

## Supplementary information for

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

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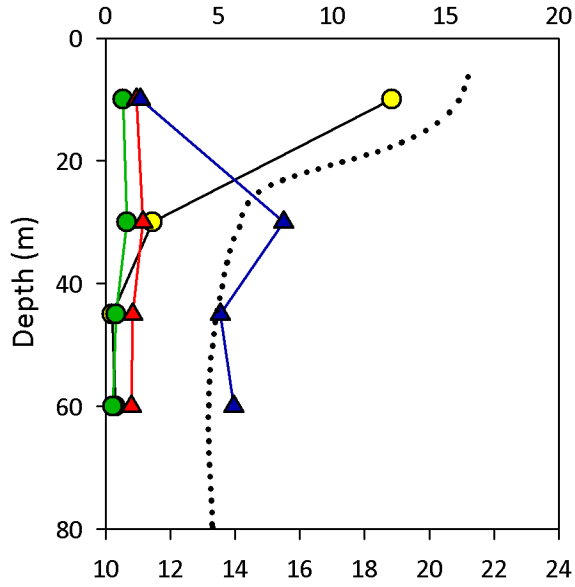
#### **This file includes:**

**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.

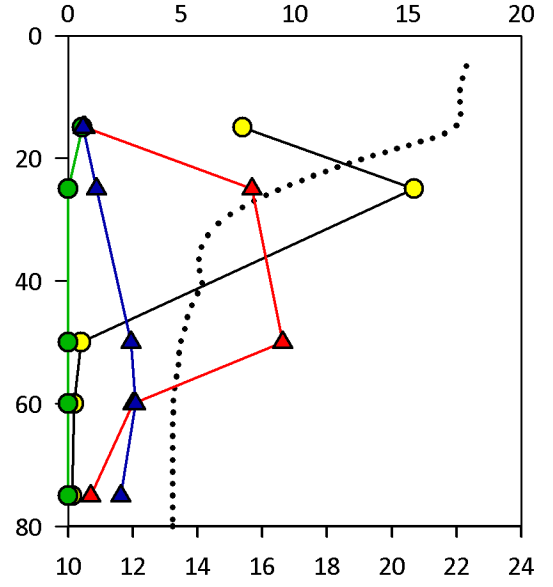
### BOUSSOLE

% Relative Hybridization



### DYF

% Relative Hybridization

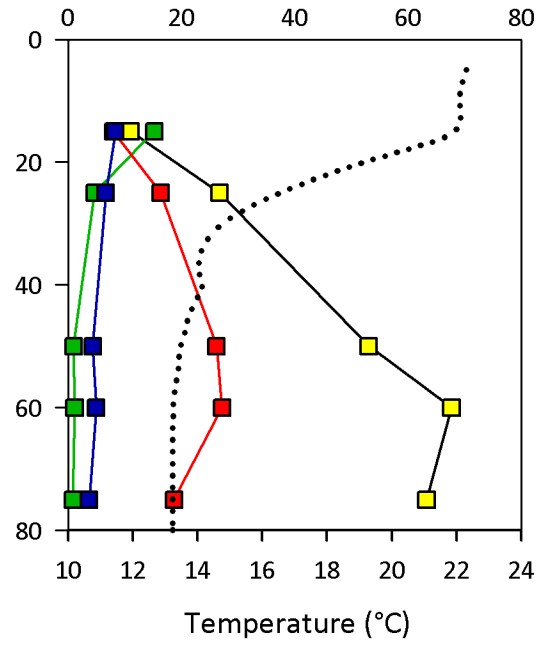
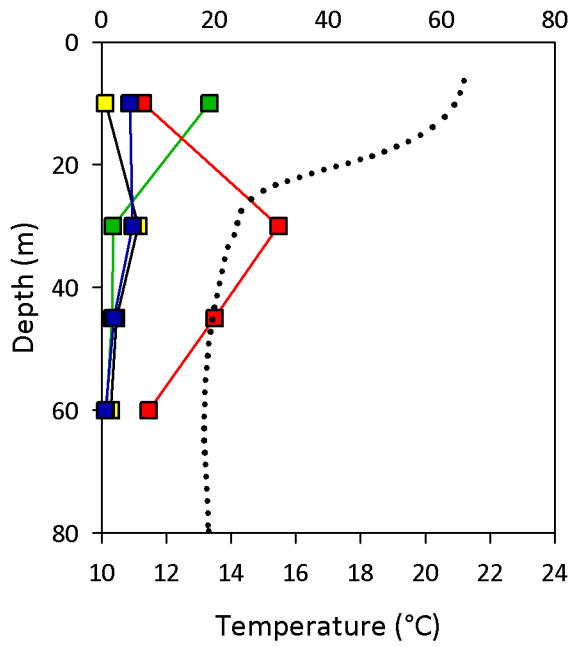


### *Prochlorococcus*

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

### *Synechococcus*

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



# BOUSSOLE

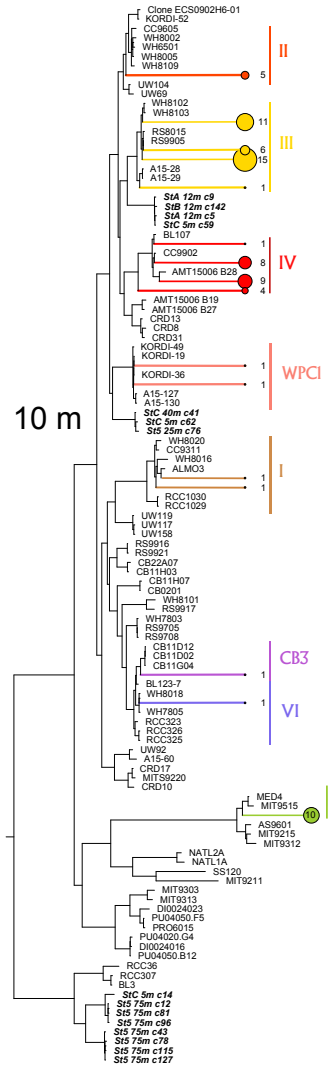
# Sta. A

# Sta. B

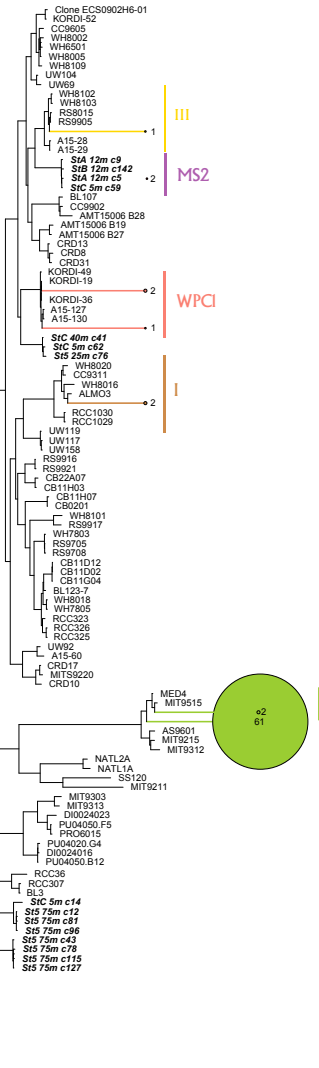
# Sta. 5

# Sta. C

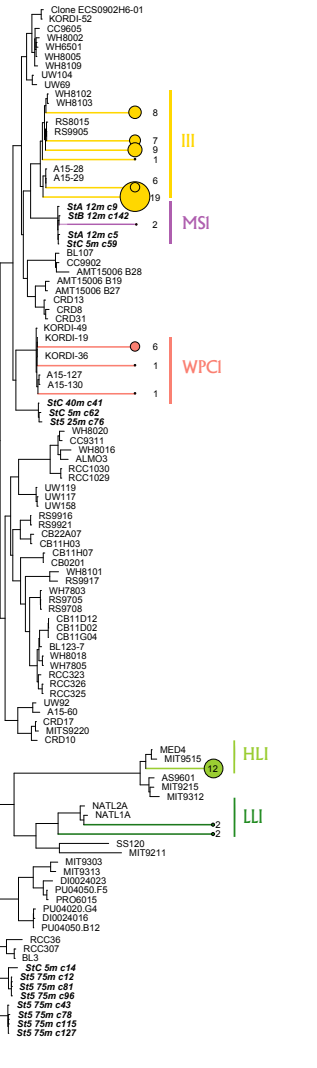
"SURFACE"



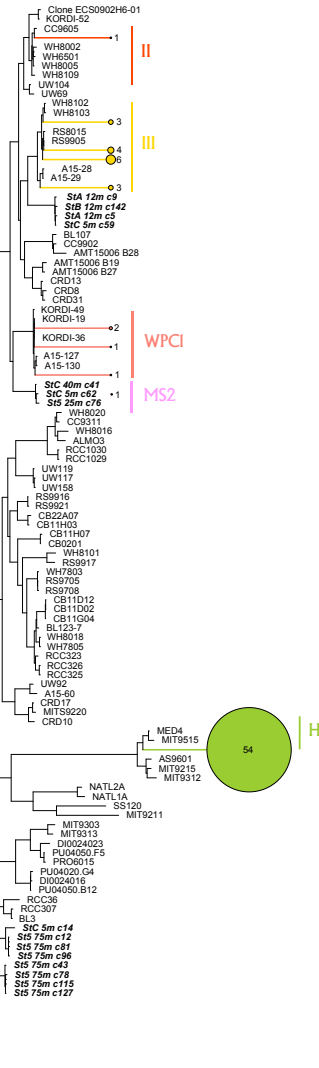
12 m



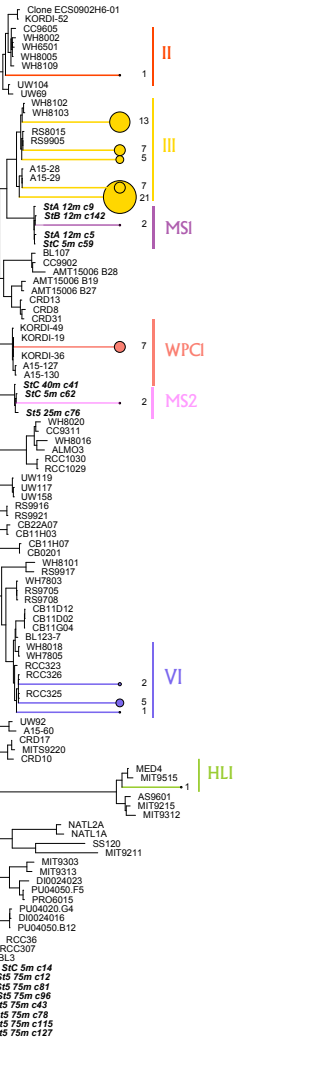
12 m



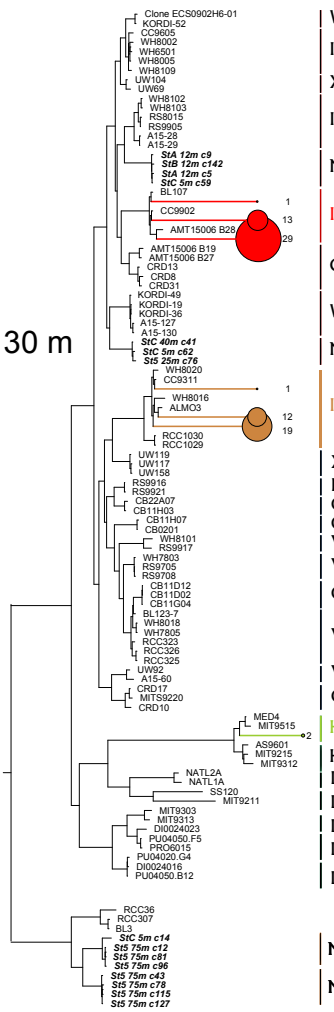
25 m



5 m



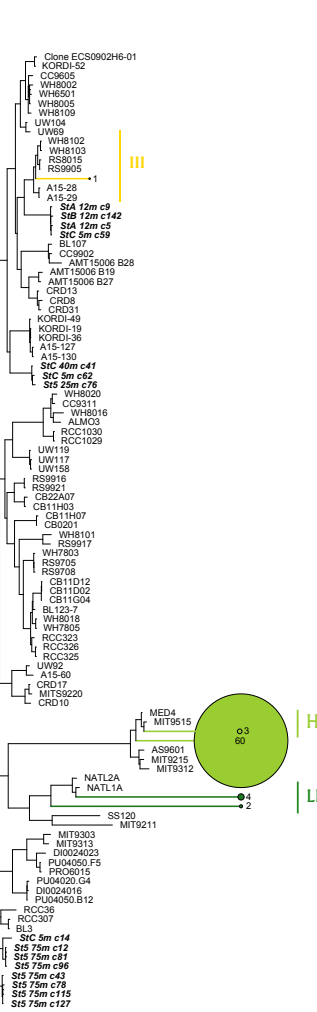
"MID-DEPTH"



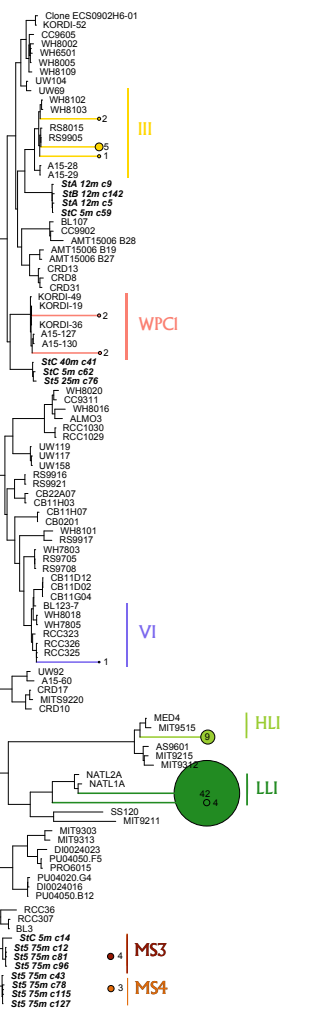
50 m



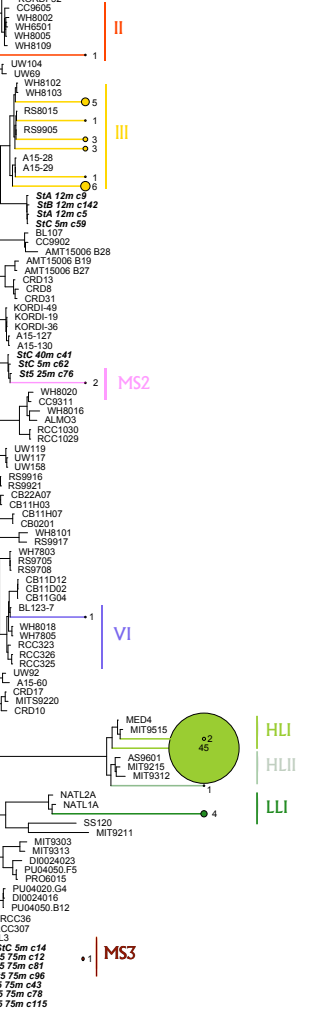
50 m



75 m



40 m



Subcluster 5.1A

Subcluster 5.1B

subcluster 5.3A

subcluster 5.3B

*Prochlorococcus*