

Greenhouse gas emissions and microbial community structuring in NZ pasture soils

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It is well established that microbial communities contribute to ecosystem processes like N cycling. While regulators of communities and emissions have been independently established using a few sites, validation of these regulators by comprehensive studies across large geographic, climactic and edaphic ranges are lacking. Prior work using 13 NZ and Irish soils, were able to link microbial community composition and N₂O emission potential with pH and soil classification. Here we combined high-resolution denitrification kinetics and 16S rRNA gene amplicon sequencing in a study covering 50 pasture soils from across 11 of New Zealand's major soil groups, 10 geographical zones and under different grazing systems (high input dairy units to dry-stock grazing). Our results confirmed pH as a conserved regulator of both microbial community structuring and emission potential. However, community structuring based on soil classification was less clear within the 50 soils data set, whereas rainfall was identified as a potentially important driver of community composition. Further, we identify specific microbial populations associated with emissions, and partition the effect of other edaphic factors in predicting microbial community and emissions potential.