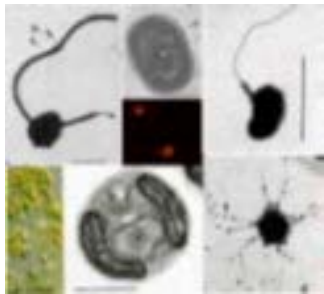


Molecular Characterisation Of Cyanobacterial Population Structure In The Mediterranean Sea

Sophie Mazard, Nick Fuller,
Frédéric Partensky, David Scanlan,
Nyree West.



PICODIV

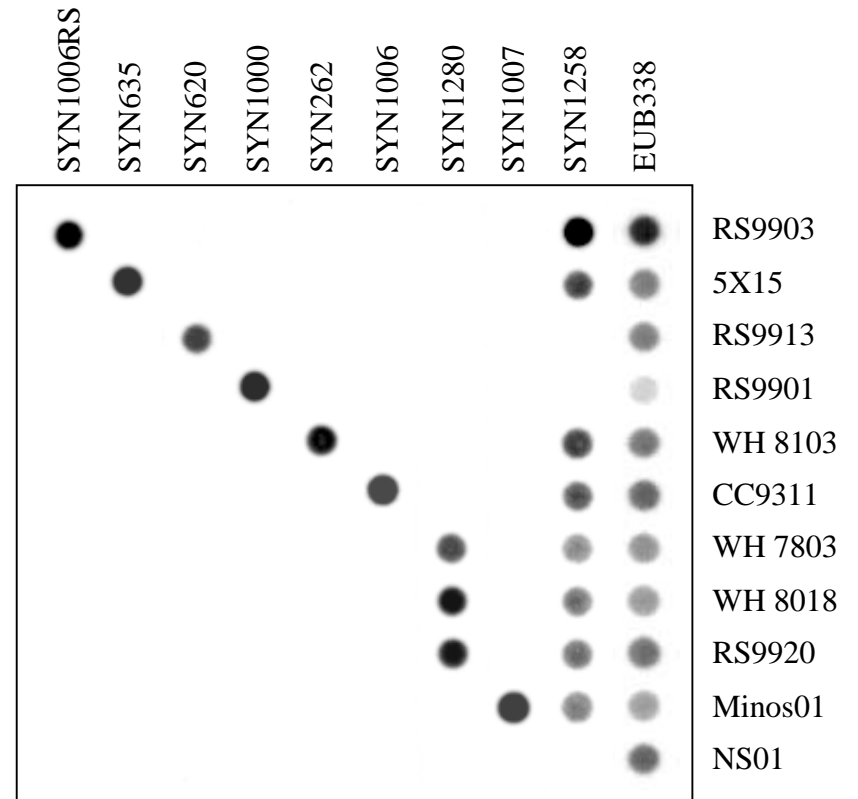
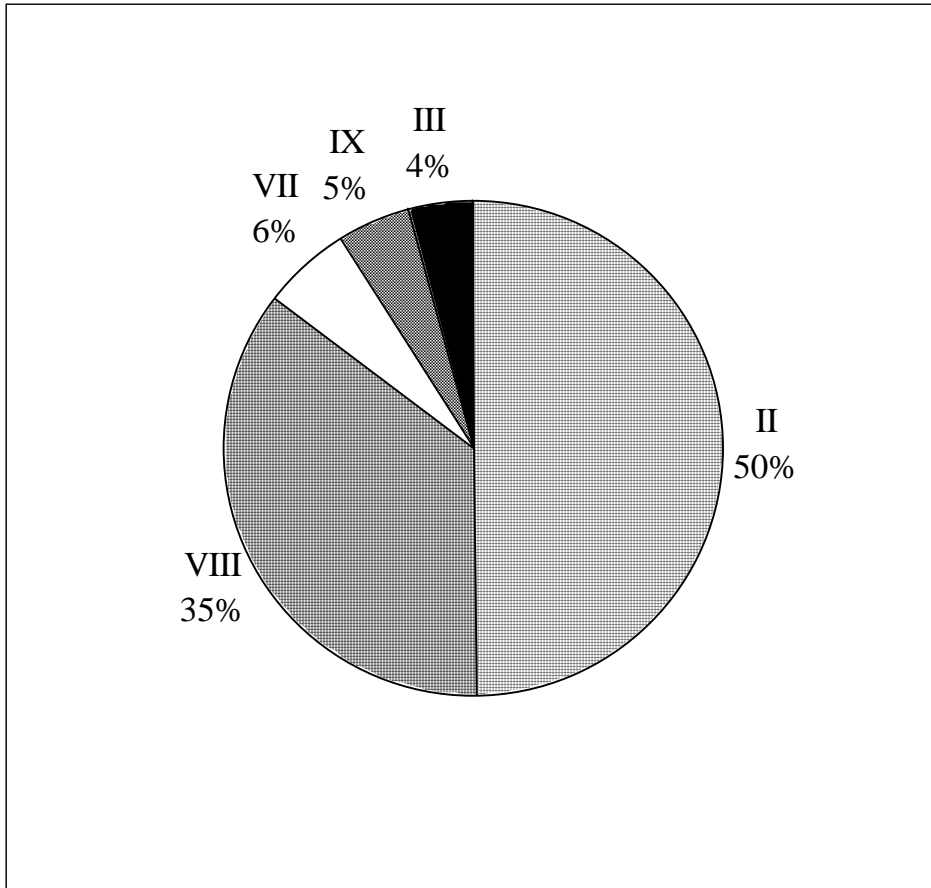


Synechococcus Marine cluster A [Sub-cluster 5.1]



% of each clade represented in cultured isolates

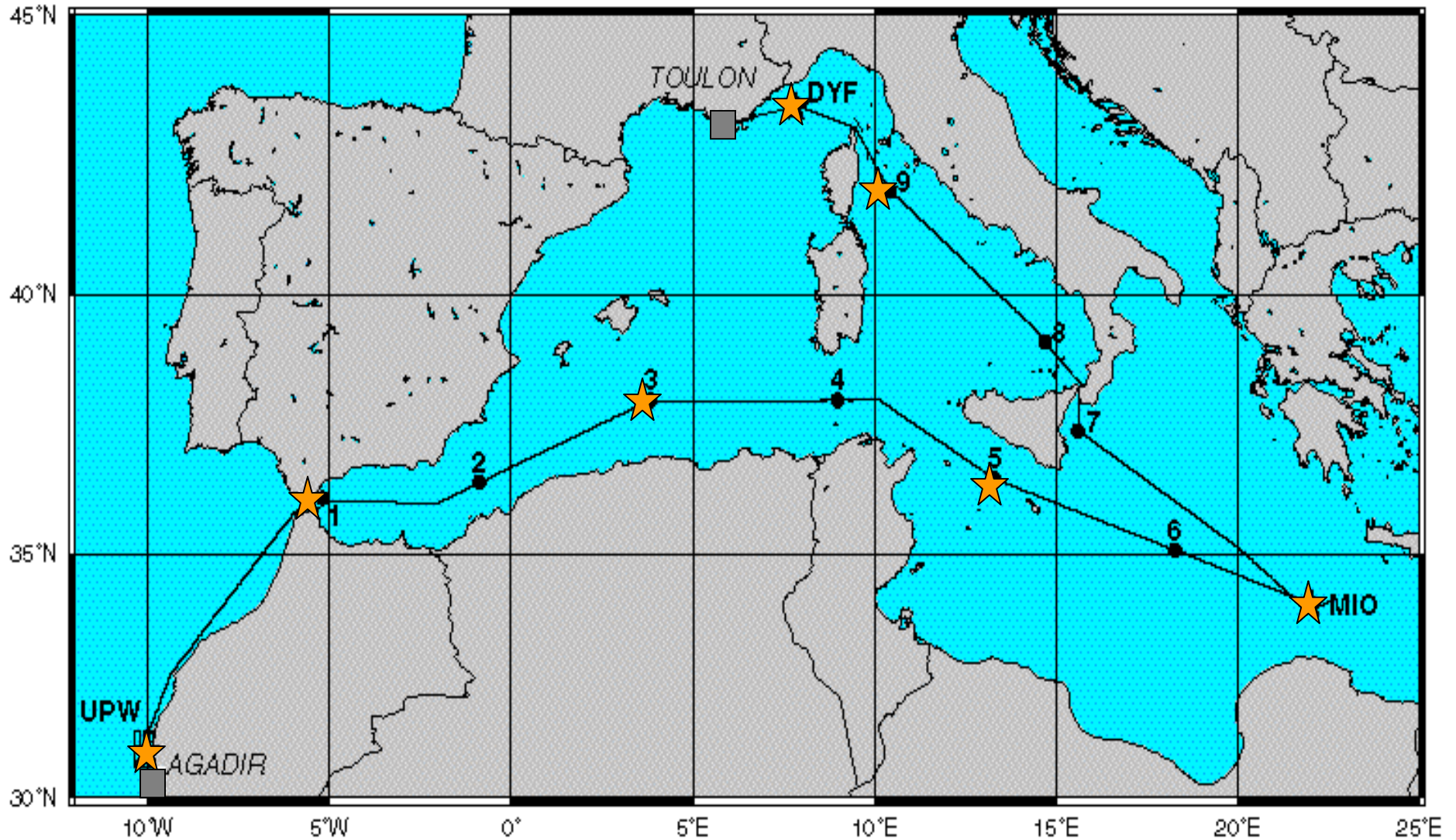
16S rDNA specificity dot blots



Fuller et al. 2003

Position of Stations during the PROSOPE cruise

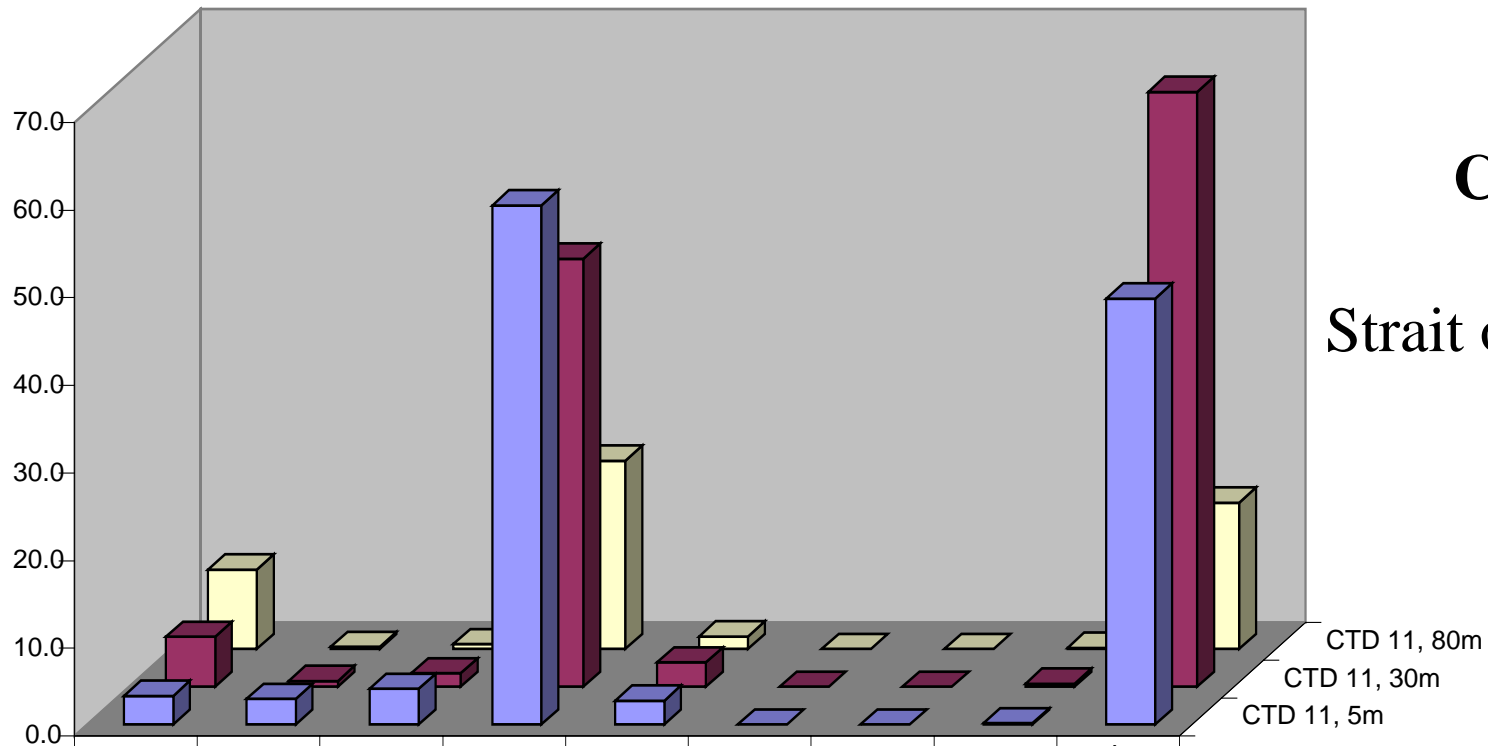
Organised by Hervé CLAUSTRE
Sites analysed



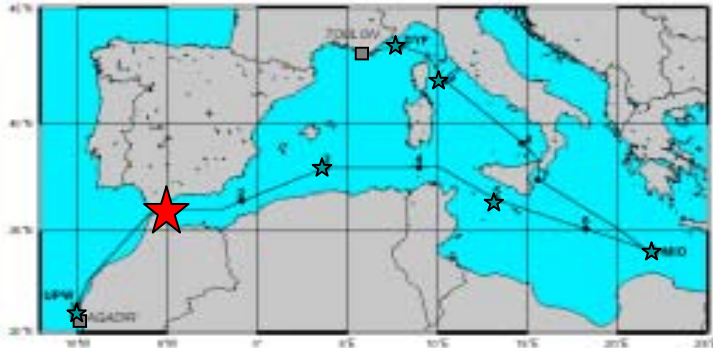
| Station | CTD | N. depth |
|---------|-----|----------|
| UPW | 2 | 3 |
| 1 | 11 | 3 |
| 3 | 17 | 5 |
| 5 | 23 | 2 |
| MIO1 | 28 | 5 |
| MIO4 | 51 | 1 |
| 9 | 70 | 5 |
| DYF2 | 81 | 5 |
| DYF | 95 | 5 |

CTD11

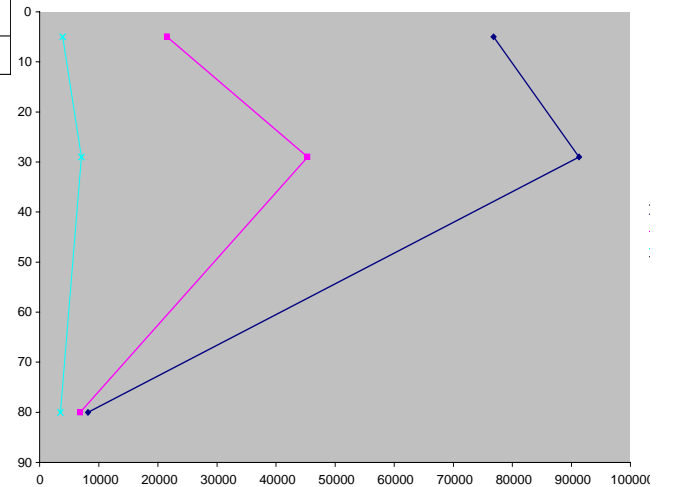
Strait of Gibraltar



| | I | II | III | IV | V, VI, VII | VIII | IX | X | I-VII,X,MITS, 303 |
|---------------|-----|-----|-----|------|------------|------|-----|-----|-------------------|
| ■ CTD 11, 5m | 3.3 | 2.9 | 4.1 | 59.2 | 2.7 | 0.0 | 0.0 | 0.2 | 48.6 |
| ■ CTD 11, 30m | 5.7 | 0.7 | 1.5 | 48.8 | 2.8 | 0.0 | 0.0 | 0.4 | 67.9 |
| □ CTD 11, 80m | 9.1 | 0.2 | 0.5 | 21.5 | 1.4 | 0.0 | 0.0 | 0.1 | 16.7 |

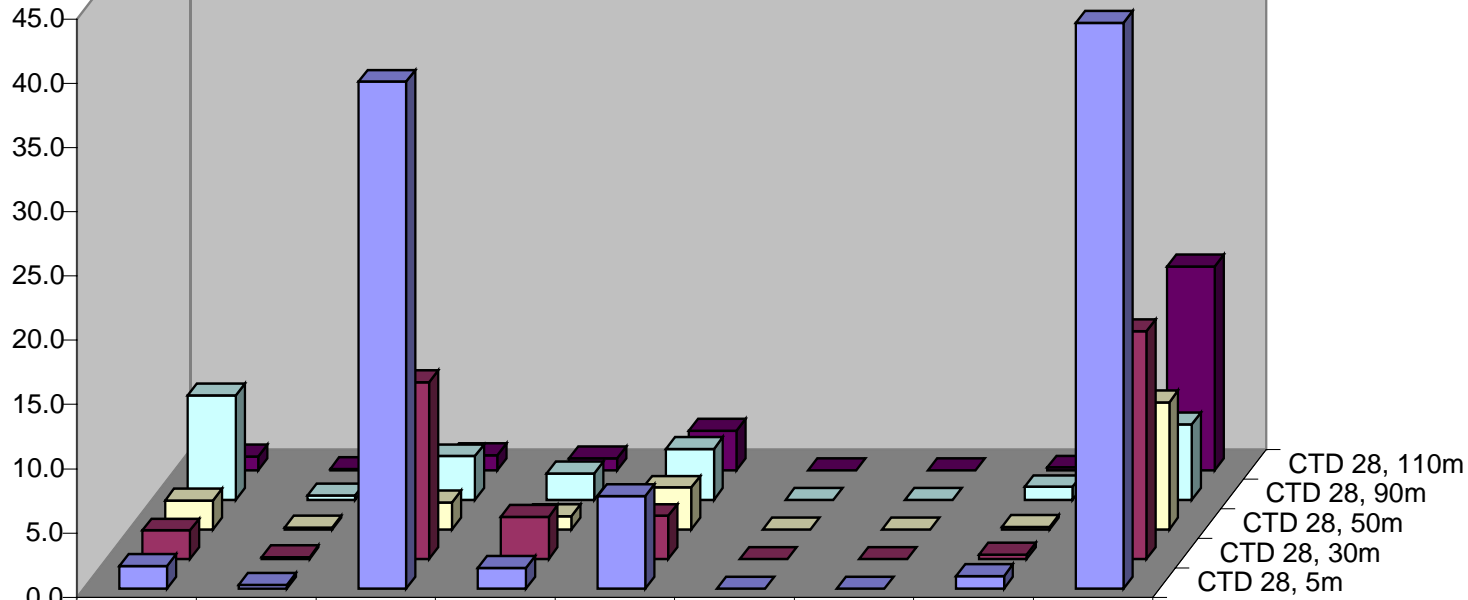


- *Synechococcus*/ml
- *Prochlorococcus*/ml
- Picoeukaryotes/ml

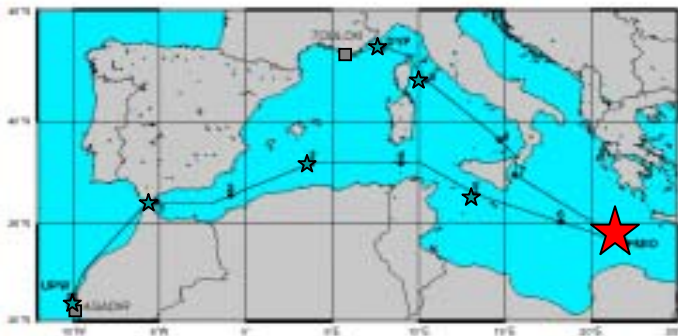


CTD28

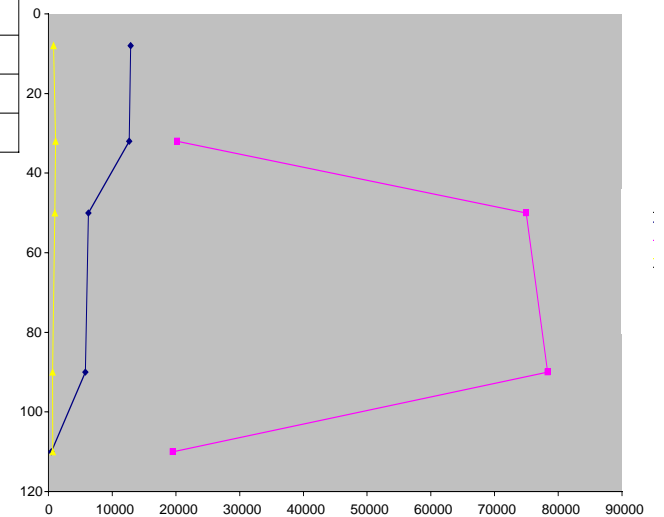
MIO



| | I | II | III | IV | V, VI, VII | VIII | IX | X | I-VII, X, MIT 9303 |
|----------------|-----|-----|------|-----|------------|------|-----|-----|--------------------|
| ■ CTD 28, 5m | 1.7 | 0.3 | 39.4 | 1.6 | 7.2 | 0.0 | 0.0 | 1.0 | 44.0 |
| ■ CTD 28, 30m | 2.2 | 0.2 | 13.8 | 3.3 | 3.4 | 0.0 | 0.0 | 0.4 | 17.7 |
| ■ CTD 28, 50m | 2.2 | 0.2 | 2.1 | 1.0 | 3.3 | 0.0 | 0.0 | 0.2 | 9.9 |
| ■ CTD 28, 90m | 8.1 | 0.3 | 3.4 | 2.1 | 4.0 | 0.0 | 0.0 | 1.0 | 5.9 |
| ■ CTD 28, 110m | 1.1 | 0.1 | 1.2 | 1.0 | 3.1 | 0.0 | 0.0 | 0.2 | 15.9 |

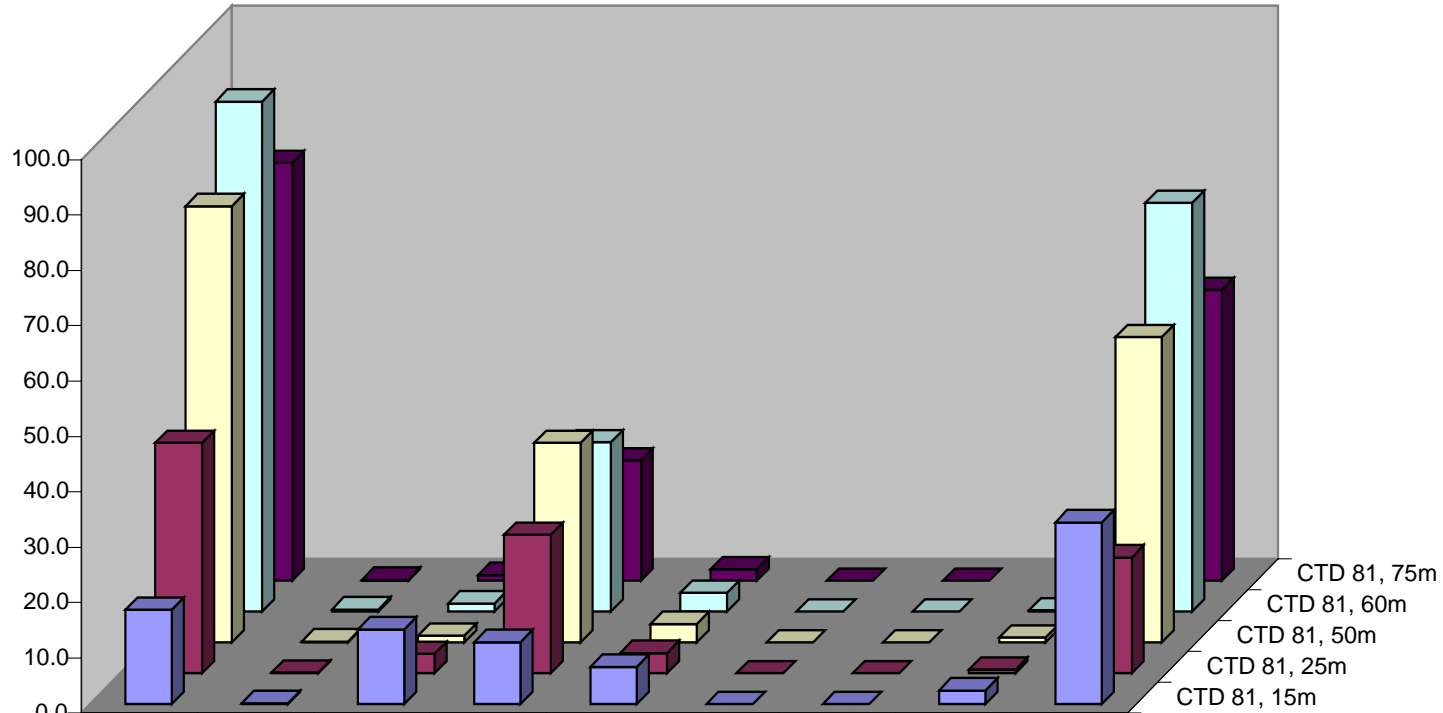


- *Synechococcus*/ml
- *Prochlorococcus*/ml
- Picoeukaryotes/ml

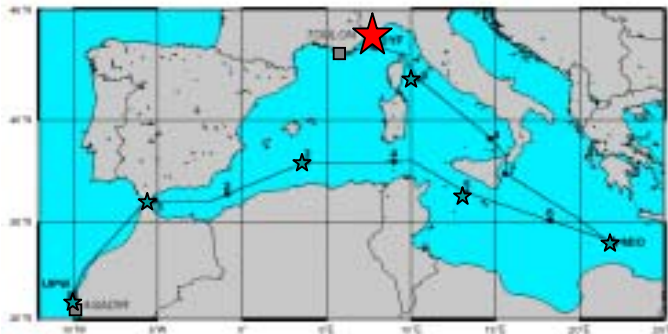


CTD81

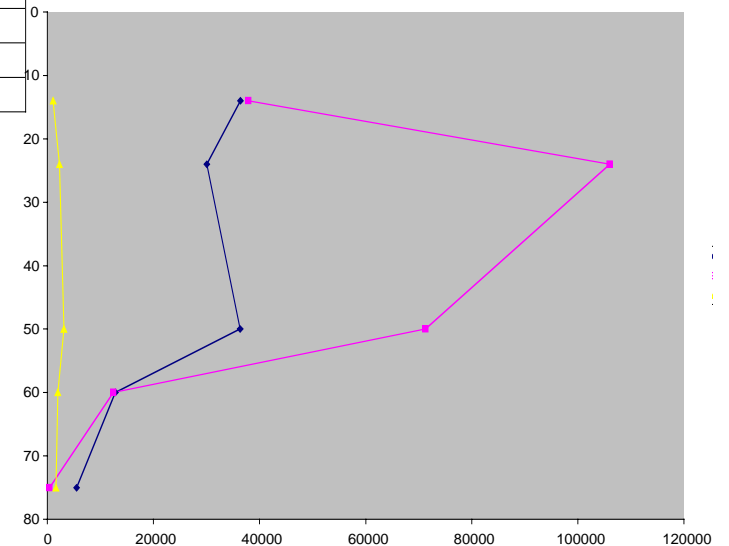
DYF



| | I | II | III | IV | V, VI, VII | VIII | IX | X | I-VII,X,MITg 303 |
|---------------|------|-----|------|------|------------|------|-----|-----|------------------|
| ■ CTD 81, 15m | 17.0 | 0.2 | 13.5 | 11.2 | 6.7 | 0.0 | 0.0 | 2.4 | 32.8 |
| ■ CTD 81, 25m | 41.6 | 0.1 | 3.5 | 25.0 | 3.7 | 0.0 | 0.0 | 0.6 | 20.9 |
| ■ CTD 81, 50m | 78.8 | 0.1 | 1.2 | 36.0 | 3.3 | 0.0 | 0.0 | 0.9 | 55.1 |
| ■ CTD 81, 60m | 92.1 | 0.4 | 1.5 | 30.5 | 3.4 | 0.0 | 0.0 | 0.2 | 73.8 |
| ■ CTD 81, 75m | 75.5 | 0.1 | 1.0 | 21.7 | 2.1 | 0.0 | 0.0 | 0.1 | 52.5 |



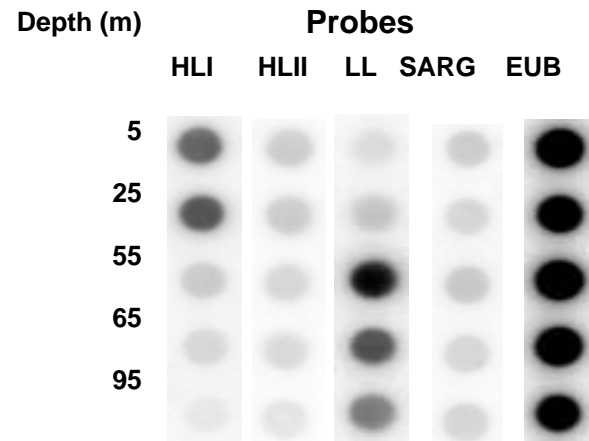
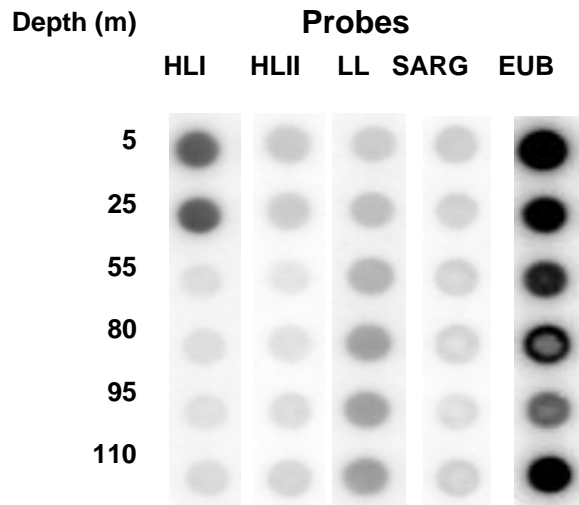
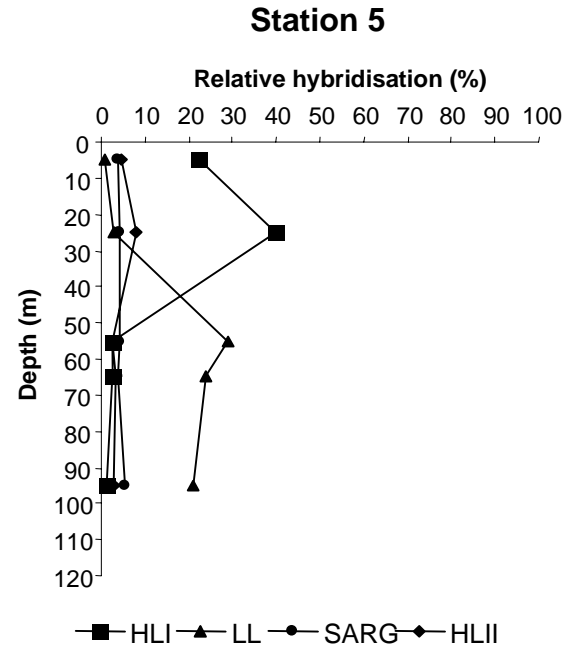
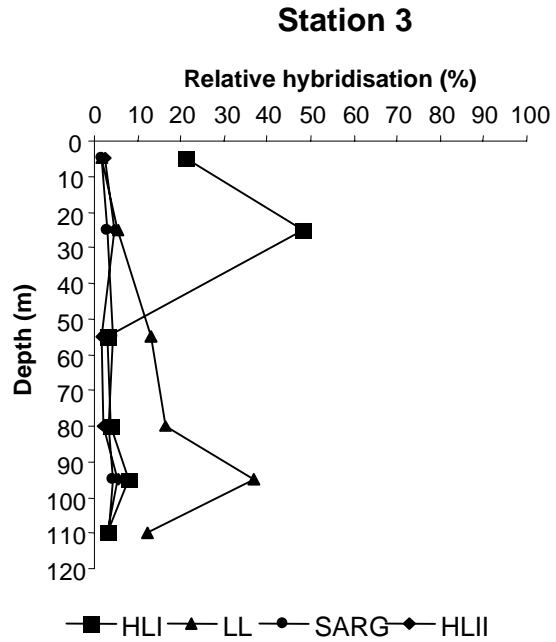
— *Synechococcus*/ml
— *Prochlorococcus*/ml
— Picoeukaryotes/ml



General trends

- ★ Virtual absence of clade II, V/VI/VII, VIII, IX and X.
- ★ Presence of clade III only in surface waters down to ~30m, And more particularly in non-coastal water.
- ★ Presence of clade I, increasing with depth (max 60m)
Dominant clade in coastal waters from the north (DYF).
- ★ Presence of clade IV in coastal waters (lower in Non-coastal waters. Dominant clade from the south.

Vertical distribution of *Prochlorococcus* 16S rDNA genotypes at 2 stations



Future work

- ★ Repeat of the Dot Blots with the *Synechococcus* probes
- ★ Dot Blot analysis of the same environmental samples with *Prochlorococcus* specific probes