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Assessing assemblages from foraminiferal propagule banks: A combined approach of culture experiments and eDNA metabarcoding

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Shallow-water banks of foraminiferal propagules (tiny juveniles <63 μm) harbor a hidden assemblage composition that has altered our understanding of traditional distribution patterns. Propagules can be transported well beyond their environmental limits and remain dormant until local conditions become suitable. Therefore, the composition of propagule assemblages is expected to differ from “adult” assemblages. This offers various opportunities for a better understanding of foraminiferal reactions to environmental changes and also of the variability of living foraminiferal populations throughout the year.

To date, propagule assemblages have only been analyzed “passively” through growth experiments with propagule banks under laboratory conditions. Here, we apply for the first time a combination of a multi-week cultivation experiment and eDNA metabarcoding of the different size fractions.

Sediment samples were taken from a shallow lagoon in Corfu (Greece) and sieved over 63 μm to separate the propagule bank from the coarser fraction. The in-situ material of the sampling site was used as a baseline for the subsequent experiment (T0). The finer fraction (<63 μm) was set up in a culture experiment for 15 weeks under stable conditions (22°C, 38 psu, constant aeration). The cultures were repeatedly harvested for grown foraminifera (>63 μm) every 5 weeks (T1–T3). At the same intervals, samples were taken and re-sieved over 63 μm for eDNA metabarcoding of both size fractions.

The morphology-based count data of the foraminiferal specimens revealed significantly different assemblage compositions after each harvest (T0–T3). The differences between the in-situ (T0) and

the experimental samples (T1–T3) were most distinct, indicating a specific composition of the propagule bank. The differences between in-situ and experimental assemblages as well as the shifting assemblage compositions over time were mirrored by the metabarcoding data from the respective intervals. Our results highlight the potential for metabarcoding to complement and expand insights gained from morphology-based approaches in foraminiferal studies.