

Monitoring soil biodiversity in nature reserves in England – a role for metabarcoding

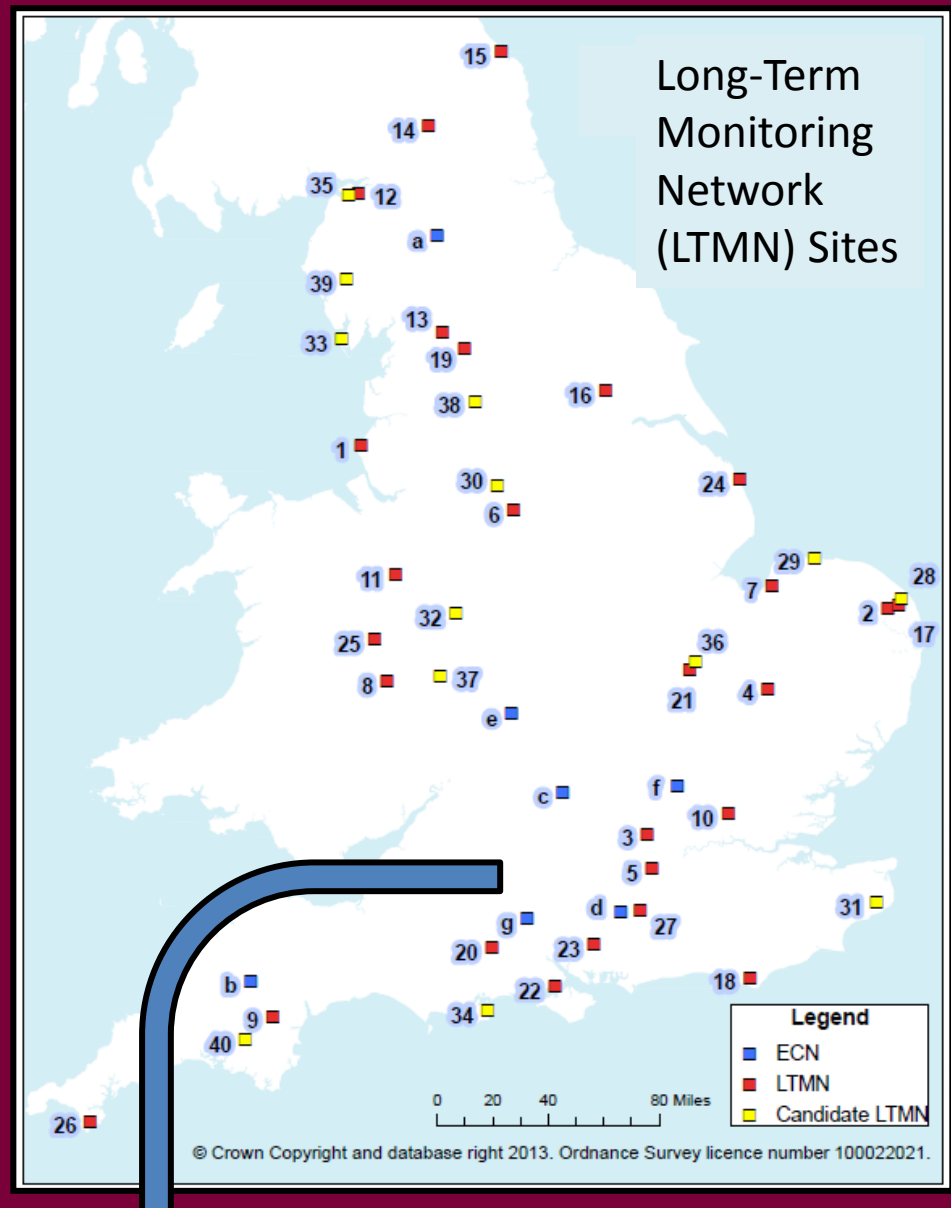


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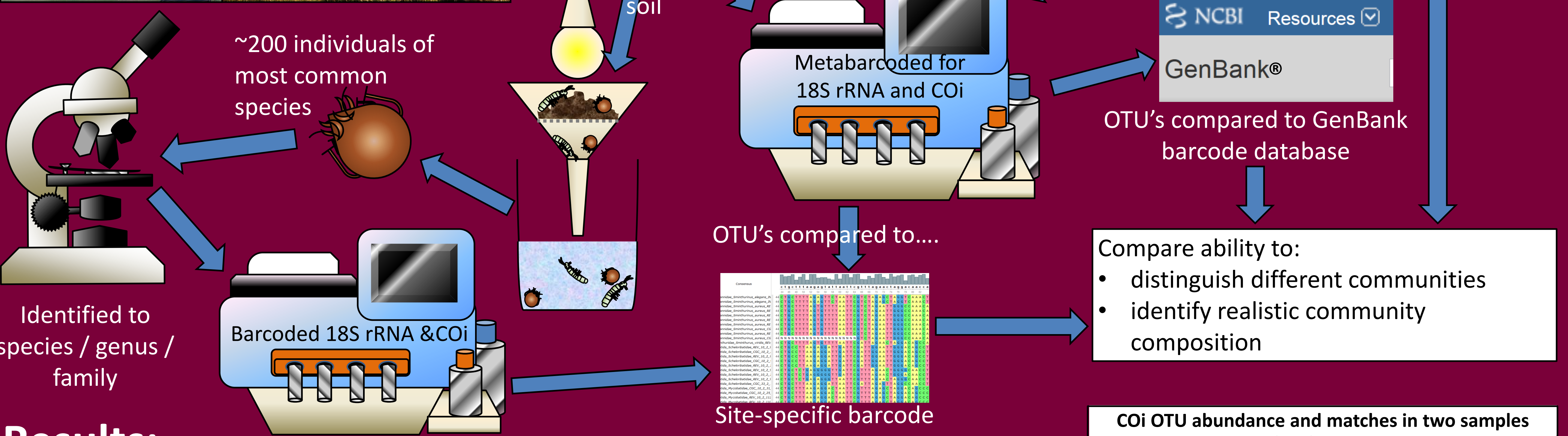
Rationale:

Natural England assesses soil biodiversity as part of our monitoring across 40 National Nature Reserves to detect long-term environmental trends. Tullgren extracts of soil mesofauna are proving challenging to identify using trained volunteers. Could metabarcoding be a rapid, cost-effective approach for monitoring soil mesofauna and characterising their communities?

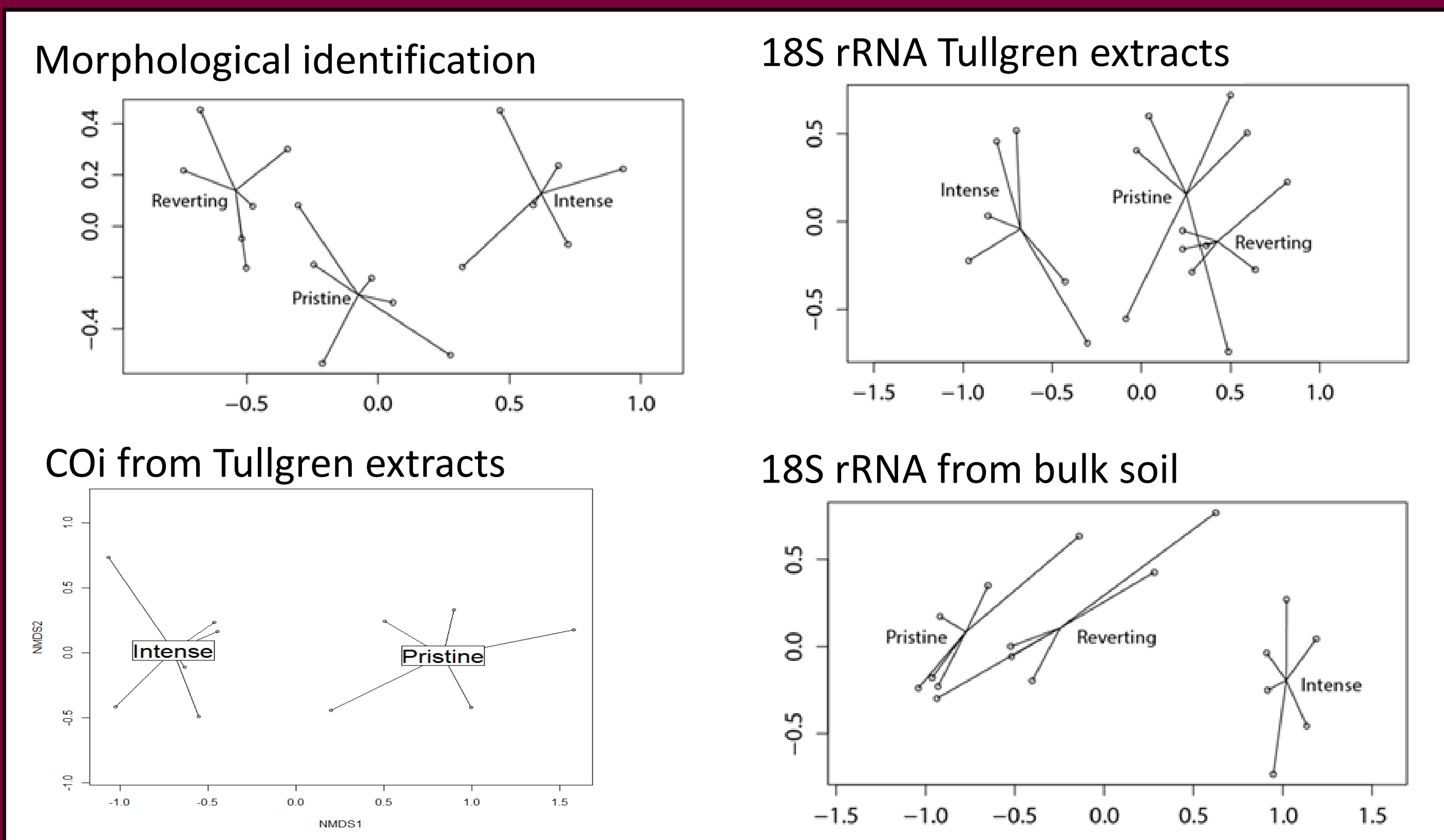


Method:

Two sets of six samples were taken from three chalk grasslands: ancient species-rich, agriculturally improved and naturally reverting grassland.



Results:



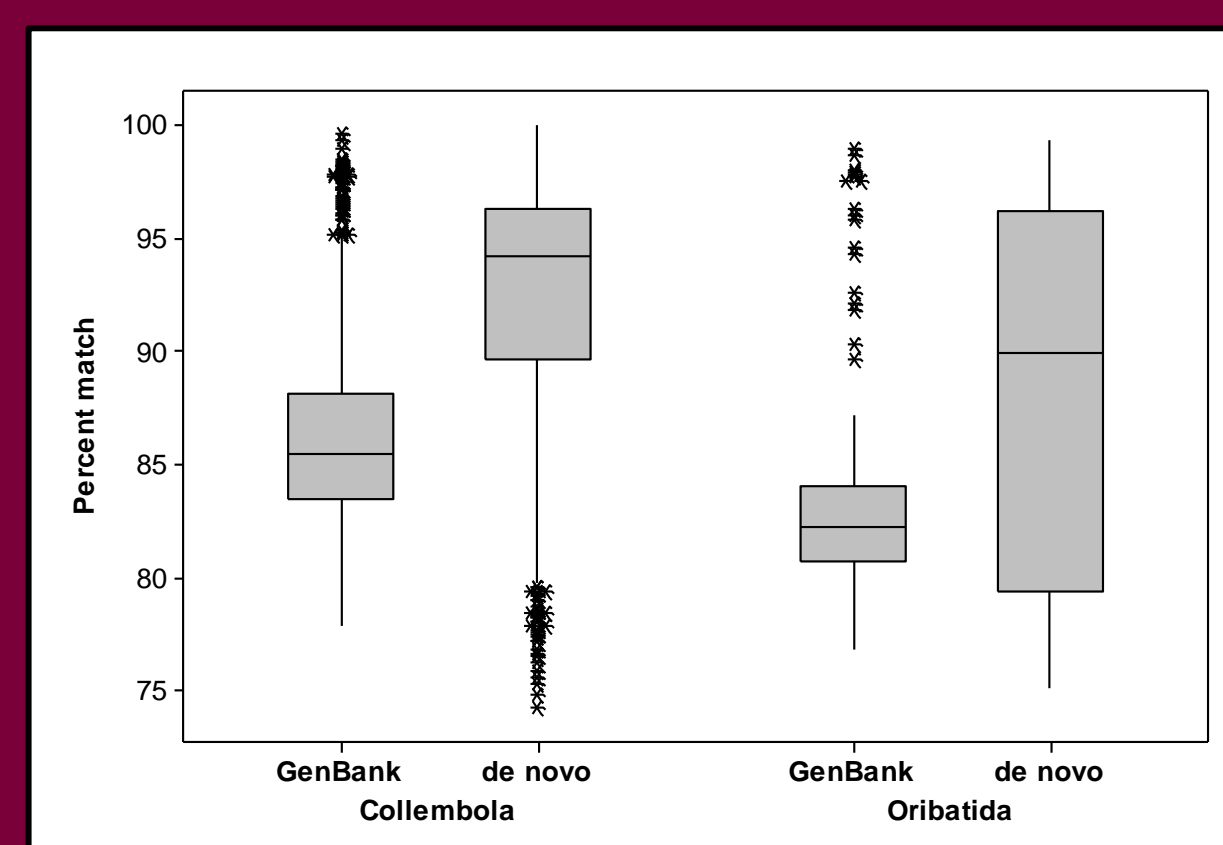
Compatibility: All approaches showed distinct and congruent differences in soil communities between grassland types. Above: first and second axes from non-metric multidimensional scaling analysis.

Methods: The minibarcode primers used for COI analysis of bulk soil resulted in poor amplification, and require more optimisation. Folmer primers worked well for collembola and oribatids in Tullgren extracts.

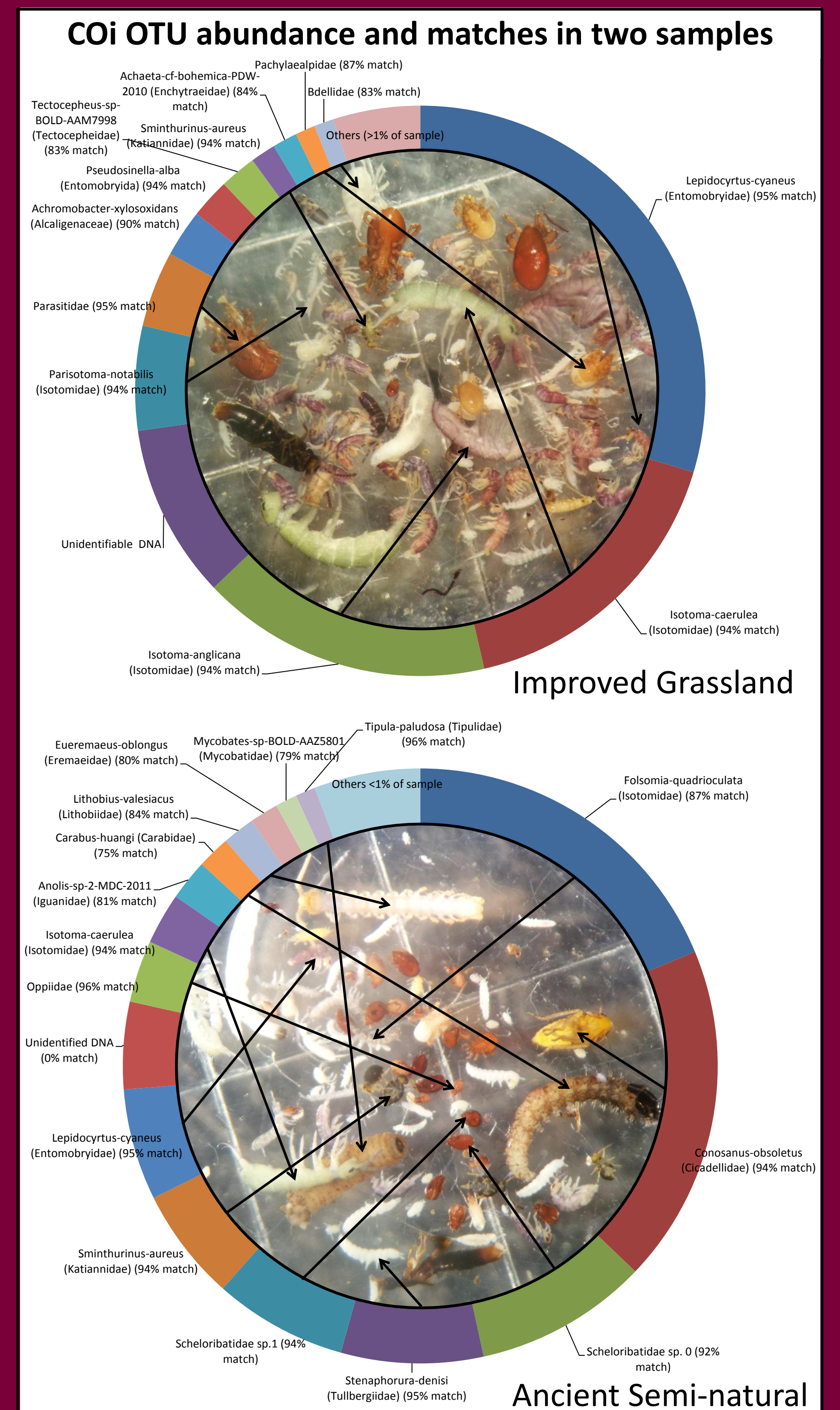
Conclusions:

- Metabarcoding shows good potential for rapid characterisation and monitoring of soil mesofauna communities, but better COI primers are needed for some groups and for bulk soil approaches.
- More effort to generate barcodes for more soil species will help identify realistic soil communities.

Community composition: 18S rRNA represented broad soil communities (mesofauna, plants, algae, fungi and protists) but gave a poor match to ecologically appropriate species in GenBank. There were more collembola OTUs in agriculturally improved grassland and more acari in the species-rich grassland soil in Tullgren extracts.



The *de-novo* site-specific database significantly improved matching of COI metabarcode OTUs over GenBank alone, describing more ecologically realistic communities.



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