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Nitrogen gas emissions and their genetic potential in tropical peatlands of French Guiana

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In the current study, nitrogen gas (N2, N2O) emissions from tropical peatlands (French Guiana) were measured and their relationships with the soil chemical parameters, water regime, and abundances of genes encoding denitrification associated nitrite and nitrous oxide reductases were analysed.

The measurements and soil sampling (from 0-10 cm layer) were carried out in October 2013 in two sites (undisturbed and drainage influenced) of the northern part of French Guiana. In both study sites, three transects along the groundwater depth gradient with three sampling points in each transect were established. At each sampling point, N2O emissions were measured in six sessions during three days using static closed chambers. N2 emission from the top-soil samples were measured in the laboratory applying He-O (N2) method. Soil pHKCl, NO_3-N, NH4-N, soluble P, K, Ca and Mg, totN and soil organic matter content were determined from the collected samples. Bacterial 16S rRNA gene, (and marker genes for measuring denitrification potential) nirS, nirK, nosZ clade I and clade II copies were quantified in the soils using qPCR method. Whole genome shotgun sequencing of DNA extracted from soil samples was performed on Illumina NextSeq system. Metagenomes were used for microbial profiling, identifying functional genes and relating them to biogeochemical cycles and biological processes.

N2O emissions were significantly lower and N2 emissions higher ($p<0.05$ in both cases) in natural sites (mean values -0.3 and 10 μg m-2 h-1 for N2O, and 1477 and 637 μg m-2 h-1 for N2 in natural and drained sites, respectively). Results from molecular analyses show that the bacterial community was significantly more abundant ($p<0.001$) in the natural site while the N2O production potential (by the abundance of nir genes) was not different between the two sites. N2O reduction potential (by the abundance of nosZ genes) was higher ($p<0.01$) in the natural area where also the lower mineral N content and high groundwater level was detected. A systematic variation in nir and nosZ genes abundances along the groundwater depth gradient in both areas was notable.

Variation in dominant bacterial groups between drained site samplings was more noticeable, than along the groundwater depth gradient in natural site. However ten out of twenty four bacterial genera (over 1% of taxonomically classified sequences) were shared between two sites (mostly Mycobacterium, Rhodopseudomonas, and Streptomyces). Archaea were dominated in natural sites by methanogens (Methanomicrobia, Methanobacteria, and Methanococci), while archaeal classes in drained sites were more evenly distributed.