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Multi-taxa eDNA metabarcoding to monitor the degradation and restoration of belowground biota in agricultural soils

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Land use change drives shifts in the taxonomic and functional diversity of soil organisms. Soil biota response will depend on both local scale agricultural management, and regional scale environmental conditions, with the diverse pool of soil taxa unlikely to respond in a uniform manner. To monitor the effect of land management and potential restoration efforts, we require techniques which can be deployed at various spatial scales, and which account for the high diversity of these communities. In this presentation, we describe the role of eDNA metabarcoding targeting a broad range of taxa to detect and parameterise these responses. We present the results of studies of habitat conversion of humid and dry forests in French Guiana and Colombia respectively, before detailing how the method will be used to monitor agricultural pasture in the UK undergoing conversion to “regenerative” management. In these studies, we combine measures of alpha and beta diversity to account for shifts in species abundance dependent on habitat management, and assignment of functional groups to infer shifts in soil biota functioning. Overall, we find that results track expected shifts in biota, for example a replacement of a broad diversity of plant eDNA to a community signal largely dominated by grasses. Agricultural soils are characterised by a greater proportion of bacteria and protists associated with the cycling of labile nitrogen. We conclude by pointing to the weaknesses of the method, and highlighting the importance of complimentary methods in spite of fruitful deployment across varied habitats.