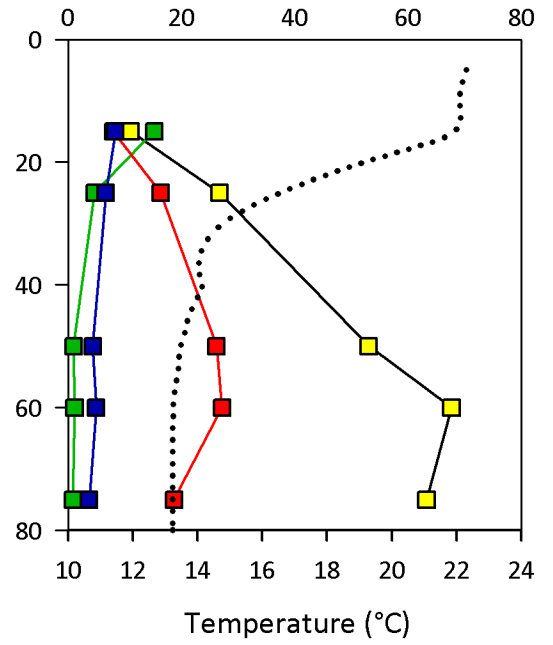
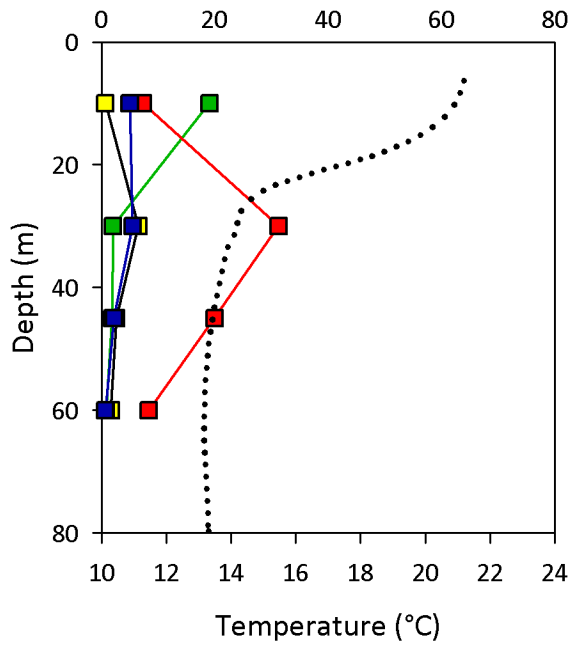


Prochlorococcus

- HLI
- HLII
- ▲— LLI/LLIV
- ▲— LLII
- Temperature

Synechococcus

- I
- III
- IV
- V/VI/VII
- Temperature



BOUSSOLE

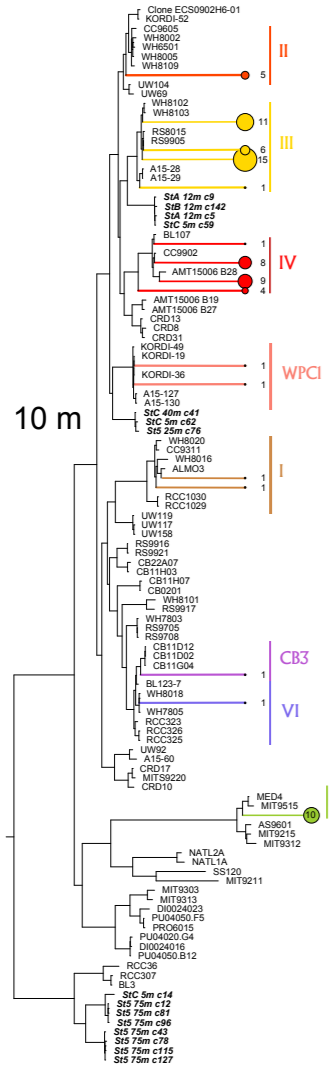
Sta. A

Sta. B

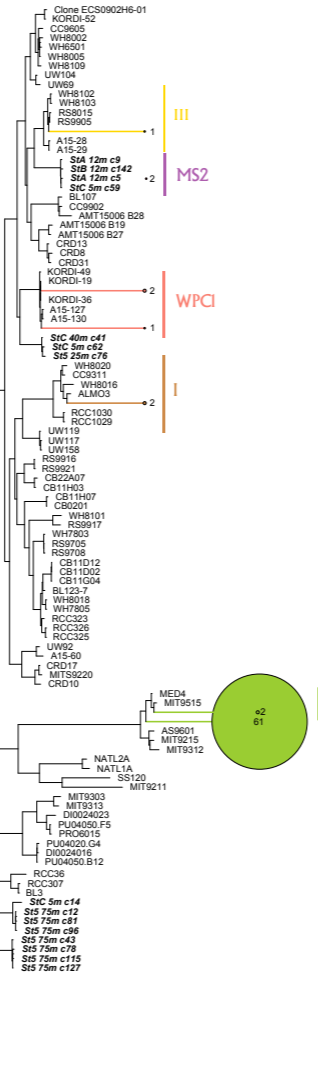
Sta. 5

Sta. C

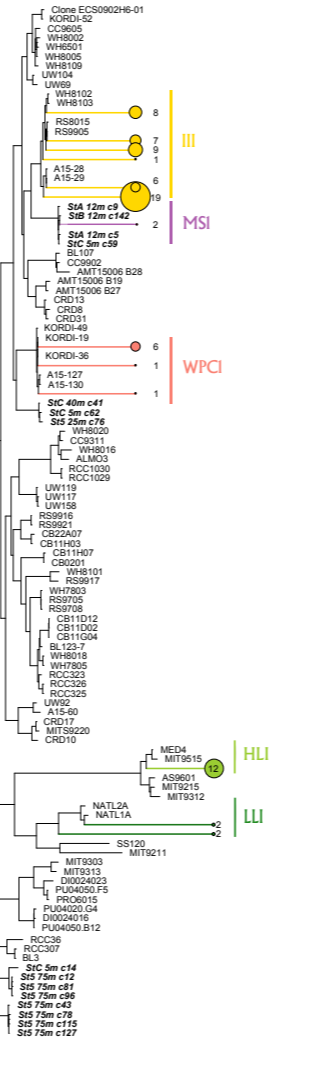
"SURFACE"



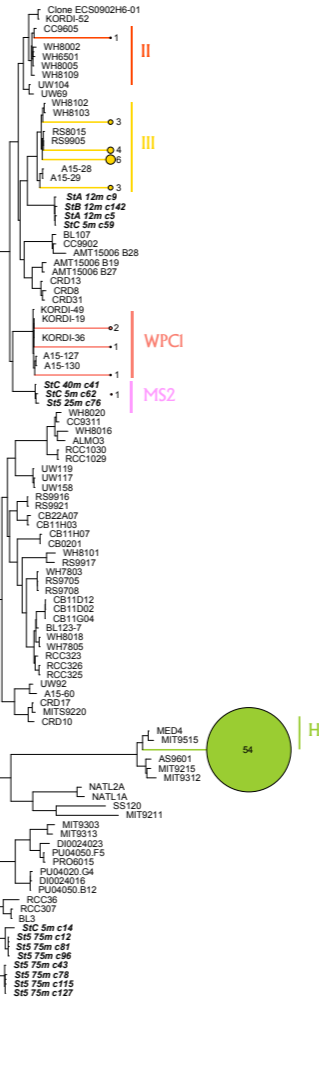
12 m



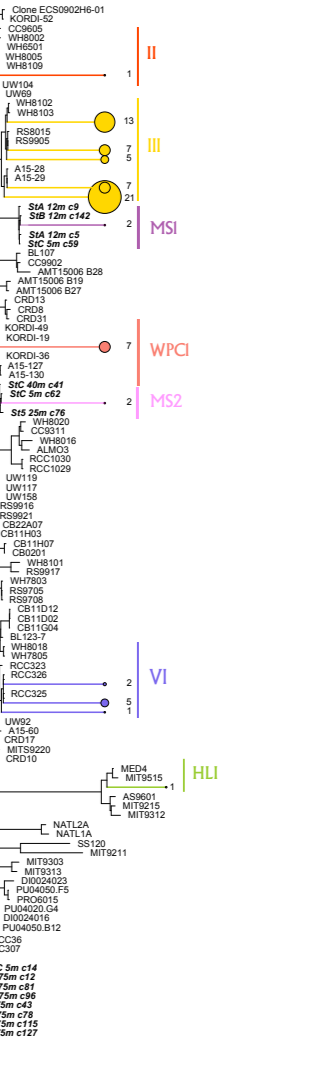
12 m



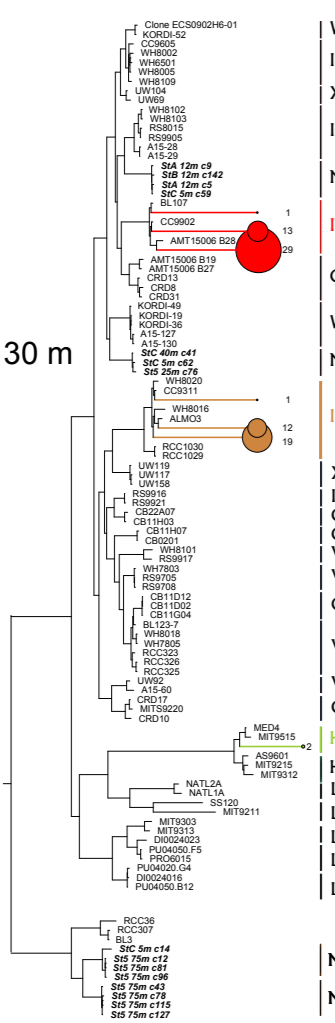
25 m



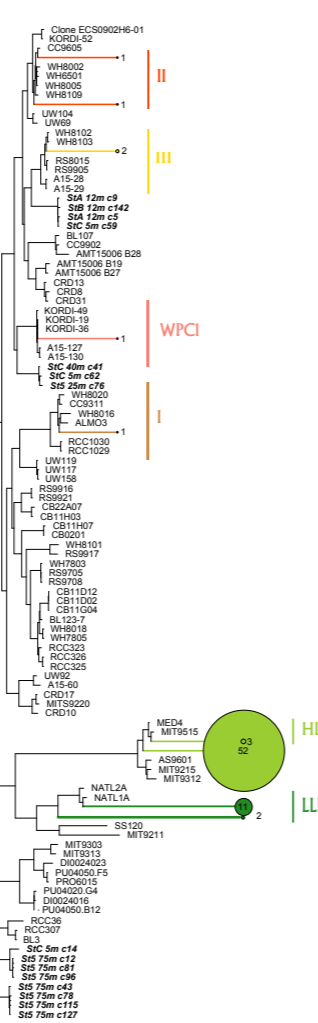
5 m



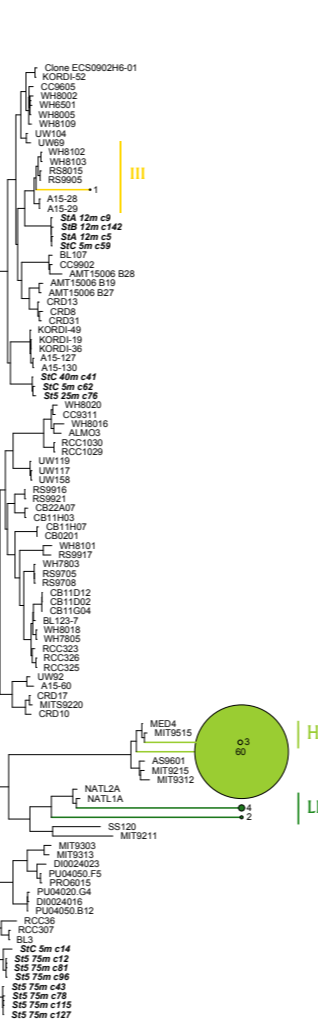
"MID-DEPTH"



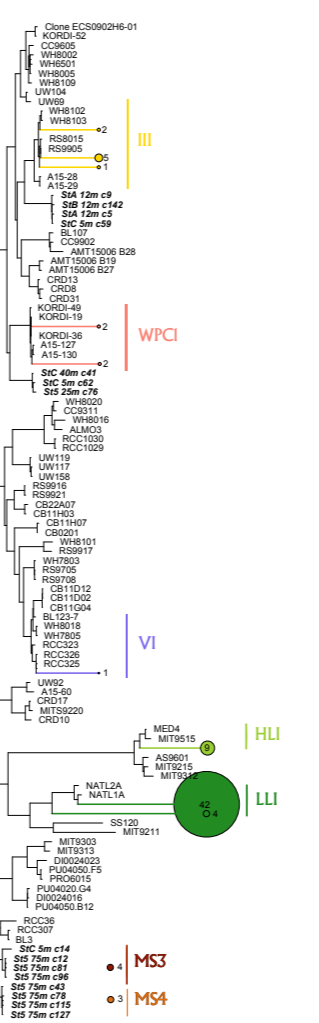
50 m



50 m



75 m



40 m



Subcluster 5.1A

Subcluster 5.1B

subcluster 5.3A

subcluster 5.3B

Prochlorococcus

MS3

MS4

MS3

MS4