

Development of metabarcoding for tracking changes of soil fauna community under stress by application of ash

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Background

Ash is a waste product from combustion of bio-fuel in power plants. Application of ash on soil ensures nutrient recycling, but detrimental ecotoxicological consequences may arise because ash is a complex mixture that may contain compounds affecting soil invertebrates and their food and habitat condition. Here, we study the effects of ash on the abundance and composition of the soil fauna community. DNA metabarcoding, which couples the principle of DNA barcoding with next generation sequencing technology, has the potential to simplify community diversity monitoring.

Method

We start out by comparing the morphospecies approach (Fig. 1B), coupling a morphospecies sorting with DNA barcoding, with three molecular approaches, differing in the types of DNA extracted from soil samples: total soil DNA, extracellular DNA and DNA gained from animals collected from the soil. In order to target all faunal groups, we use a set of three mini-barcodes based on the mitochondrial cytochrome oxidase I encoding gene (COI), histone 3 protein encoding gene (H3) and 18S regions, respectively (Fig. 1A).



Perspectives

Compared to classic biodiversity data sets, samples subject to metabarcoding are taxonomically more comprehensive, many times quicker to produce, less reliant on taxonomic expertise and auditable by third parties. Metabarcoding allows for the precise estimation of pairwise community dissimilarity (β diversity) and within-community phylogenetic diversity (α diversity).

The long term monitoring data could help maintain the soil ecosystem and improve the management of ash.

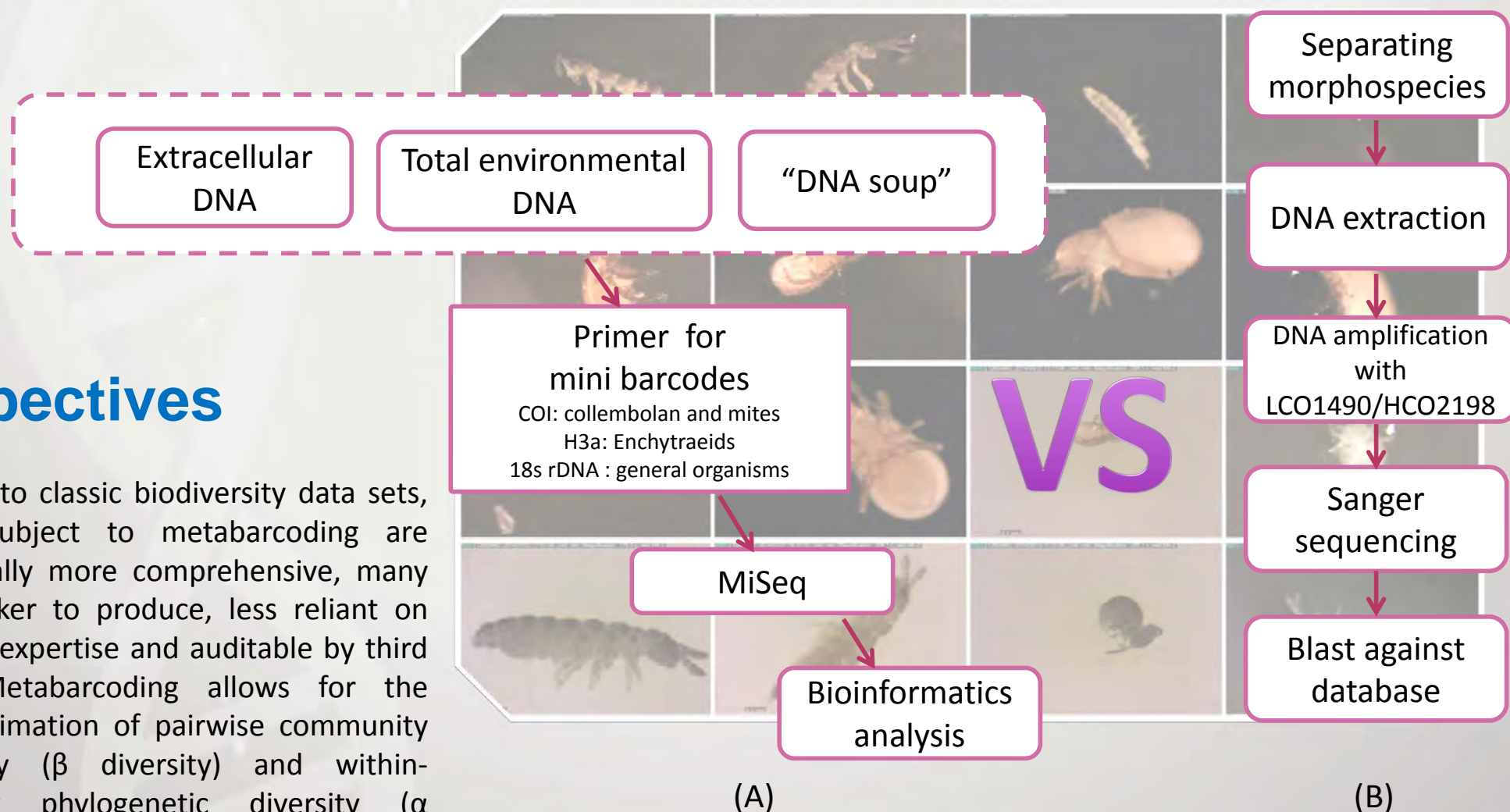


Fig.1: Diagramtic of the development of DNA metabarcoding to be used to detect changes in the soil mesofauna biodiversity.

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