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Assessment of foraminiferal richness from deep-sea benthos using Illumina massive sequencing technology

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New massive sequencing technologies are especially relevant to assess the diversity of environmental samples from the Deep Sea since they allow retrieving extensive genetic information from limited amount of material uneasy to collect at such remote places.

We collected unsieved sediment samples from the Deep Sea of five distinct geographic regions and sequenced a very short (36 nt) fragment of the foraminiferal SSU rDNA hypervariable region.

Among the numerous phylotypes resulting from our analyses, some of them have been identified to the genus or species level and most of identified OTUs were assigned to monothalamous (single chambered) taxa. Our results, in which multi-chambered orders account for only a minority part of the richness, contrast with the classical view of foraminiferal diversity based on micropaleontologically oriented study of fossilized species.

This study emphasizes the usefulness of such technology for environmental biomonitoring perspectives regarding climate changing and human activities impact on deep-sea environment.

キーワード: benthic foraminifera, deep sea, massive sequencing

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