

## Supplementary Information S.I. 1

**Supplementary Table S1.** Relationship between chlorophyll *a* levels of each species growing as monoculture, measured with a laboratory fluorimeter (Turner BioSystems, USA), and their density and biovolume, which were measured with a particle counter (CASY™ Roche Innovatis AG, Germany). Each regression was performed across the range of densities that were observed in our experiment. N = samples size, R<sup>2</sup> = variance explained by the regression.

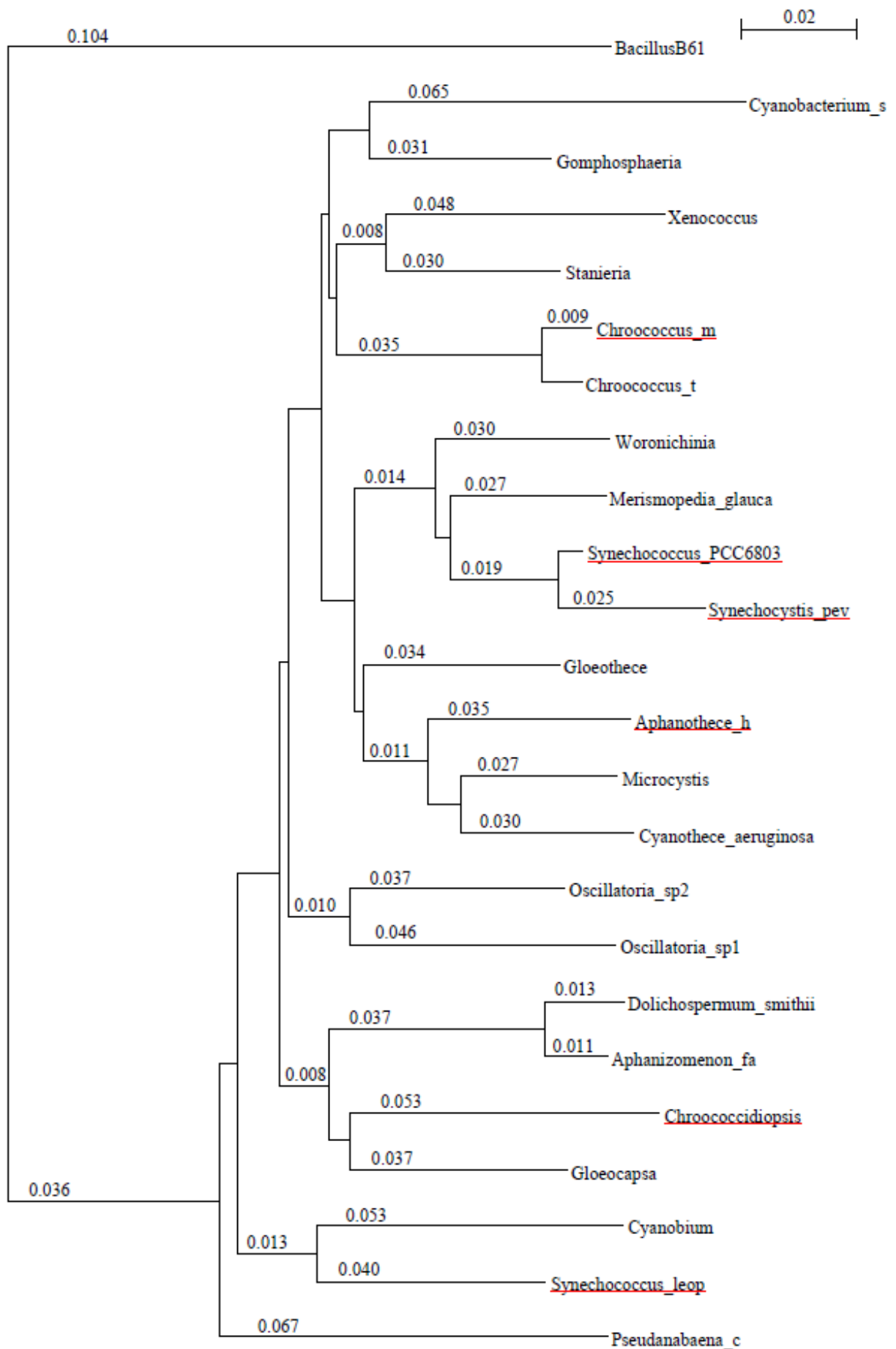
Species	Fluorimeter-particle counter (density)		Fluorimeter-particle counter (biovolume)	
	R <sup>2</sup>	N	R <sup>2</sup>	N
<i>Synechococcus leopoliensis</i>	0.830	15	0.902	15
<i>Synechocystis sp PCC 6803</i>	0.887	20	0.953	20
<i>Synechocystis pevalekii</i>	0.943	15	0.981	15
<i>Chroococcus minutus</i>	0.830	20	0.915	20
<i>Chroococciopsis cubana</i>	0.972	13	0.993	13
<i>Aphanothece hegewaldii</i>	0.833	20	0.943	20

**Supplementary Table S2.** Comparison of monoculture counts of each species used in the experiment when counted under a light microscope, or on the particle counter (CASY™ Roche Innovatis AG, Germany). Each regression was performed across the range of densities that were observed in our experiment. N = samples size, R<sup>2</sup> = variance explained by the regression.

Species	R <sup>2</sup>	N
<i>Synechococcus leopoliensis</i>	0.998	7
<i>Synechocystis sp PCC 6803</i>	0.999	8
<i>Synechocystis pevalekii</i>	0.999	8
<i>Chroococcus minutus</i>	1.000	10
<i>Chroococciopsis cubana</i>	0.891	8
<i>Aphanothece hegewaldii</i>	0.886	7

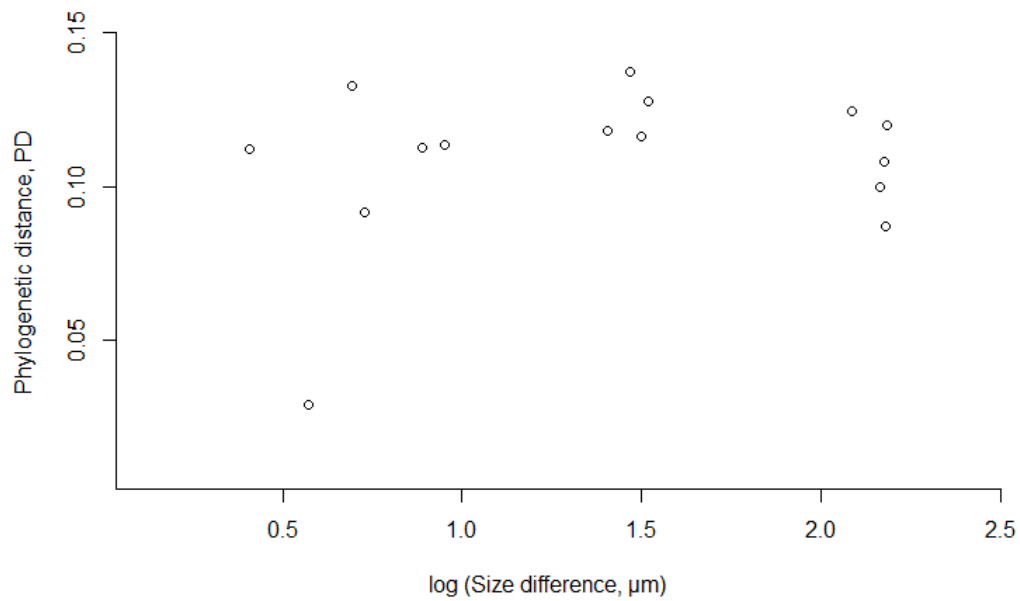
## **Supplementary Information S.I. 2**

**Supplementary Figure S1.** Maximum Likelihood phylogeny constructed using RAxML version 7.2.8 (Stamatakis et al 2008). This molecular phylogeny includes 23 common freshwater cyanobacterial species estimated using partial 16S ribosomal RNA sequences and *Bacillus subtilis* strain B6-1 as outgroup, all available on GenBank. We aligned gene sequences with ClustalX2 (Neighbour-joining distance method) and excluded positions with gaps and correcting for multiple substitutions. Species used in this experiment are underlined in red.



### Supplementary Information S.I. 3

**Supplementary Figure S3.** Relationship between cyanobacterial size differences ( $\mu\text{m}$ ) and phylogenetic distance, for each pairwise combination ( $N = 15$ ). No correlation was found between the two variables ( $R^2 = 0.05$ ,  $P = 0.4$ ).



### References

Stamatakis, A., Hoover, P. & Rougemont, J. (2008). A Rapid Bootstrap Algorithm for the RAxML Web Servers. *Syst. Biol.*, **57**, 758–771.