Geophysical Research Abstracts
Vol. 19, EGU2017-6546-1, 2017
EGU General Assembly 2017

Nitrogen biogeochemistry in tropical peatlands: nitrogen gas emissions and metagenomic insights into related microbial groups

Kuno Kasak, Mikk Espenberg, Kristjan Oopkaup, Teele Ligi, Marika Truu, Jaak Truu, Martin Maddison, Järvi Järveoja, Alar Teemusk, and Ülo Mander

University of Tartu, Institute of Ecology and Earth Sciences, Department of Geography, Tartu, Estonia (kuno.kasak@ut.ee)

Tropical peatlands constitute considerable amount of global peatland areas and are one of the most important and vulnerable terrestrial ecosystems in terms of impact on the atmospheric greenhouse gas composition. Anthropogenic actions, especially drainage and agriculture, are transforming biochemical cycles in tropical peatlands substantially. It is well known that drainage of tropical peatlands will result in huge amount of carbon loss, however a comprehensive study of the nitrogen cycling genetic potential in tropical areas is still less known.

In the current study, nitrogen gas (N2, N2O) emissions from tropical peatlands (French Guiana, South America) were measured and their relationships with the soil chemical parameters, water regime, and abundances and diversity of genes in nitrogen cycle was assessed. The measurements and soil sampling were carried out in October 2013 in two sites (undisturbed and drainage influenced) of the northern part of French Guiana. At both sampling sites, N2O emissions were measured in six sessions during three days using static closed chambers. N2 and N2O 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. The bacterial and archaeal 16S rRNA genes and functional genes involved in nitrogen cycle (nirS, nirK, nosZI, nosZII, bacterial and archaeal amoA, nifH, nrfA, ANAMMOX bacteria specific 16S rRNA genes) in soil were quantified by using quantitative PCR method. DNA extracted from soil samples was sequenced 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 site (mean values -0.3 and 9.9 μg m-2 h-1 for N2O, and 1477.3 and 637.2 μg m-2 h-1 for N2 in natural and drained sites, respectively). Results from molecular analyses showed that drainage had a clear impact on the communities of nirS, nirK, nosZ, amoA archaea and nifH gene possessing microorganisms and the structure of these communities were mainly related to different nitrogen forms in tropical peatlands. The bacterial community was more abundant 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 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.