

## **Diatom resting stages in surface sediments: a pilot study comparing Next Generation Sequencing and Serial Dilution Cultures**

Roberta PIREDDA<sup>a\*</sup>, Diana SARNO<sup>a</sup>, Carina B. LANGE<sup>b,a</sup>,  
Maria Paola TOMASINO<sup>c,a,d</sup>, Adriana ZINGONE<sup>a</sup> & Marina MONTRESOR<sup>a</sup>

<sup>a</sup>Stazione Zoologica Anton Dohrn, Department of Integrative Marine Ecology,  
Villa Comunale, 80121 Naples, Italy

<sup>b</sup>Department of Oceanography, COPAS Sur-Austral & Centro FONDAP-IDEAL,  
University of Concepción, Barrio Universitario, Concepcion, Chile

<sup>c</sup>Institute of Biomembranes and Bioenergetics,  
National Research Council, Bari, Italy

<sup>d</sup>Current address: CIIMAR – Interdisciplinary Center of Marine  
and Environmental Research, University of Porto, Portugal

**Abstract** – Several diatom species produce resting stages as part of their life cycle. These resting stages accumulate in the sediments where they can remain for a long time before being re-suspended in the water column and switching to active growth. Until now, the abundance and diversity of viable diatom resting stages have been assessed using the Serial Dilution Culture (SDC) method. In the present study, surface sediment samples from the Gulf of Naples were used to compare results obtained with the SDC method with those provided by HTS metabarcoding based on DNA extracted from the same sediment sample; the marker used was the V4 region of 18S rDNA. HTS metabarcoding showed a marked dominance of polar centric diatoms, among which *Chaetoceros* species were the most represented, in terms of both sequence and ribotype number. Almost all the most abundant ribotypes identified with metabarcoding matched records of species observed in SDCs. In some cases, however, this marker region could not distinguish between morphologically and phylogenetically distinct species, e.g., *Skeletonema pseudocostatum* and *S. tropicum*. As expected, molecular analysis provided a higher number of ribotypes as compared to the number of taxa recorded by SDC. Despite the well-known biases of both methodologies for quantitative assessments, our results show that DNA metabarcoding *via* HTS sequencing is a promising approach to explore the diversity of diatom resting stages. This study also confirms the importance of curated reference sequences to fully interpret the diversity stored in environmental sediment samples.

**Diatoms / HTS / metabarcoding / V4 / 18S rDNA / resting stages / SDC / sediments / LTER-MC / Gulf of Naples**

---

\* Corresponding author: robpiredda@gmail.com