Plant-derived environmental DNA complements diversity estimates from traditional arthropod monitoring methods but outperforms them detecting plant-arthropod interactions

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Abstract

Our limited knowledge about the ecological drivers of global arthropod decline highlights the urgent need for more effective biodiversity monitoring approaches. Monitoring of arthropods is commonly performed using passive trapping devices, which reliably recover diverse communities, but provide little ecological information on the sampled taxa. Especially the manifold interactions of arthropods with plants are barely understood. A promising strategy to overcome this shortfall is environmental DNA (eDNA) metabarcoding of arthropods from plant material they have interacted with. However, the accuracy of this approach has not been sufficiently tested. In four experiments, we exhaustively test the comparative performance of plant-derived eDNA from surface washes of plants and homogenized plant material against traditional monitoring approaches. We show that the recovered communities of plant-derived eDNA and traditional approaches only partly overlap, with eDNA recovering various additional cryptic taxa. This suggests eDNA as a useful complementary tool to traditional monitoring. Despite the differences in recovered taxa, estimates of community α - and β -diversity between both approaches are well correlated, highlighting the utility of eDNA as a broad scale tool for community monitoring. Last, eDNA outperforms traditional approaches in the recovered with eDNA. Our results highlight the value of plant derived eDNA analysis for large-scale biodiversity assessments that include information about community level interactions.

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