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Nitrous oxide emission from tropical and sub-tropical peatlands

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In the current study nitrous oxide (N2O) emission from tropical peatlands in French Guiana, Uganda, Myanmar, Malaysia (Sabah, Borneo) and from sub-tropical peatlands in Taiwan was measured and their relationships with soil chemical parameters, water regime, and abundances of genes encoding denitrification-associated nitrite and nitrous oxide reductases were analysed.

From June 2013 to November 2017, 7–10-day gas- and soil-sampling campaigns were organised. In each country we established two sites, one in natural peatlands and another one in peatlands affected by human activities (e.g. drainage, intensive agriculture, fertilisation etc.). In all sites three sampling points were established. At each sampling point, N2O emissions were measured in 3-6 sessions during two to three days using static closed chambers. Soil pH, NO_3-N, NH4-N, P, K, Ca and Mg, TN and organic matter content were determined from the collected samples. In French Guiana fen samples, the bacterial and archaeal 16S rRNA genes and functional genes involved in nitrogen cycling (nirS, nirK, nosZI, nosZII, bacterial and archaeal amoA, nifH, nrfA, ANAMMOX bacteria genes) in soil were quantified by using quantitative PCR method.

In all areas N2O emissions were significantly higher in the affected sites than in the natural sites. Statistical analyses showed a strong positive correlation between the N2O emissions and soil NO_3-N content ($p<0.05$), while soil moisture and water table level showed a negative correlation with N2O emission ($p<0.05$) in all sites. Highest N2O emissions originated from arable sites in Uganda and from oil palm plantation in Borneo, where the emissions were up to 1055 μg m-2 h-1 and 1144 μg m-2 h-1, respectively. N2O emissions from natural sites showed relatively low values, fluctuating around zero. Metagenomic insight into French Guiana peatlands showed that drainage had a clear impact on the communities of nirS, nirK, nosZ, archaeal amoA and nifH gene possessing microorganisms. The structure of the communities was mainly related to different N forms. The bacterial community was more abundant ($p<0.001$) in the natural site while the N2O production potential (abundance of the nir genes) was not different between the drained and non-drained sites. N2O reduction potential (abundance of nosZ genes) was higher ($p<0.01$) in the natural area where significantly lower mineral N content and high groundwater level were detected. Soil moisture and soil nitrate content are the key parameters regulating denitrification efficiency.