



Conference Abstract

# Comparative study of benthic diatom community using 18S rDNA metabarcoding and light microscopy in the Bosphorus, Turkey

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## Abstract

Diatoms are one of the major algal groups having an important role in the aquatic systems in which they constitute the main primary production with dinoflagellates in the coastal regions, and can contribute to photosynthesis at great rates. There had been intense effort to reveal diatom community with light microscopy (LM) and scanning electron microscopy (SEM), on the other hand, DNA barcoding techniques had been an interest to understand the microbiome in the last decades. Barcoding provided rapid response on the targeted organisms and introduced many new species. Recently, monocultural molecular studies showed that species could be described with accurate and reliable results. DNA metabarcoding approaches yielded to determine the whole organisms with available DNA data in the sample and major advances on next-generation sequencing platforms enable to widen the application of metabarcoding approach to various environmental samples.

The aim of this study was to perform a comparative assessment of the diatom community structures in Bosphorus of Istanbul, Turkey by LM and 18S rDNA metabarcoding. Diatom samples were collected by brushing from the submerged stones of 10 cm<sup>2</sup> of area taken from the coast of Beykoz on the Asian part of the Bosphorus, Istanbul and processed for LM and metabarcoding in June 2020. To concentrate the sample, the scrapes of the biofilm filtered from a 0.22-micron filter, and eDNA was extracted from that filter paper using MN

NucleoSpin Soil DNA isolation kit (Macherey-Nagel, Germany) following the manufacturer's protocol and diatom community profile was analyzed by targeting the V4 region of the 18S rRNA gene using Illumina® MiSeq™.

DNA metabarcoding results revealed two classes Bacillariophyceae (91%) and Mediophyceae (9%) (Fig. 1). While small-celled *Hyalosira delicatula* Kützing was the most abundant taxa with 40% abundance and it was followed by *Licmophora* spp. (33%). 28% of *Licmophora* sequences could not be assigned to any species and remained as unidentified, *Licmophora gracilis* (Ehrenberg) Grunow (4%), and *L. flabellata* (0.9%) detected at lower abundances. Besides, one of the common genera of diatoms, *Navicula* spp., showed a relative abundance of 4% and another common genus *Nitzschia* spp. were represented only by *N. commutata* Grunow and composed 0.5% of the community.

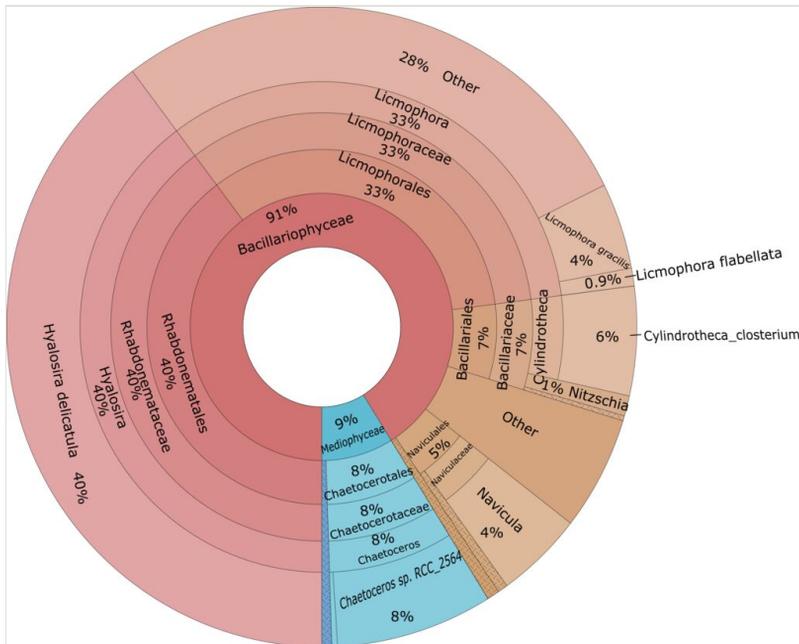


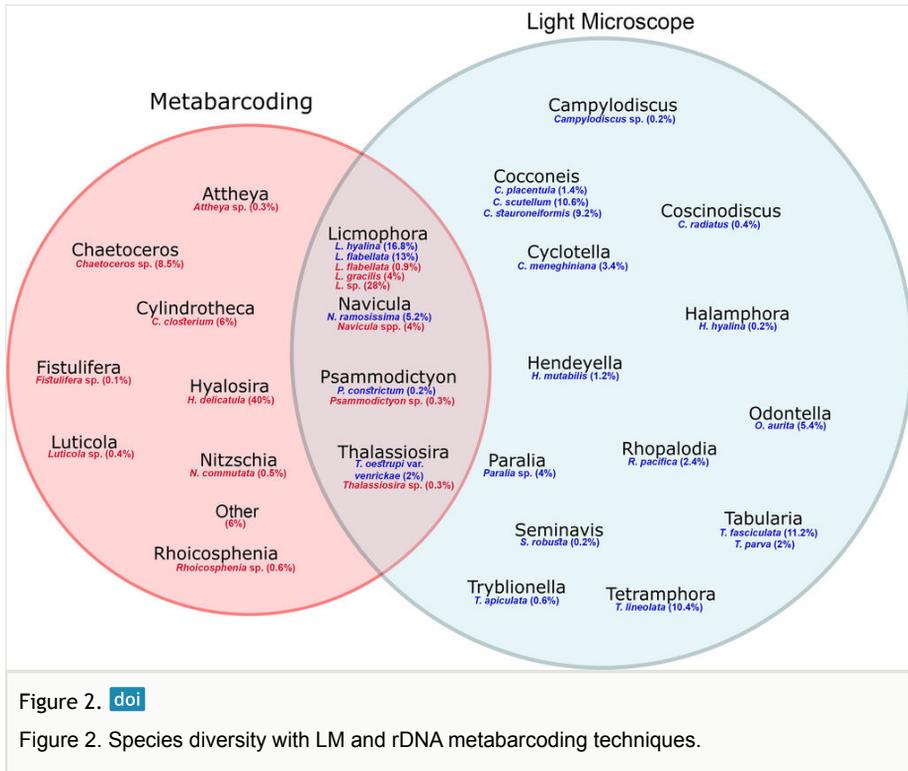
Figure 1. [doi](#)

Figure 1. Diatom composition of the station by 18S rDNA

While 18S rDNA metabarcoding revealed 11 genera, LM investigation identified 17 genera belonging to 21 species. 4 genera were common in both techniques and *Licmophora flabellata* was detected in both LM and metabarcoding methods. Interestingly, small celled taxa which could be easily overlooked in LM was detected with 18S metabarcoding. The results presented a promising number of genera which could be detected by both methods (Fig. 2).

DNA metabarcoding of diatoms is a new area of research in the coastal waters and there are few studies performed so far and this is the first study relying on the rDNA metabarcoding of diatoms in the aquatic systems in Turkey. The comparison of the taxa

using microscopy methods and metabarcoding techniques indicated some significant differences in the diatom composition. However, the results here with 18 species with metabarcoding vice-versa 21 taxa with microscopy methods confirms poor biodiversity in the Bosphorus. However, this study based on one sampling effort in one station for the comparison of the two methods, we had LM results from more stations in different seasons supporting the lower biodiversity. eDNA data is scarce from the coastal areas and our results comprise a promising number of genera. Results of this study could provide data for further research, which high number of diatoms could be determined with eDNA metabarcoding.



## Keywords

diatom diversity, amplicon sequencing, eDNA, Illumina® MiSeq™

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**Conflicts of interest**

Authors declare no conflict of interest.