## Microbial nitrogen cycle in sub-tropical peatland cloud forest and wetland ecosystems of Reunion Island

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## Abstract:

Peatlands play an important role in the regulation of carbon and nitrogen cycles. Nitrogen-rich peatlands under warm and dry conditions can be a source of  $N_2O$ , which is a potent greenhouse gas. Research on microbial activity, particularly in relation to  $N_2O$  emissions in sub-tropical peatlands and wetlands, is very limited. In the current study, we investigated two peatland cloud forest sites in Reunion Island, namely Plaine des Cafres (characterized by dominant species *Erica reunionensis* and *Alsophila glaucifolia*) and Forêt de Bébour (featuring *Erica reunionensis* exclusively), alongside one RAMSAR wetland site located in Saint Paul. Our objective was to clarify the microbial dynamics associated with the nitrogen cycle in sub-tropical peatland forests and wetlands.

Soil samples were collected from the study sites for physical-chemical and microbial analyses. DNA extraction was performed on soil samples, followed by quantification of genes associated with the nitrogen cycle using quantitative polymerase chain reaction. In addition, soil samples underwent analyses to assess levels of ammonium (NH4-N) and nitrate (NO3-N). Soil N<sub>2</sub>O fluxes were determined by collecting gas samples from the chamber headspace of static soil chamber systems at 20-minute intervals during one-hour sessions. The concentration of N<sub>2</sub>O was determined from gas samples using a gas chromatographer (Shimadzu-2014).

A substantial amount of NH<sub>4</sub>-N was found across all sites (mean: 77.2 mg/kg), correlating significantly with the abundance of *nifH* gene ( $R^2 = 0.7$ , p<0.01). This indicates high rates of microbial nitrogen fixation. Soil NO<sub>3</sub>-N content varied substantially, with Plaine des Cafres and Forêt de Bébour sites exhibiting notably higher levels (means: 53.67 mg/kg and 139 mg/kg, respectively) compared to the wetland in Saint Paul (mean: 2.5 mg/kg). Archaeal and COMAMMOX *amoA* gene abundances were high across all three sites, indicating archaeal nitrification and complete ammonia oxidation. The *nir:amoA* ratio was highest in wetland soil, explaining the low NO<sub>3</sub>-N content. The *nir:nosZ* ratio was less than 1 in all sites indicating the dominance of N<sub>2</sub>O consumers in soil, with wetland exhibiting the lowest ratio. The high abundance of denitrifiers and dominance of *nosZ*-type denitrifiers in the peatland forests and the wetland of Reunion Island can explain the observed low N<sub>2</sub>O fluxes in all sites with no significant variation.