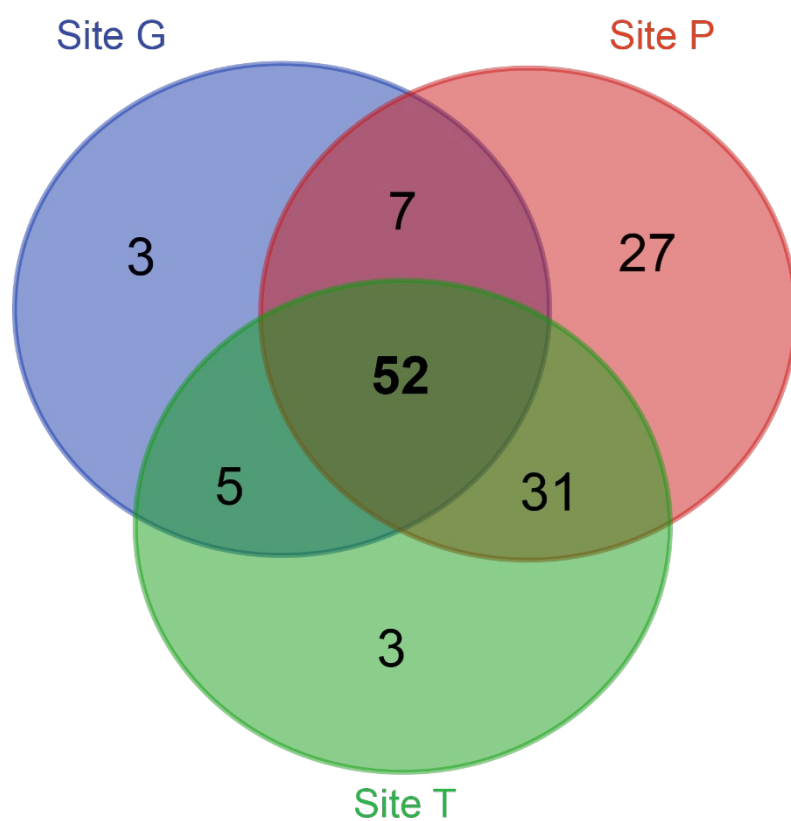
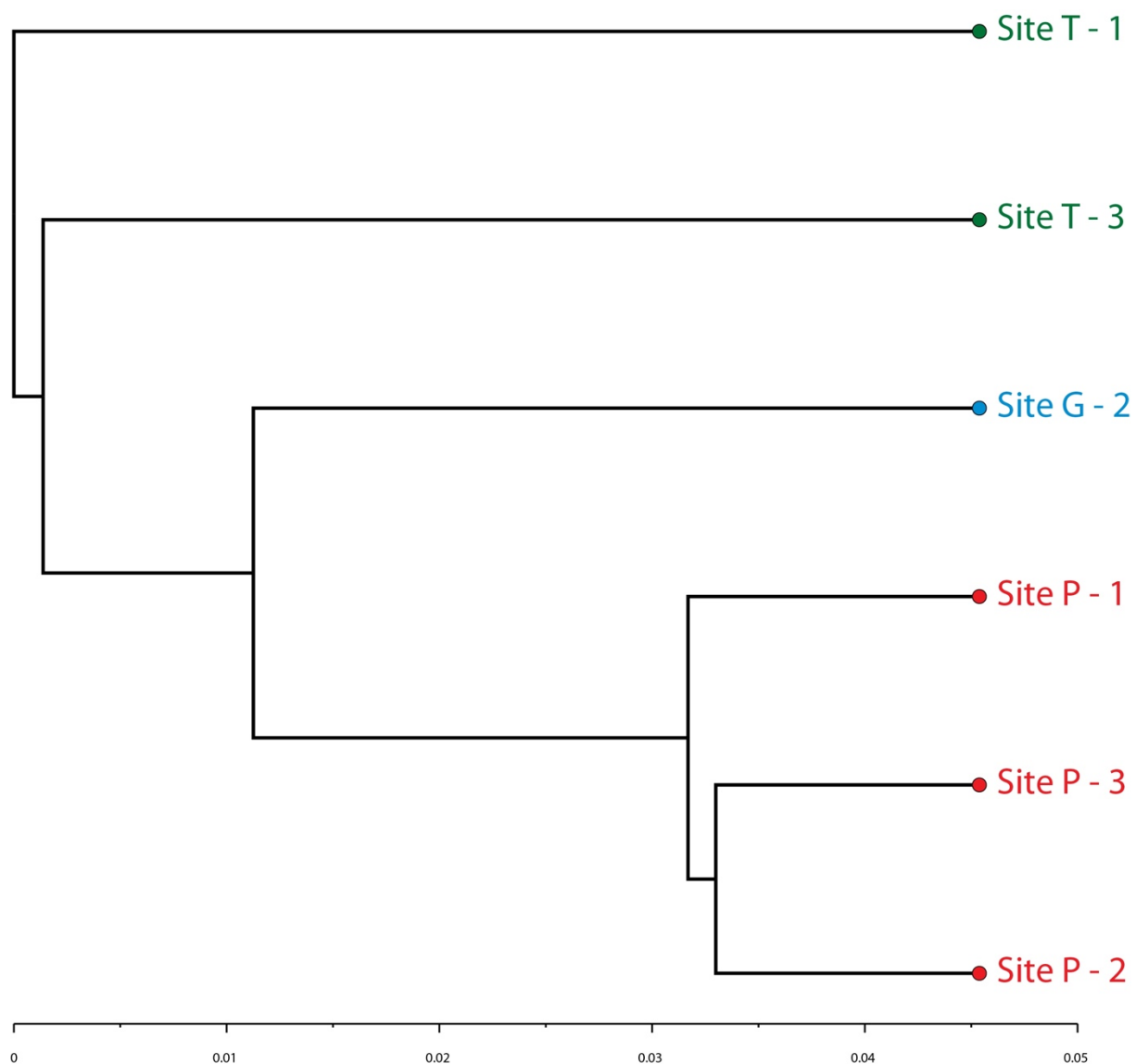


Suppl. Figure 1. Rarefaction curve after normalization of the samples to 1983 sequences.

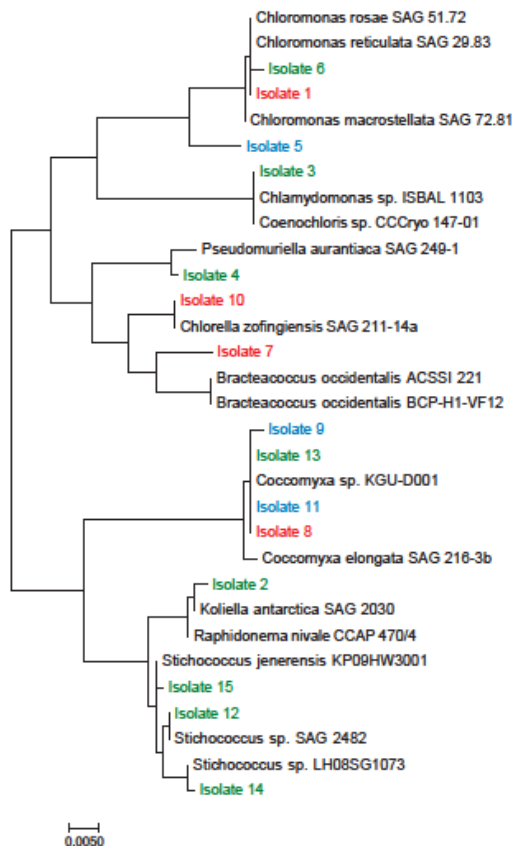


Suppl. Figure 2. Venn's diagram showing the distribution of cyanobacterial OTUs in the three sites based on sequencing of the 16S rRNA gene results.

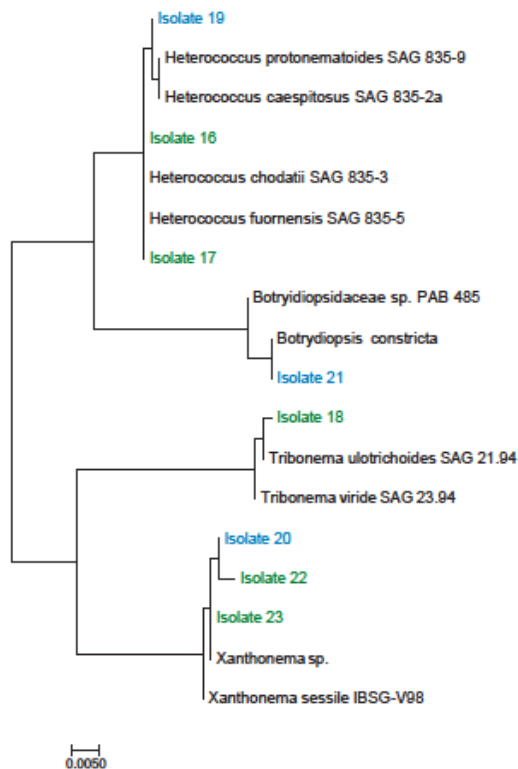


Suppl. Figure 3. Weighted Paired Group Method of Averaging (WPGMA) cluster diagram of cyanobacterial OTUs obtained from Illumina-based 16S rRNA gene sequencing.

a.



b.



Suppl. Figure 4. Phylogenetic tree of the eukaryotic microalgae isolated from the three studied localities: Site T (green), Site P (red) and Site G (blue). The tree was obtained by a maximum likelihood analysis of 18S rRNA gene: *a* – Chlorophyte and *b* – Xanthophyceae.