

# Soil nematode communities 18S metabarcoding techniques: Comparing and improving DNA extraction

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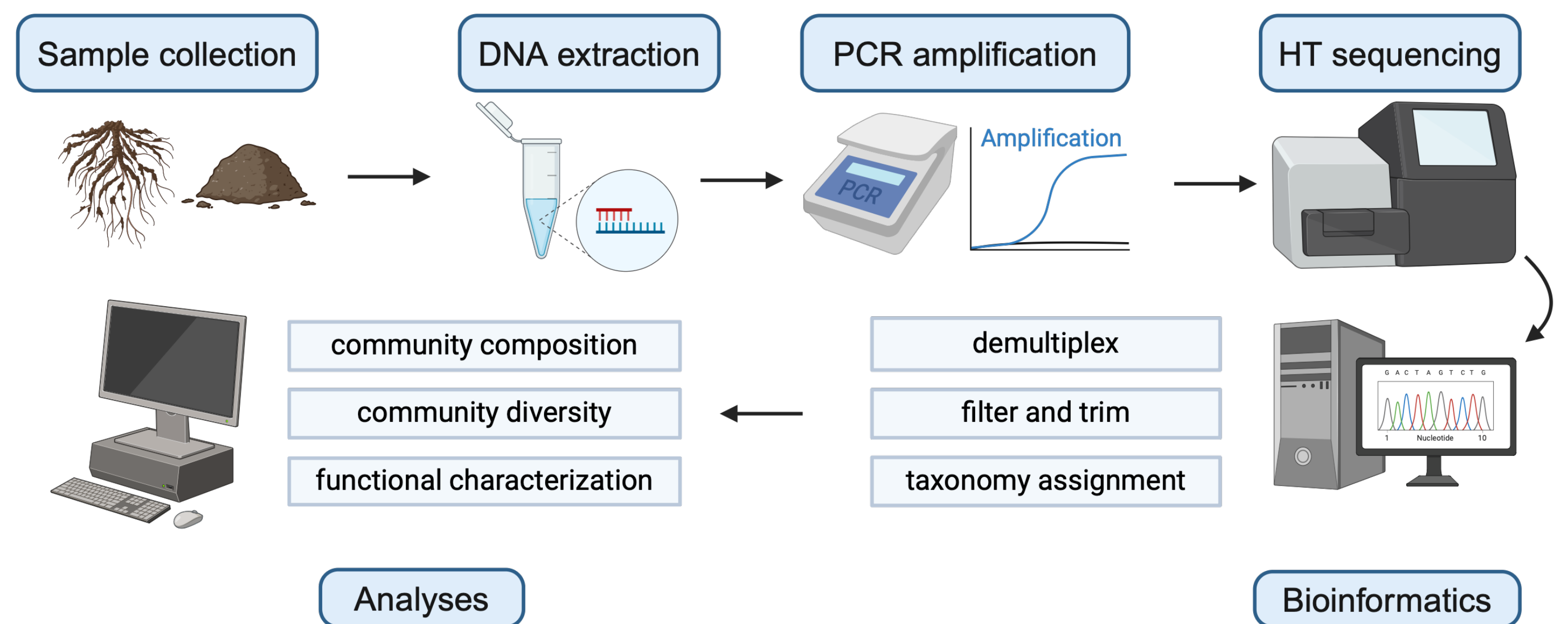
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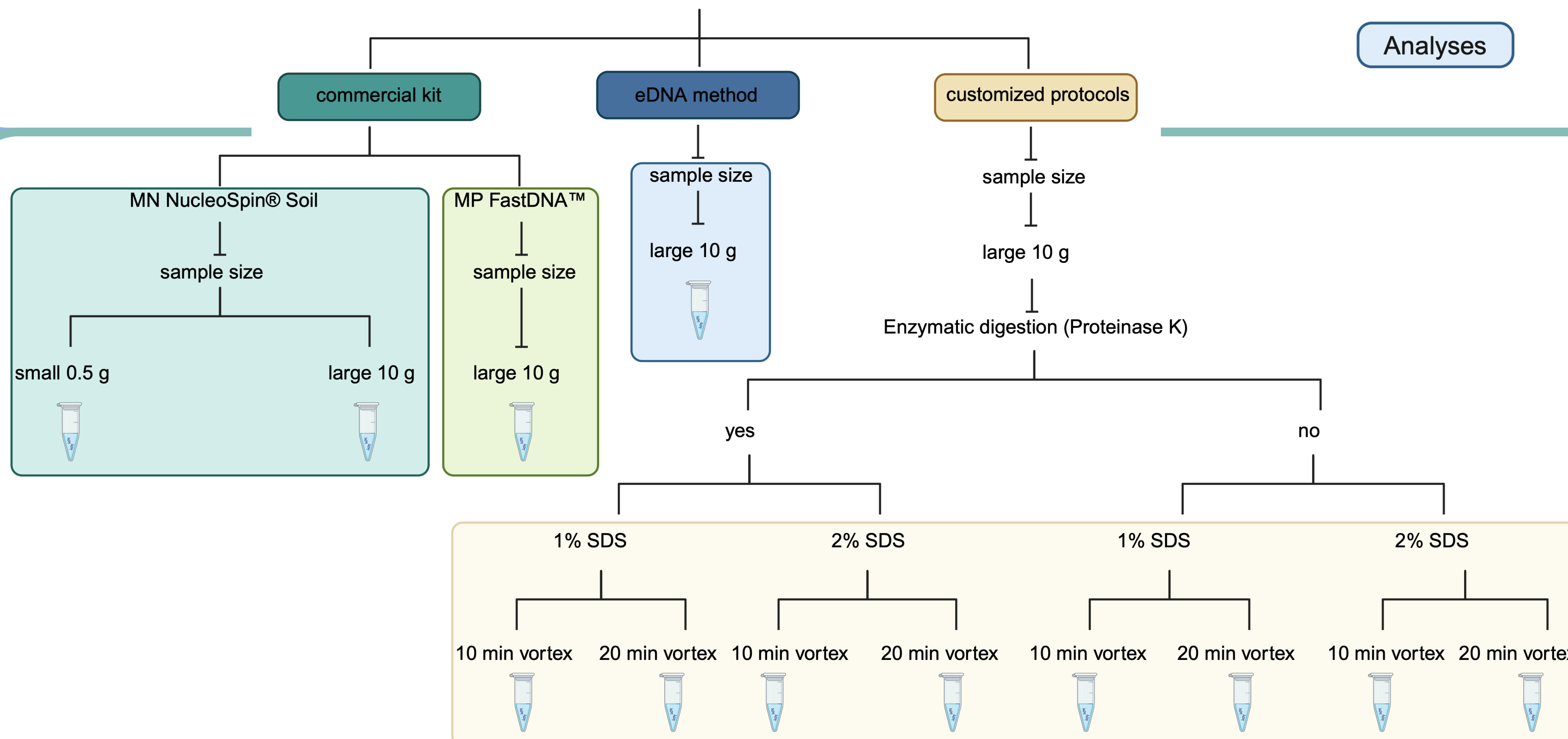
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## Background & Objectives

- Nematodes are abundant and diverse in soil, serving as vital bioindicators for soil ecology and health.
- Metabarcoding techniques are not standardized and are still under development for soil animals.
- To improve the quality of nematode metabarcoding data, we explored the effect of various DNA extraction procedures adapted to larger soil samples on soil nematode biodiversity estimates.



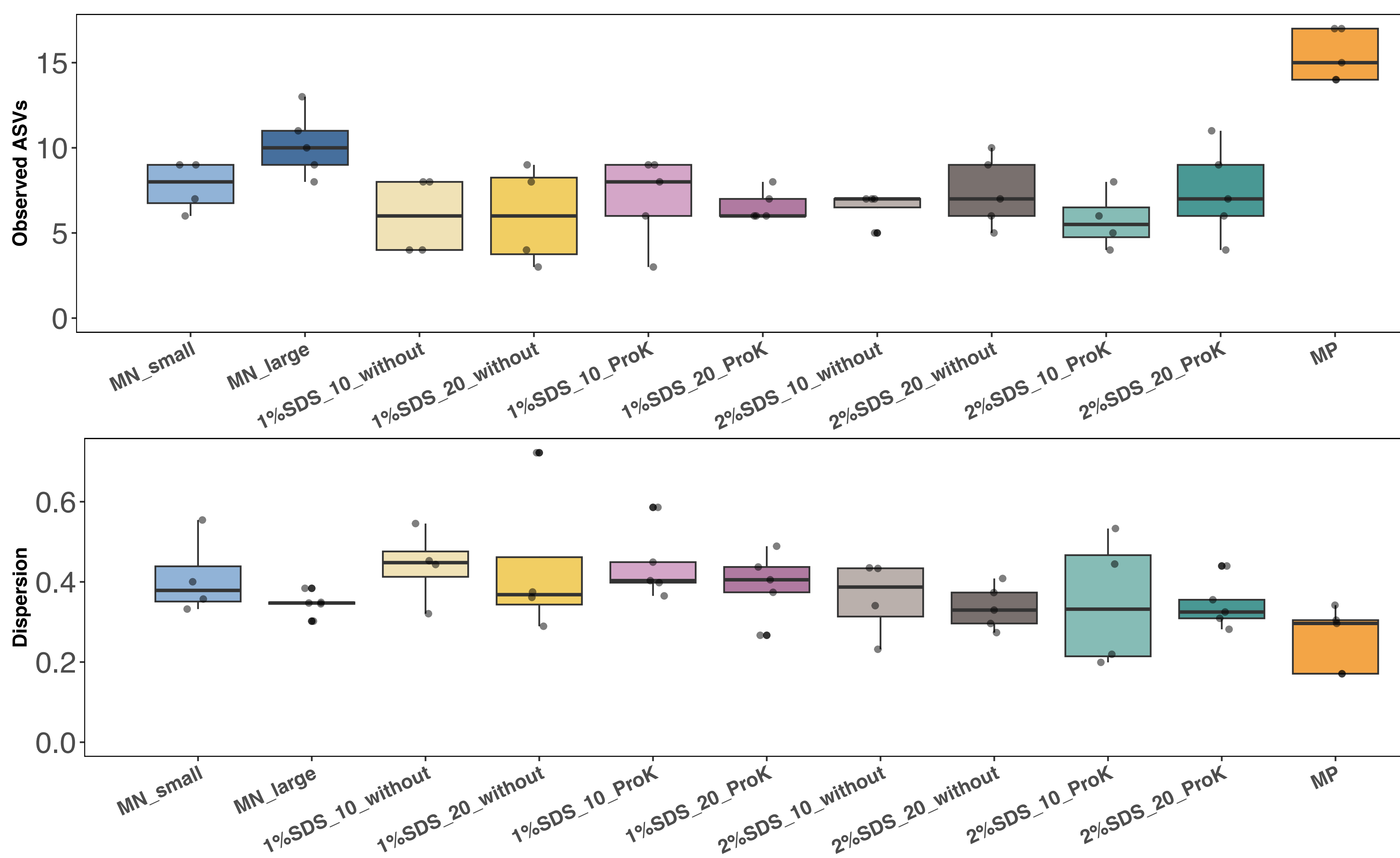
## DNA extraction methods



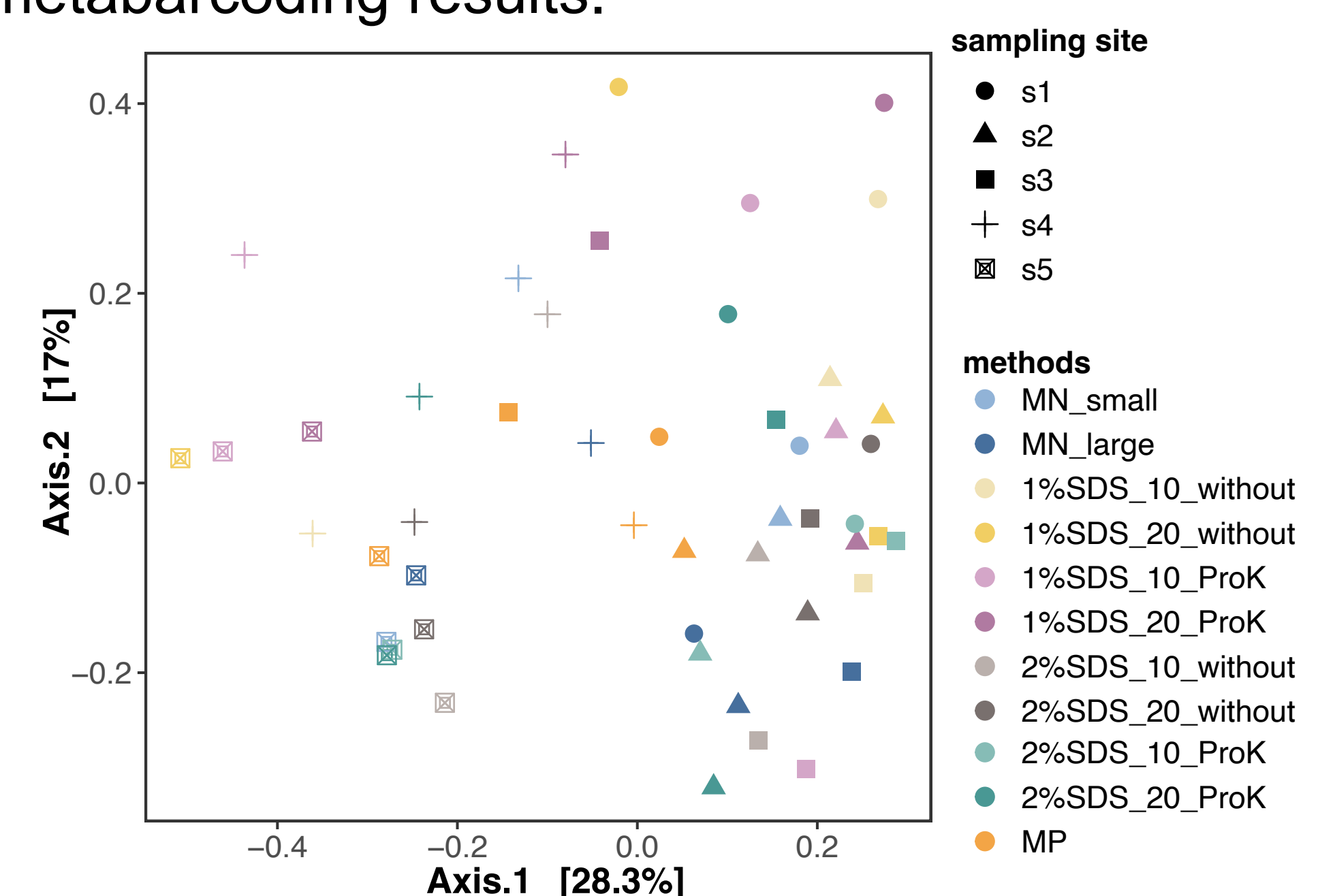
## Materials & Methods

- Total DNA was extracted from soil samples and sequenced with a nematode-specific 18S rRNA primer set (Nemf/18Sr2b) on an Illumina MiSeq platform.
- Different DNA extraction methods were tested for large soil samples (10 g), focusing on the effectiveness of different lysis buffers, bead beating durations, and enzymatic digestion applications.
- Sequencing data were filtered, trimmed, merged using the DADA2 pipeline, followed by taxonomy assignment using the PR2 reference database.

## Results

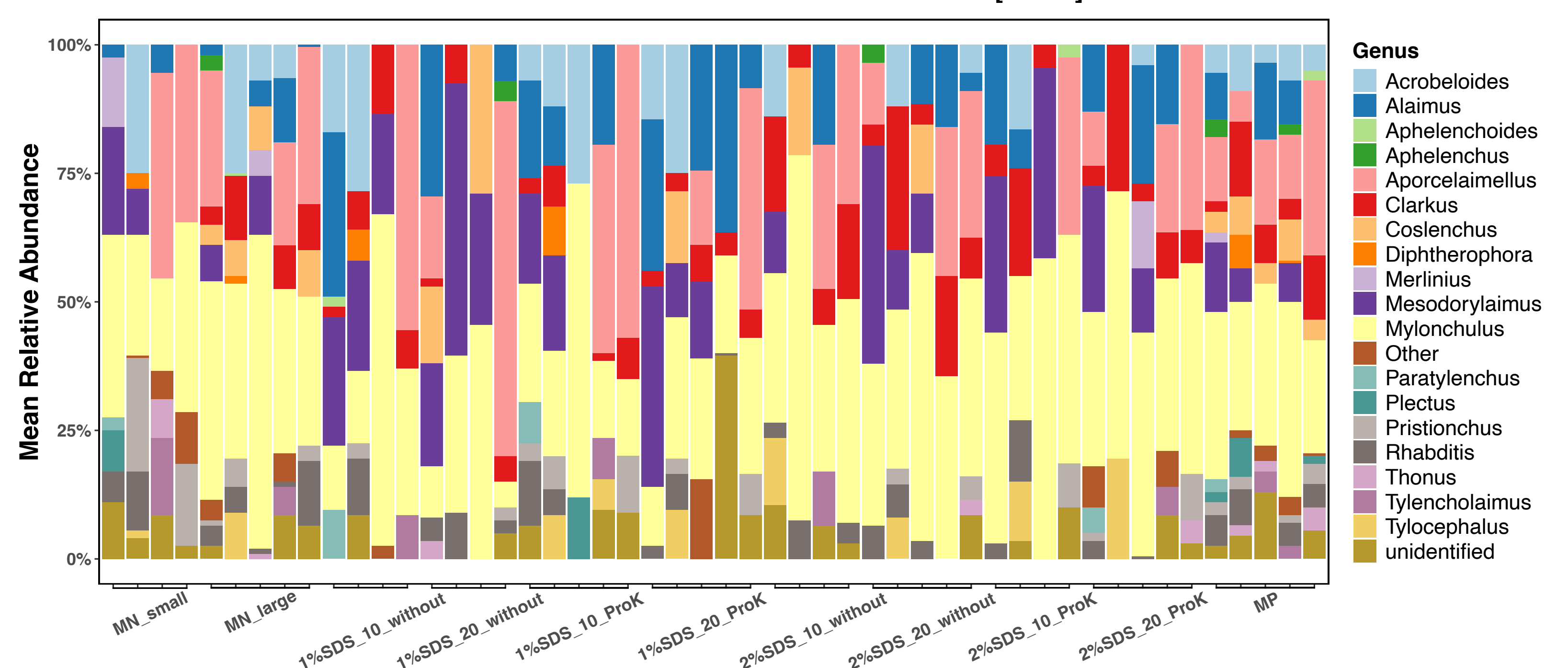


- DNA extracted by MP FastDNA™ Kit resulted in significantly higher nematode alpha diversity, and lower variability between samples compared to all other methods.
- The clustering of samples is influenced more significantly by the sampling sites than by the DNA extraction methods.
- Mylonchulus*, *Aporcelaimellus*, and *Mesodorylaimus* are the most prominent nematode genera according to metabarcoding results.



## Remarks & Conclusions

- Commercial kits outperformed both eDNA and customized extraction protocols, exhibiting more consistent results between replicates.
- Kits that used larger soil samples detected higher alpha diversity, but similar dominant taxa as those which used smaller sample sizes.
- DNA extraction methods must be adapted to the scientific objectives.



Gefördert durch

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