

Soil nitrification/denitrification kinetics coupled with population dynamics demonstrate diverse life-strategies for different microbial functional groups

Md Sainur Samad¹, Charlotte Johns², Dr Karl Richards³, Dr Gary Lanigan³, Prof Lars Bakken⁴, Dr Cecile de Klein⁵, Prof Timothy Clough², [Dr Sergio Morales¹](#)

¹Department of Microbiology and Immunology, Otago School of Medical Sciences, University of Otago, ²Department of Soil and Physical Sciences, Lincoln University, ³Teagasc, Environmental Research Centre, ⁴Department of Environmental Sciences, Norwegian University of Life Sciences, ⁵AgResearch Invermay

Nitrous oxide (N₂O) emission under ruminant urine patches is often ascribed to heterotrophic denitrification and possibly ammonia oxidation. Phenotypic evidence (gas kinetics) supports this notion, however genotypic information is still lacking, particularly transcription profiles and identification of populations linked to them. In this study we examined microbial nitrification, denitrification and nitrogen fixation processes, in order to determine community changes linked to N₂O emissions under urea deposition in pasture soils. Using repacked soil cores (1.1 mg m⁻³) in tension tables we mimicked a urine-N deposition event for over 60 days by applying urea under two different moisture contents: near saturated (high moisture content i.e. -1.0 kPa) and field conditions (low moisture content i.e. -10 kPa). Simultaneous measurements of soil chemistry (pH, NH₄⁺, NO₂⁻, NO₃⁻), N₂O emission, microbial community composition (OTUs) and functional gene abundance (for nitrification, denitrification and nitrogen fixation) at DNA (gene) and RNA (transcript) levels were performed to determine the active populations and pathways during the urine cascade. We revealed that microbial diversity (Shannon) and richness both declined under urea treatment, with different response curve and community composition under differing soil moisture conditions (high vs. low). We were also able to link soil conditions, as well as functional responses, to specific taxonomic groups (by 16S amplicon sequencing). Results suggest that different populations within nitrifiers and denitrifiers have unique responses to urea deposition, suggesting different strategies for energy utilization from urea (i.e. growth vs. maintenance or survival). Response at different times also indicates the potential for niche differentiation between ammonia oxidizing archaea and bacteria.