



A national-scale field study to evaluate potential N₂O emissions: Community composition predicts soil potential denitrification in Irish grasslands

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Community composition predicts soil potential denitrification in Irish grasslands



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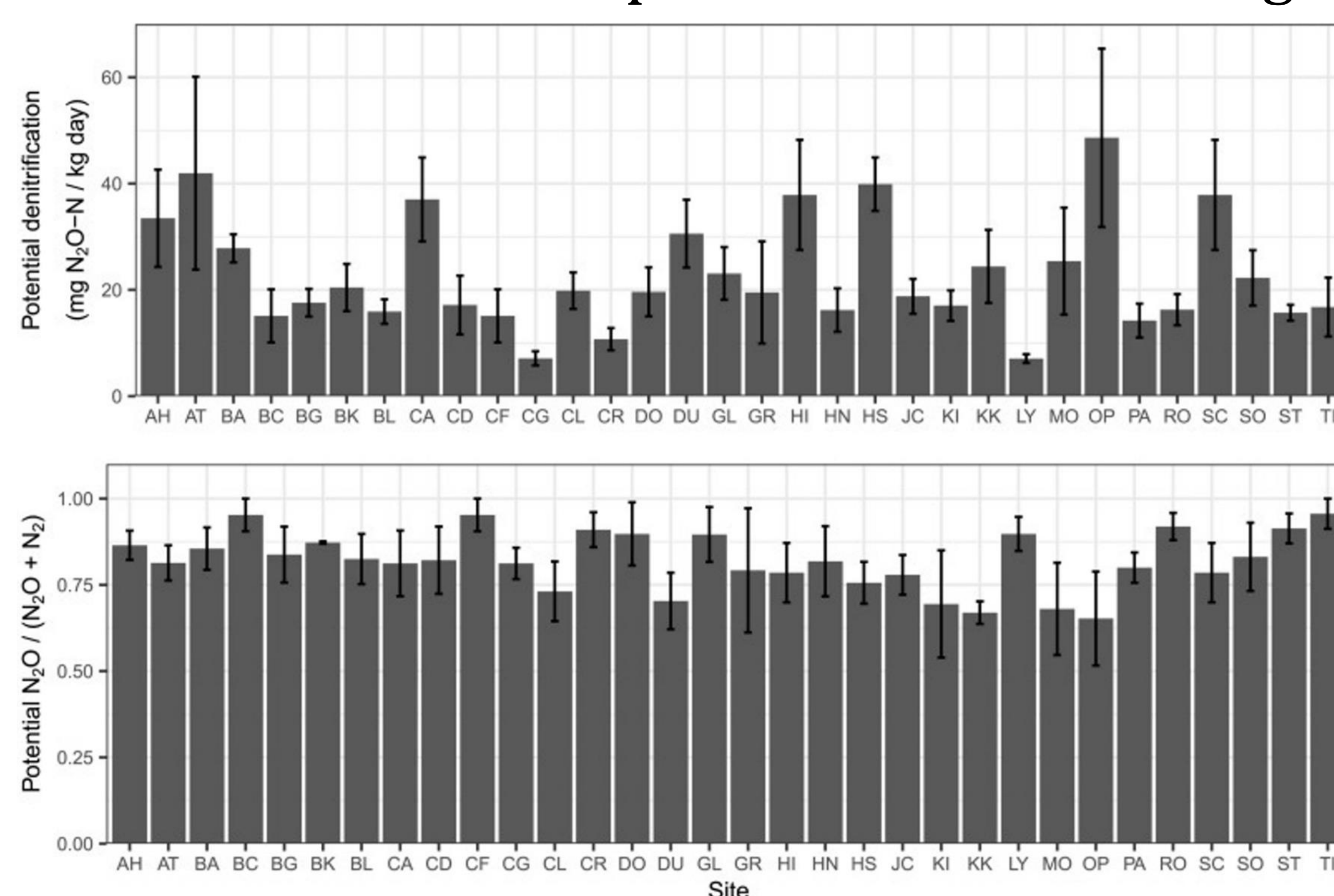
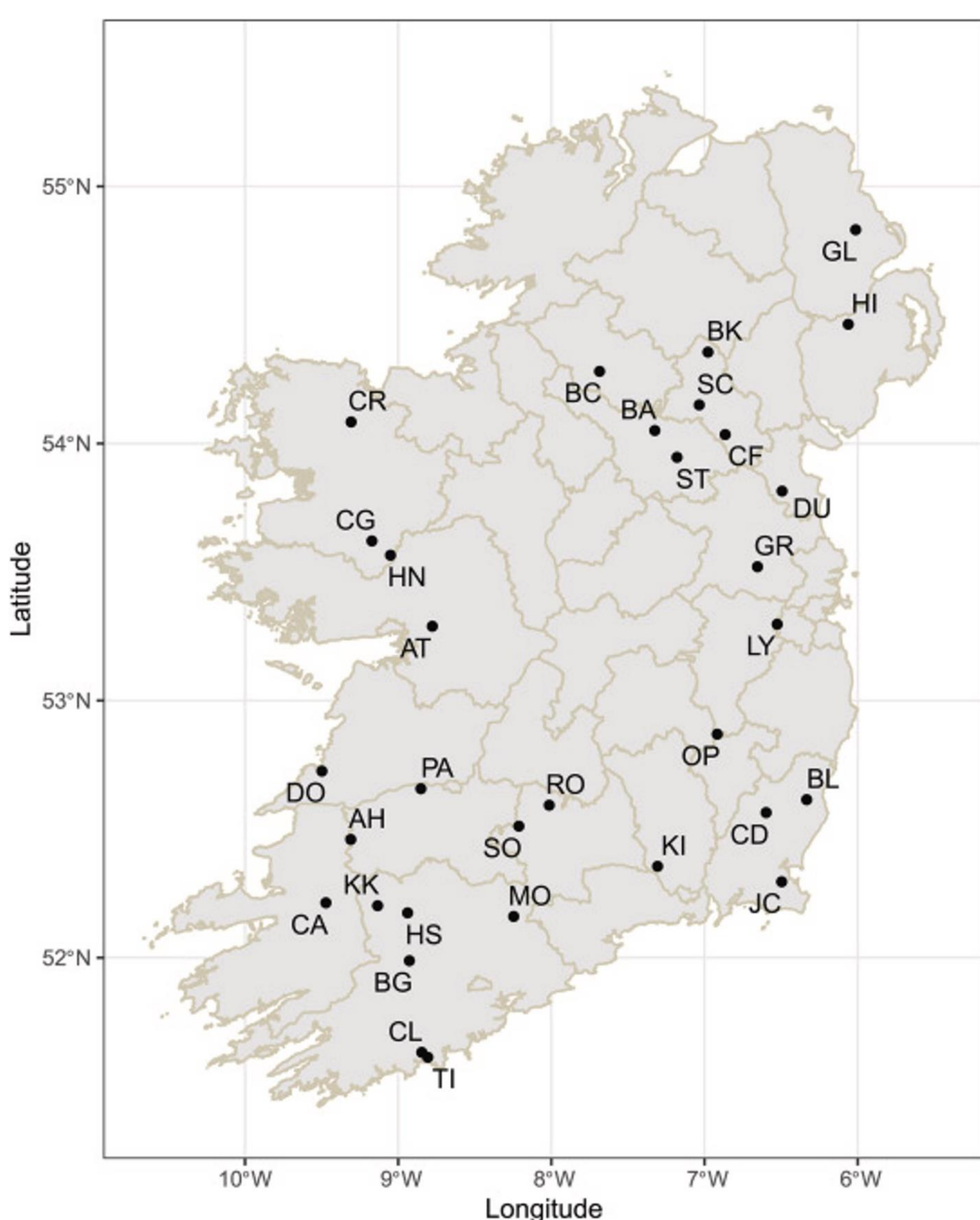
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A national-scale field study to evaluate potential N₂O emissions:

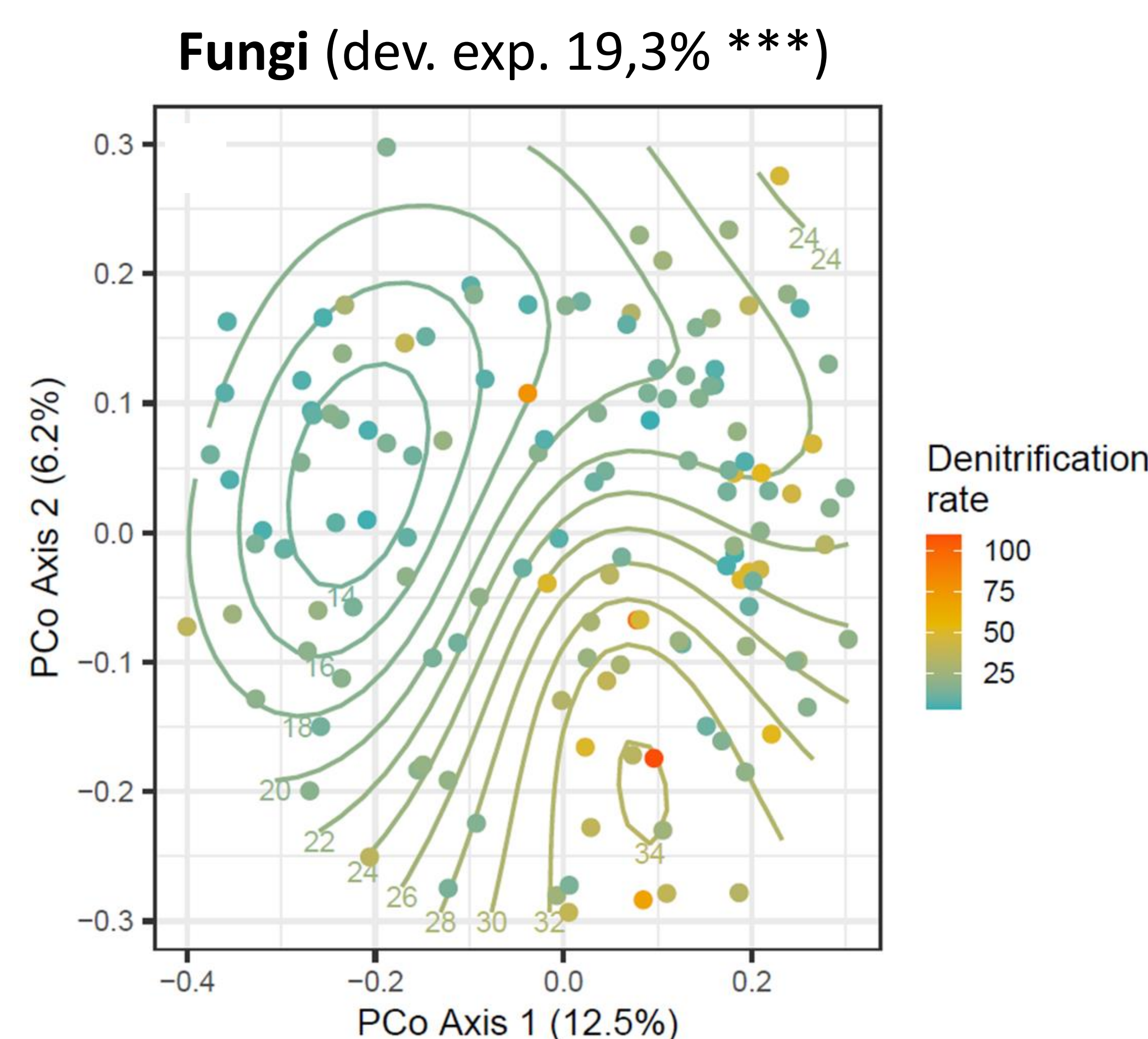
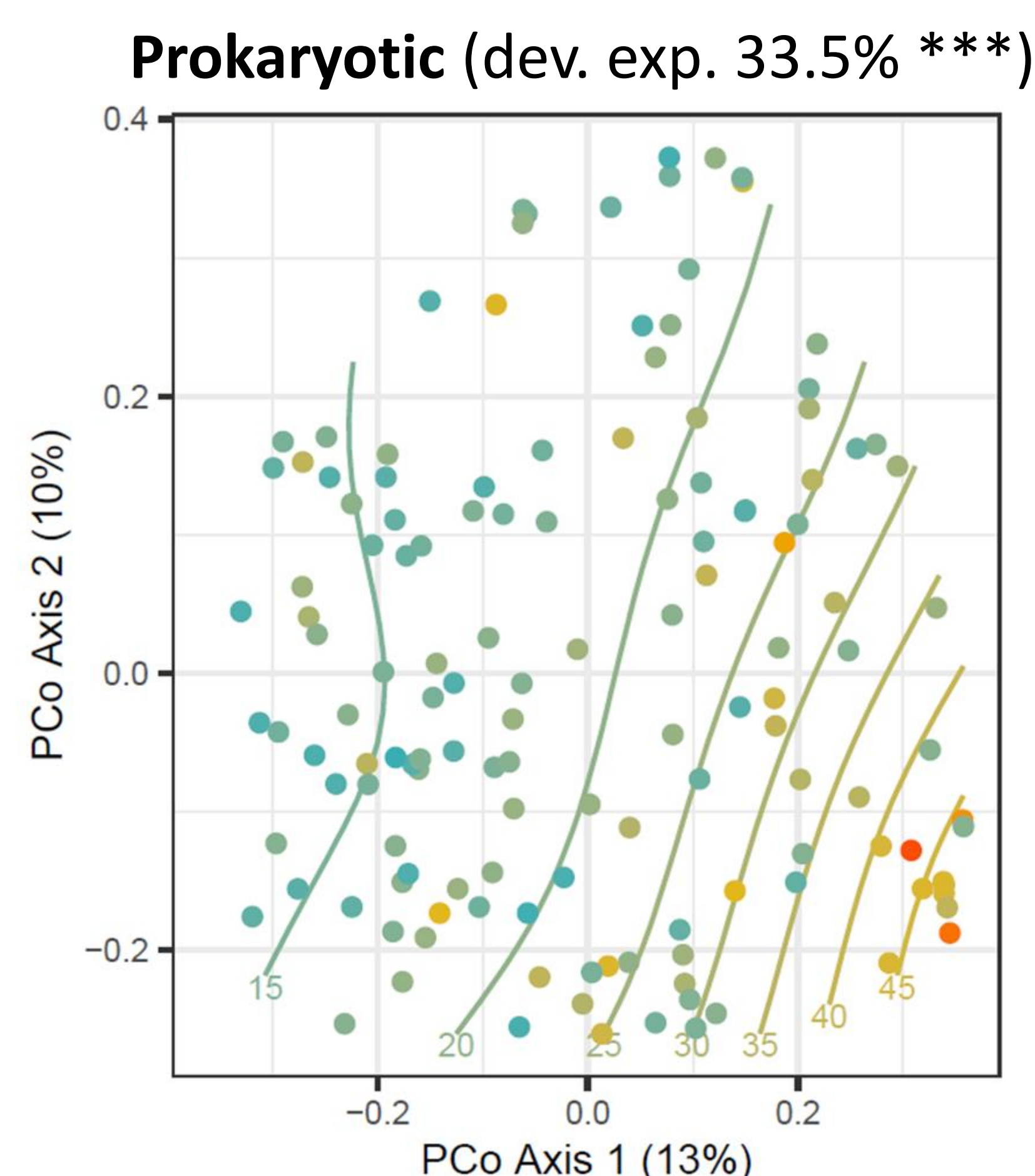
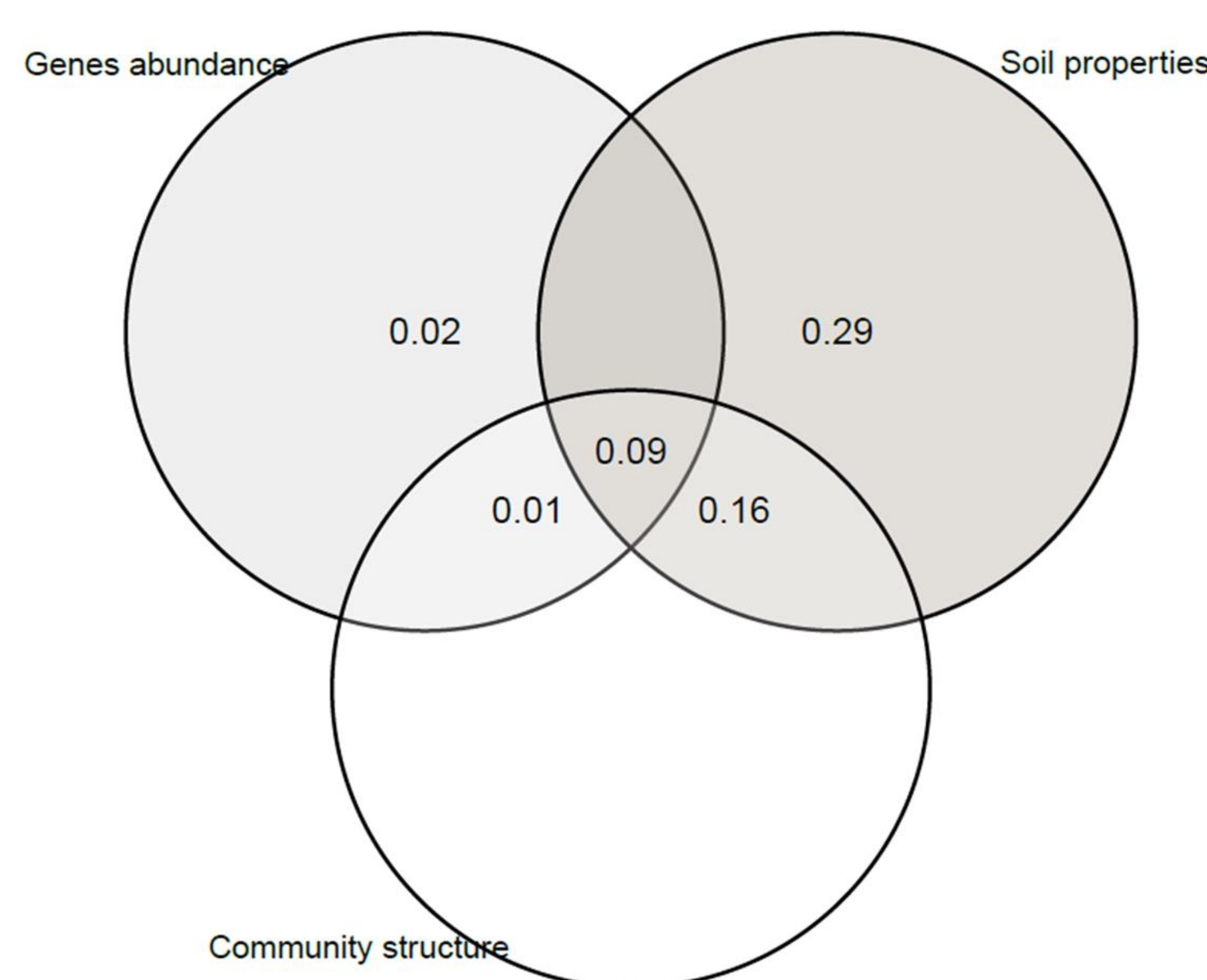
136 samples collected in 32 sites in Ireland, together with soil physicochemical properties, climate, functional genes abundance and soil communities composition. Soil potential denitrification was assessed under optimal conditions using incubations.



Soils' potential denitrification varied greatly between sites and even at the same sites, with soil P, N and pH being the most predictive. In most of the soils, emissions were in the form of N₂O rather than N₂.

Among biotic factors, prokaryotic community composition was more predictive than the denitrifiers community abundance:

We evaluated the prokaryotic (16S) and fungal (ITS) community composition using Illumina sequencing and determined the abundance of genes involved in denitrification (*nirK*, *nirS*, *nosZ* clade I and II) with qPCR.



The prokaryotic community composition better predicted the potential denitrification rate. The relative abundance of **Actinobacteriota** and **Crenarchaeota** was positively correlated to potential denitrification ($R = 0.35$ & 0.41 , respectively).

Long story short...

- Soil phosphorus was as important predicting PD as was pH and total nitrogen.
- The prokaryotic community was more predictive of soil PD than the fungal community.
- Soil community structure, rather than denitrifiers' community abundance, was an important predictor.
- Actinobacteriota and Crenarchaeota were correlated to complete denitrification.

Our open access paper



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