Cyclidium glaucoma

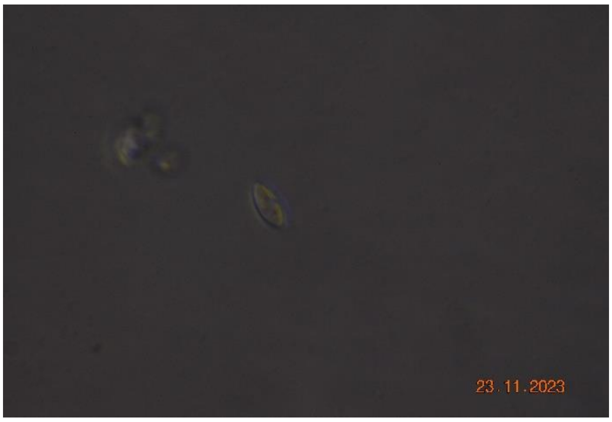

Figure 1: Photograph of the isolated ciliate.

Abstract

As part of the course “Diversity and evolution of microbial eucaryotes” at Uppsala university, samples for algal sequences were collected and identified. The results show that the collected species is most likely *Cyclidium glaucoma.*

Sampling

The sample was collected from a water source near Växjö, Sweden, by lake Torsjö (figure 2). The water source is located in a grazing pasture and surrounded by trees such as oak, birch and spruce. (figure 2)

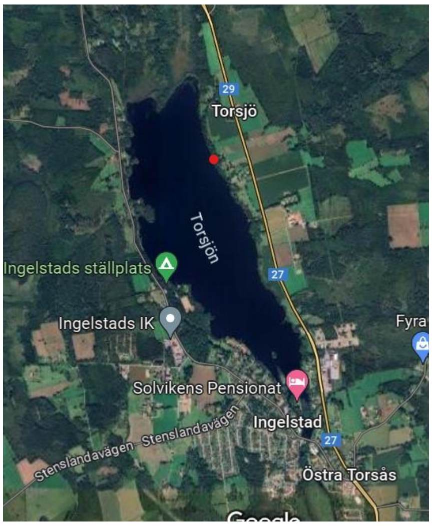

Figure 2: Picture of lake torsjö, the red dot marks the sample site.

Figure 3: Picture of the sample site with surrounding greenery.

Materials and methods

Purification

The sample was cultured using MWC and Z8 algal mediums, promoting algal growth in a 6X8 well plate. The sample did not show sufficient algal growth so well B5, treated with MWC, was chosen for purification and sequencing as it appeared to contain ciliates (figure 4).

Phylogeny

Phylogeny was determined using different computing programs. After receiving the sequences, Snapgene (SnapGene) was used to trim and assemble the sequences. The assembled sequence was analyzed using BLAST® (Altschul *et al.* 1990), and sequences likely phylogenetically similar were collected. Together with significant protist groups, these sequences were analyzed using the MAFFT program (Rozewickii *et al*, 2019) and assembled into a phylogenetic tree using iqtree (Minh *et al*, 2020) and iTool (Letunic &

Bork, 2021). The result of this is shown in figure .

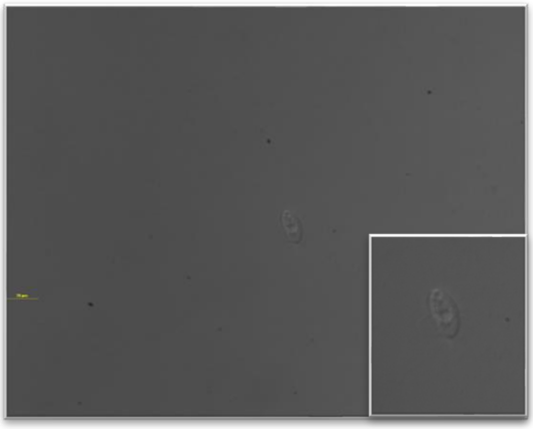

Figure 4: Photograph of the cultured ciliate.

Discussion

As shown in figure 4, the cultured species is a ciliate, part of the alveolate group in the SAR phylum. The species is closest to *Cyclidium glaucoma*, a common ciliate in water habitats across the salinity spectrum. (Fenchel *et al.* 2015)

Due to it being very common the collected species could very well be *c. glaucoma* the somewhat low commonality value during the BLAST and the low bootstrap could be due to contamination, which was an issue throughout the whole laboration process.

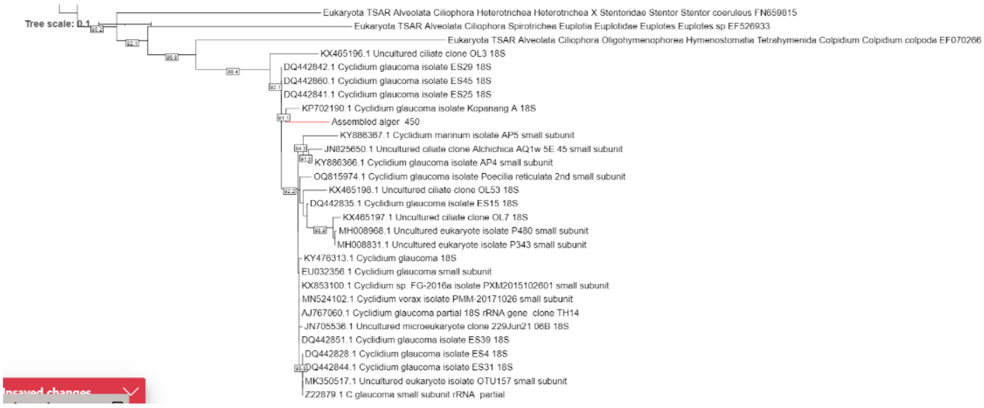

Figure 4: The resulting phylogenetic tree, the isolated species is shown in red.

References

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Letunic I and Bork P (2021) Nucleic Acids Res doi: 10.1093/nar/gkab301 Interactive Tree Of Life (iTOL) v5: an online tool for phylogenetic tree display and annotation (full article)

SnapGene software, version 7.1 (www.snapgene.com)

Rozewicki, Li, Amada, Standley, Katoh 2019 (Nucleic Acids Research 47:W5-W10) MAFFT-DASH: integrated protein sequence and structural alignment (describes web interface for sequence and structural alignments)