

Ultra-deep sequencing of foraminiferal microbarcodes unveils hidden richness of early monothalamous lineages in deep-sea sediments

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Abstract

Deep-sea floors represent one of the largest and most complex ecosystems on Earth but remain essentially unexplored. The vastness and remoteness of this ecosystem make deep-sea sampling difficult, hampering traditional taxonomic observations and diversity assessment. This problem is particularly true in the case of the deep-sea meiofauna, which largely comprises small-sized, fragile, and difficult-to-identify metazoans and protists. Here, we introduce an ultra-deep sequencing-based metagenetic approach to examine the richness of benthic foraminifera, a principal component of deep-sea meiofauna. We used Illumina sequencing technology to assess foraminiferal richness in 31 unsieved deep-sea sediment samples from five distinct oceanic regions. We sequenced an extremely short fragment (36 bases) of the small subunit ribosomal DNA hypervariable region 37f, which has been shown to accurately distinguish foraminiferal species. In total, we obtained 495,978 unique sequences that were grouped into 1,643 operational taxonomic units, of which about half (841) could be reliably assigned to foraminifera. The vast majority of the operational taxonomic units (nearly 90%) were either assigned to early (ancient) lineages of soft-walled, single-chambered (monothalamous) foraminifera or remained undetermined and yet possibly belong to unknown early lineages. Contrasting with the classical view of multichambered taxa dominating foraminiferal assemblages, our work reflects an unexpected diversity of monothalamous lineages that are as yet unknown using conventional micropaleontological observations. Although we can only speculate about their morphology, the immense richness of deep-sea phylotypes revealed by this study suggests that ultra-deep sequencing can improve understanding of deep-sea benthic diversity considered until now as unknowable based on a traditional taxonomic approach.

[DNA barcoding](#) [next-generation sequencing](#) [small subunit ribosomal RNA](#) [microbial eukaryote](#) [cosmopolitanism](#)

Footnotes

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Data deposition: The sequence data reported in this paper have been deposited at the NCBI Sequence Read Archive.

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