

### **GP3: Nano- and microplankton diversity inhabiting a coastal upwelling system: a metabarcoding approach**

Pilar Díaz-Tapia<sup>1</sup>, Antonio Bode<sup>1</sup>, Marta M Varela<sup>1</sup>

<sup>1</sup>*Centro Oceanográfico de A Coruña, Instituto Español de Oceanografía (IEO), España*

\*Presenting author: [pilar.diaz@ieo.es](mailto:pilar.diaz@ieo.es)

Small eukaryotic plankton has been traditionally characterized using conventional microscopy techniques. Current advances in sequencing technologies allow the cost-effective study of the diversity within microbial plankton based on DNA sequences. This technique has been implemented in the last 15 years for investigating prokaryotic diversity, but its application to unravel the diversity and distribution of eukaryotic organisms is still incipient. Alleged advantages of this approach include the ability of detecting the smaller fraction of the community that tends to be overlooked in microscopy studies, as well as improving the resolution of taxonomic identification for groups whose morphological study is challenging due to the paucity of morphological characters. In this study we characterize the diversity of the nano- and microplankton marine communities using microscopy and rDNA sequencing techniques. The aim of this work is to compare results of both techniques, assessing whether rDNA data can provide new insights into the study of the diversity of eukaryotic planktonic communities. Twenty monthly samples were collected in a station off the Ría de A Coruña (NW Iberian Peninsula). Planktonic samples for DNA studies were collected by filtering seawater samples through a 3 µm pore size polycarbonate filter. DNA was extracted, the V4 region of the 18S rRNA was PCR amplified and subsequently sequenced using the High Throughput Sequencing (HTS) platform Illumina. Amplicon sequence variants (ASVs) were differentiated using DADA2 implemented in R. Sequences were aligned against PR2 v4.12.0 and SILVA 132 18S rRNA databases as references. Microscopic identification of plankton taxa (phytoplankton and protozoa) was made using the Uthermöhl technique. In total 1182 ASVs were identified based on rDNA data, which contrasts with only 65 species identified by microscopy. Morphological identifications of eukaryotic plankton were restricted mainly to diatoms, dinoflagellates and ciliates, while rDNA data allowed the detection of additional taxonomic groups (i.e. protist). Some of them were very abundant, such as the algae Cryptophyceae and Mamiellophyceae or the heterotrophs Ascomycota or parasitic Stramenopiles. Therefore, our study further evidenced that DNA metabarcoding is a valuable tool to uncover part of the great diversity within microbial plankton, improving the detection of small eukaryotes.