

EFFICACY OF SUBSURFACE DENITRIFICATION TO ATTENUATE NITRATE IN SHALLOW GROUNDWATERS

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Leaching of nitrate (NO_3^-) from grazed pastoral systems and other intensive land uses has been implicated as a key water contaminant in the deterioration of surface and ground water quality in New Zealand's agricultural catchments. The impact of NO_3^- leaching from agricultural soils, however, strongly depends on its losses, flow pathways and potential attenuation (removal) in subsurface environment.

Microbial denitrification, a multistep sequence of N reduction reactions, has been identified as one of the effective mechanisms attenuating NO_3^- in subsurface environment including shallow groundwaters. Environmental benefit of subsurface denitrification, however, may be limited if subsurface denitrification is incomplete and the terminal product of NO_3^- reduction is N_2O (a harmful greenhouse gas) rather than N_2 (an inert and harmless gas making up 78% of the atmosphere).

We are undertaking a field study assessing whether NO_3^- reduction in shallow groundwater is due to incomplete and environmentally harmful (i.e. N_2O release) or complete and environmentally benign (i.e. N_2 release) denitrification and what are the main processes and factors driving complete denitrification. We have been collecting monthly shallow groundwater samples from 6 pastoral farms located in various hydrogeological settings in Manawatu and Rangitikei River catchments. The study sites have been identified as oxidized or reduced shallow groundwater conditions.

The shallow groundwater samples are being collected and analyzed for redox parameters (i.e. dissolved oxygen, oxidation-reduction potential (ORP), pH, nitrate, nitrite, ammonium, dissolved organic carbon, iron, manganese, and sulfate) and dissolved gases N_2O and N_2 , using the standard in-field and laboratory equipment and practices. Also, the collected groundwater samples are analysed for quantification of denitrifier genes (*nosZ*, *nirS*, and *nirK*) using Quantitative Polymerase Chain Reaction (qPCR).

We found that different study sites show variability in denitrification parameters and denitrifier gene abundances. A preliminary analysis of these results will be presented and discussed in detail at the Workshop.

Editor's Note: An extended manuscript has not been submitted for this presentation.