

Revegetation rewilds the soil bacterial microbiome of an old field

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The global biodiversity crisis is being driven by land clearing and land-use change. Targeted action is required and requires effective and functional landscape restoration, as emphasised by IPBES. Successful restoration requires accurate and detailed monitoring to inform adaptive management interventions. Unfortunately, traditional monitoring methods often require taxonomic expertise and time consuming, expensive, and often unstandardized field surveys. Additionally, functionally diverse microbial communities often go unmonitored. High-throughput amplicon sequencing of environmental DNA (eDNA; e.g. soil) has been shown to be a scalable, efficient, and standardisable way of quantifying microbial communities. I will present a novel use of high-throughput amplicon sequencing of soil eDNA to monitor bacterial community turnover in an old field that has undergone revegetation. We sampled soil eDNA across a revegetation chronosequence, an open old field, and remnant stands. We sequenced the standard bacterial barcode 16S rDNA to quantify bacterial community turnover across this chronosequence. We show that revegetation of this old field returns soil bacterial communities to a remnant state ca. 8 years post revegetation. Land-use legacy effects did not hinder revegetation driving the changes in belowground bacterial communities over time. Our study is a first step in demonstrating that high-throughput amplicon sequencing of soil eDNA is a rapid, scalable, and standardisable tool for monitoring soil microbiomes during old field restoration.