

High-throughput sequencing of marine biodiversity archives: Promises and challenges

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The evolution of the marine environment is commonly studied based on microfossil species capable of biomineralization. However, beyond calcareous or siliceous remains, ancient DNA (aDNA) molecules preserved in the sea floor represent a valuable, yet largely untapped archive of biodiversity. This archive has been investigated as a complement to classical palaeoceanographic proxies using high-throughput sequencing technologies (HTS) [1,2]. Although exhaustive DNA sequence datasets offer promising insights into past marine environments, unexpected contamination events are still challenging current inferences.

The large diversity of marine micro-eukaryotes without doubt entails sensitive biomarkers of changes. Nevertheless, the aDNA proxy deserves further validation. Therefore, we (i) compare molecular and microscopic data focusing on the extensively studied microfossil group of Foraminifera and (ii) describe the ability and relevance of detecting non-fossilized taxa based on illumina HTS of ribosomal gene markers.

In low [2] and high [3] latitude environments, non-fossilized taxa dominate as in modern communities [4]. We found a limited match between fossil species and their aDNA markers both in terms of sequence abundance and occurrence across sediment core samples, especially in the case of rare taxa. Such inconsistencies might result from the many biases known to affect sequencing datasets.

However, HTS is prone to a new pervasive type of caveat leading to undetectable cross-contamination patterns among multiplexed samples. We document, alleviate and make beneficial from this phenomenon to develop a powerful filtering method towards high-throughput accuracy.

Robust experimental planning is the key to optimize the value of aDNA information buried in marine sediments and understand past and present marine biodiversities.

[1] Coolen *et al* (2013) *Proc. Natl. Acad. Sci. USA* **110**, 8609–8614. [2] Lejzerowicz *et al* (2013) *Biol. Lett.* **9**. [3] Pawłowska *et al* (in revision) *Geobiology*. [4] Lecroq *et al* (2011) *Proc. Natl. Acad. Sci. USA* **108**, 13177–13182.