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METABARCODING REVEALS BIODIVERSITY TRENDS IN FOREST ECOSYSTEMS

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ABSTRACT

The bottleneck of morphological taxonomy is a major obstacle to the detection of biodiversity trends. Here, we demonstrate the use of DNA metabarcoding to gather biodiversity data for forest arthropods, generating statistically powerful datasets that can detect fine-scale trends and guide environmental management.

In collaboration with Forest Research, Malaise trapping was carried out for eight consecutive weeks in fifteen stands of a UK plantation forest, each with a crop of either pure pine, pure oak or mixed oak/pine. Sequencing of the 120 bulk samples generated a dataset of more than 600 arthropod species across many taxonomic groups. Pure pine sites had lower species richness than oak or mixed sites but contained many specialists, suggesting that even monocultures can make an important contribution to regional biodiversity within a varied matrix of plantation forest stands. Arthropod community composition was explained by undergrowth density and the ratio of conifer/broadleaf trees, and it also showed a very regular succession over the eight week sampling period. This study demonstrates the power of the approach for revealing community-level trends and underlines the crucial importance of controlling for time when undertaking biodiversity surveys.

Metabarcoding allows invertebrate biodiversity to be treated as a true response variable that can be measured repeatedly over time and space. In the context of climate change, it can function as a highly sensitive surveillance tool to (1) detect community changes associated with a changing environment, (2) map changes in species distributions, and (3) provide early warning of the arrival of invasive non-native and pest species.



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