



## Microbial nitrogen cycle and nitrous oxide emissions in natural and managed tropical peatlands

Mikk Espenberg (1), Jaan Pärn (1), Kuno Kasak (1), Martin Maddison (1), Leho Tedersoo (2), and Ülo Mander (1)

(1) University of Tartu, Institute of Ecology and Earth Sciences, Department of Geography, Tartu, Estonia (mikk.espenberg@ut.ee), (2) Natural History Museum, University of Tartu, Tartu, Estonia (leho.tedersoo@ut.ee)

Tropical peatlands cover approximately 11% of global peatland area. However, recent studies suggest that far much more peat exists in the tropics than previously estimated and tropical peat may exceed the known area and volume even more than three times. Thus, tropical peatlands are particularly important in terms of carbon cycle and there is a growing interest in their nitrogen cycle. Management of nitrogen is economically, ecologically and environmentally critical. Quantity and distribution of nitrogen is controlled through biogeochemical processes, however, the lack of knowledge regarding microbial processes governing nitrous oxide (N<sub>2</sub>O) emissions is hindering climate-change impact estimations of tropical peatlands.

The purpose of this study was to assess the abundances of soil bacteria and archaea and their potential to perform different N transformation processes in natural and managed tropical peatlands, and link these changes to N<sub>2</sub>O and N<sub>2</sub> emissions from the peat. The peat sampling was carried out in years 2013 to 2017 at natural and drained peatland sites of seven tropical regions (Myanmar, Borneo, Taiwan, Uganda, Florida, Pantanal, and French Guiana). A total of 188 peat samples were collected from top soil (0–10 cm). Peat pH<sub>KCl</sub>, total C, organic matter content, total N, NH<sub>4</sub>-N, NO<sub>3</sub>-N, total P, Ca, Mg and K values were determined. Quantitative PCR was applied to evaluate bacterial and archaeal community size by quantifying abundance of bacterial and archaeal specific 16S rRNA genes, respectively. Genetic potential of nitrogen transformation processes was evaluated by targeting the following functional genes: nirS, nirK, nosZ clade I and nosZ clade II (denitrification); nifH (N<sub>2</sub> fixation); nrfA (dissimilatory nitrate reduction to ammonium, DNRA); bacterial and archaeal amoA (nitrification); and ANAMMOX-specific 16S rRNA genes (anaerobic ammonium oxidation). During the peat sampling, in situ N<sub>2</sub>O emission measurements were conducted using a closed chamber technique. In addition, potential N<sub>2</sub> emissions were measured from the soil using helium-atmosphere soil incubation technique in the laboratory.

Bacterial abundance varied significantly between the sites. The highest abundance was found in the year-round wet sites of Myanmar and Taiwan, while bacteria were least abundant in the ephemeral Pantanal wetlands and the deep-drained Borneo oil palm plantation. Archaea abundance was quite similar over most of the sites. We observed only low levels of the bacterial amoA gene. Thus, ammonia-oxidizing archaea were the main nitrifiers in the ecosystems. We can conclude that ANAMMOX process plays a minor role in tropical peatlands. The nirK denitrifiers were significantly more abundant compared to nirS-type denitrifiers. Conversion of N<sub>2</sub>O to N<sub>2</sub> was mainly controlled by microbes possessing nosZI genes in the wet sites and microbes possessing nosZII genes in the drained sites. In addition, DNRA influenced the N<sub>2</sub>O emissions, and N<sub>2</sub>-fixing microbes were abundant across tropical peatlands. In conclusion, drainage of tropical peatlands may cause substantial shifts in the microbially mediated nitrogen cycle.