Comparison of destructive and non-destructive DNA extraction methods for the metabarcoding of arthropod bulk samples

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Abstract

DNA metabarcoding is routinely used for biodiversity assessment, especially targeting highly diverse groups for which limited taxonomic expertise is available. Various protocols are currently in use, although standardization is key to its application in large-scale monitoring. DNA metabarcoding of arthropod bulk samples can be either conducted destructively from sample tissue, or non-destructively from sample fixative or lysis buffer. Non-destructive methods are highly desirable for the preservation of sample integrity but have yet to be experimentally evaluated in detail. Here, we compare diversity estimates from 14 size sorted Malaise trap samples processed consecutively with three non-destructive approaches (one using fixative ethanol and two using lysis buffers) and one destructive approach (using homogenized tissue). Extraction from commercial lysis buffer yielded comparable species richness and high overlap in species composition to the ground tissue extracts. A significantly divergent community was detected from preservative ethanol-based DNA extraction. No consistent trend in species richness was found with increasing incubation time in lysis buffer. These results indicate that non-destructive DNA extraction from incubation in lysis buffer could provide a comparable alternative to destructive approaches with the added advantage of preserving the specimens for post-metabarcoding taxonomic work.

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