# Towards the characterisation of underwater forests

Flash view on 3 studies about the trophic and phylogenetic diversity of protists in the global ocean

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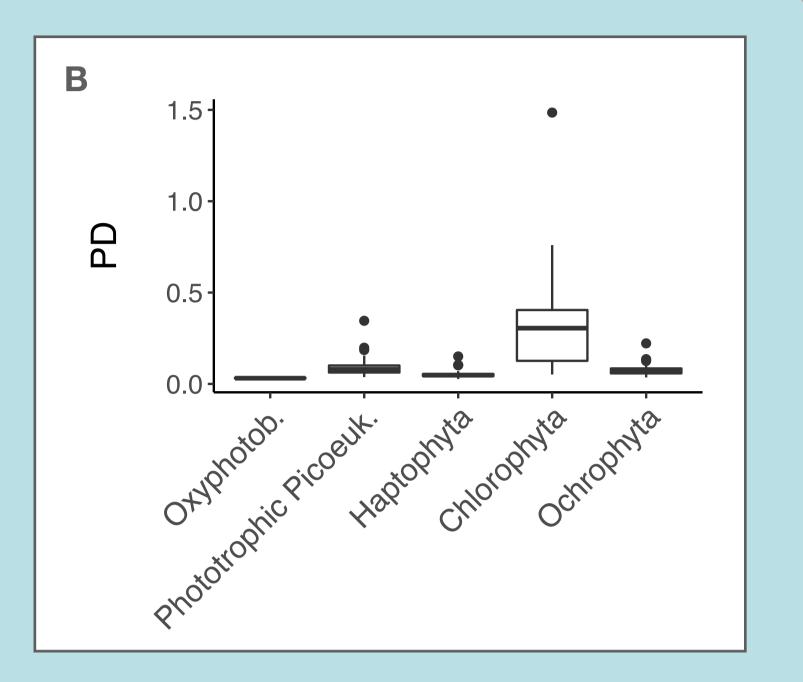
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## **Global comparative analysis of picophototrophs**\*

We compared the abundance and diversity of prokaryotes and picoeukaryotes that contribute to photosynthesis in the oligotrophic ocean.

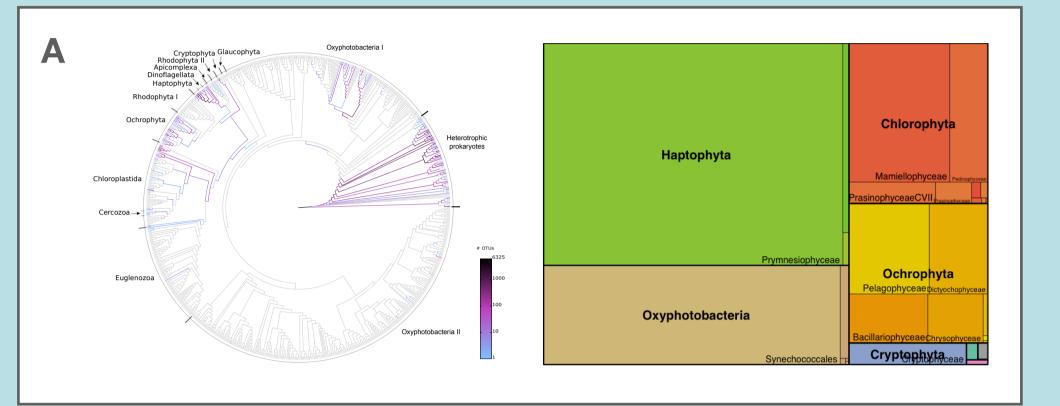
• Prymnesiophyceae, Mamiellophyceae, Dictyochophyceae and Pelagophyceae are the dominant eukaryotic groups.





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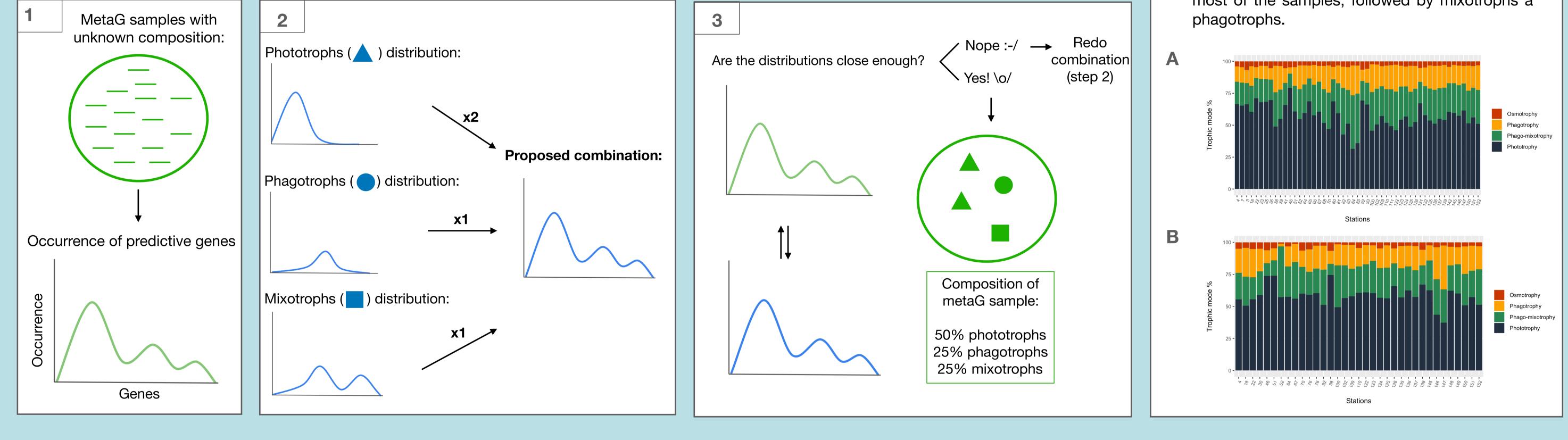
 Metagenomic and metabarcoding data showed that Cyanobacteria are 3 times more abundant than phototrophic picoeukaryotes but hold lower evolutionary diversity.



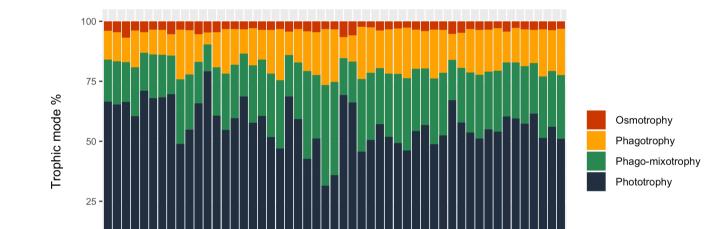
\*In collaboration with Pierre Barbera, Lucas Czech, Nicolas Henry, Pelin Yilmaz, Ewen Corre and Cédric Berney.

#### **Deciphering the global map of trophic modes\***

We adapted a model predictive for nutrition mode (2) to find out the proportion of the different trophic groups (including phago-, photo-, osmo- and mixo-trophs) in metagenomic data. The model follows these steps:



- We used the model to screen Tara Oceans metaG samples of piconano- (A) and nano- (B) size fraction.
- The results show dominance of phototrophs in most of the samples, followed by mixotrophs a

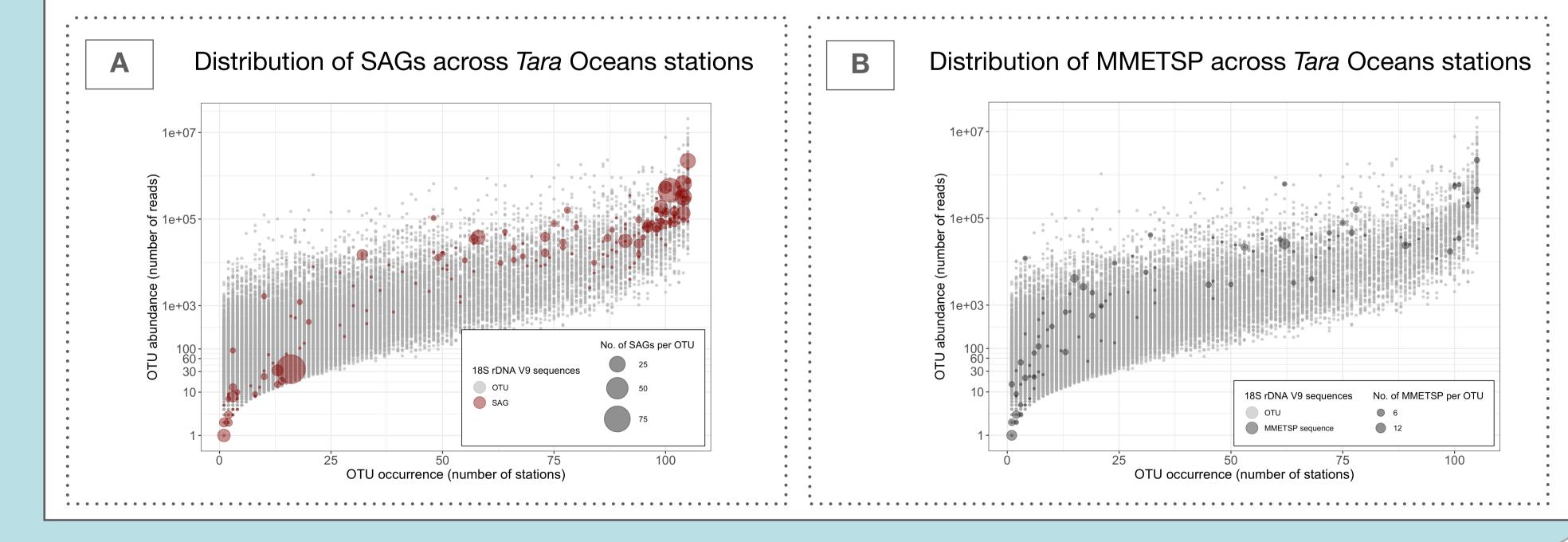


\*In collaboration with John Burns, Giulio Trigla, Eric Pelletier and Nicolas Henry

### The potential of Single-Cell Genomics to recover the dominant protists in the ocean\*

We compared a collection of 903 SAGs<sup>3</sup> (single-cell amplified genomes) and the MMETSP against *Tara* Oceans 18S rDNA V9 metabarcodes to evaluate their global occurrence and abundance.

In comparison with MMETSP, SAGs dataset represents a number of cosmopolitan and abundant taxa. This suggests that SCG is a



powerful technique for the recovery of the dominant taxa of protists in the ocean.

\*Work included in the study of Sieracki et al. (3)

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