Uppsala Universitet
Diversity and Evolution of Microbial Eukaryotes
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Identifying algae - *Cryptophyceae* : *Rhinomonas*

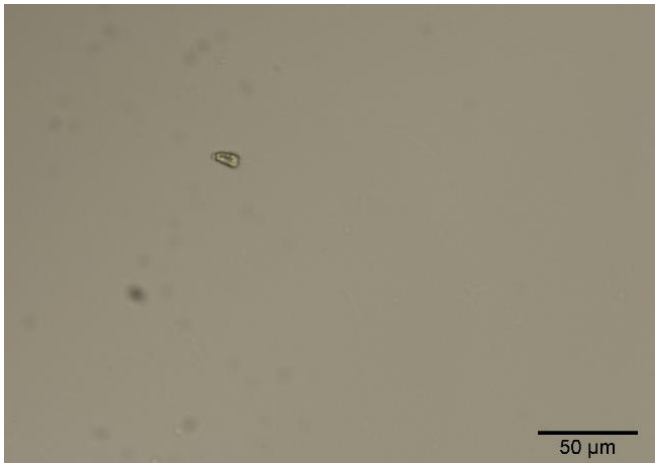

Figure 1. One algae with a flat end, in the left corner a scale is placed.

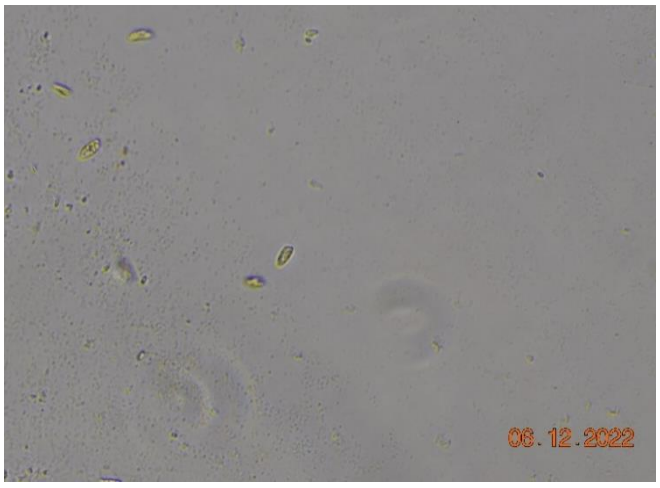

Figure 2. Several algae swimming by, yellow and red pigments can be observed.

Identification

The algae are small, approximately 20 µm long and fast moving. When moving they rotate around their own axis. The shape is oval and the algae has both yellow and red pigments. One end is flattened, cutting of the cells oval shape. Flagella where hard to observe but the hasty movement suggest at least one.

Visual identification suggest that this algae belongs to either *Cryptomonas* or *Chroomonas* (Bellinger & Sigee 2015). Sequencing of DNA and following analysis with BLAST suggest *Rhinomonas nottbecki* could be a possible species or family. The sequence was 91% similar to earlier identified samples, so the match is not completely reliable. Also note that the sequencing only worked on one of the DNA-strands, which inhibited creating a consensus-strand. Instead, the BLAST-search was done with one single-strand. This makes the result unreliable and should be seen more as guidelines then definitive answers.

Combining the two methods provides us with more insight. The algae likely belong to class *Cryptophyceae* and if the sequencing is correct, to the family *Rhinomonas. Cryptophyceae* generally mixotrophs in marine and freshwater environments (Johannesson). Even through these species can be found almost everywhere, colder climate is preferred. *Cryptophyceae* have undergone secondary endosymbiosis with *Rhodophyta*, of which the remnants still can observed in the form of a nucleomorph. Therefor the plastid is of a red alga, giving the plankton red and yellow colours.

Method

Sampling was conducted on the 10th of November, at Ekebypölen, Uppsala (59.845046” N, 17.596174” E). At the time the water was still, and the surrounding area had recently been cleared of large growing macrophytes. To ensure the sample was properly taken the water was mixed a little, so a little sediment was included, and taken at an arm. The sample was stored at room temperature overnight and then transported to the lab. The sample was diluted several times and mixed with different growth mediums, aiming to produce pure cultures of at least one

species. With established cultures PCR was performed with the primers PF1 and FAD4. Sequence analysis was done with Assseq and BLAST.

Sources

Bellinger EG, Sigee DC. 2015. Freshwater Algae: Identification, Enumeration and Use As Bioindicators. John Wiley & Sons, Incorporated, Hoboken, UNITED KINGDOM.

Johannesson MH Mahwash Jamy, Fabien Burki & Hanna. Hacrobia. WWW-dokument: //uu-microbial-eukaryotes.github.io//ebook/book/Part2/phylogenetic_classification/sections/Hacrobia.html. Hämtad 2022-12-21.