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Monitoring (functional) insect biodiversity in tropical agroecosystems: The potential for a DNA-based monitoring approach

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Abstract

Biodiversity and particularly functional insect diversity are key contributors to agroecosystem resilience and productivity, especially in tropical smallholder agroecosystems. Monitoring insect biodiversity is essential for understanding (tropical) agroecosystem functioning and guiding more sustainable agricultural management. DNA-based environmental monitoring is increasingly seen as an alternative to traditional monitoring methods that remain constrained by scalability, required expertise and cost. Here, we explore an integrated DNA-based monitoring approach to assess arthropod diversity across ten coffee farms in Anserma (Caldas, Colombia), comparing five large monoculture and five small diversified production systems.

We combined standardised trapping of flying and ground-dwelling arthropods (SLAM/ Malaise and pitfall traps), complemented by sticky trap sampling in 4 farms, across wet and dry seasons. Using a non-destructive DNA extraction protocol to allow counting the arthropods post-extraction and COI metabarcoding, we identified 1,870 taxa spanning 36 arthropod orders, revealing substantial arthropod diversity in coffee systems. We also show that DNA can be successfully extracted from sticky traps with simple scalable modifications to the sample handling process.

Our results indicate that sampling method strongly determines observed community composition, with minimal overlap between the sample types. This demonstrates that single-method approaches risk severely underestimating biodiversity. While local (alpha) diversity did not differ significantly between monoculture and diversified farms, total (gamma) diversity was significantly higher in diversified systems, indicating that management effects emerge primarily at larger spatial scales.

Species accumulation analyses revealed substantial undersampling, indicating that complete inventories of tropical arthropod diversity are unrealistic. Nevertheless, consistent patterns in community composition and management effects were detected, showing that meaningful insights can be obtained from DNA metabarcoding. This suggests monitoring should prioritise repeatable sampling and focus on ecologically relevant target groups rather than exhaustive species detection. Functional trait analyses showed limited differences between systems, likely because broad categories fail to capture ecological variation, especially across life stages.

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We conclude that scalable DNA-based monitoring can deliver robust biodiversity indicators for tropical agriculture, provided it integrates complementary sampling and appropriate analytical frameworks. However, limited reference databases remain a key constraint and future work should incorporate the generation of this type of baseline data.

Keywords: Biodiversity monitoring, DNA, insects, tropical agroecosystems