

## Abstract

# Quantifying Gas Emissions and Denitrifying Genes in a Salt-Affected Soil <sup>†</sup>

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**Abstract:** Salinity effects on microbial community relative to greenhouse gas emissions are not well understood in salt-affected soils. A better understanding of this interaction would be useful for agricultural practices to reduce nitrogen gas losses and manage environmental pollution. We hypothesized that elevated salinity would increase the abundance of denitrifier genes resulting in a low rate of gas emissions. Objectives of this study were to measure induced-soil greenhouse gas emissions and to quantify denitrifying genes in a salt-affected soil over a 3-week incubation period. This incubation study was conducted by submerging field-moist samples of an acid sulphate soil in different saline solutions. A quantitative polymerase chain reaction (qPCR) was used to quantify the abundance of resident bacterial denitrification genes in the salt-affected soil. It was found that increased salinity caused a decrease in both flux and cumulative emission of N<sub>2</sub>O from the incubated soil, relative to fresh water. Soil respiration was significantly reduced in salinity treatments compared to the treatment of distilled water. The study results showed that elevated salinity increased the denitrifying genes in the incubated acid sulfate soil. The abundance of the *nir* genes was usually high between the first and second week of incubation, while number copies of the *nosZ* gene were significantly low at those times. The study concludes that salinity controls the biological aspects of denitrification leading to a reduction of greenhouse gas emissions. Findings from this investigation extend our knowledge about the underlying molecular ecological mechanisms of denitrification that manage nitrogen cycling in salt-affected soils.

**Keywords:** denitrifying genes; gas emissions; nitrous oxide; qPCR; salinity effects

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