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Integrating microbiological and isotope methods for studying nitrification and denitrification processes in soils of drained and rewetted peatland forest

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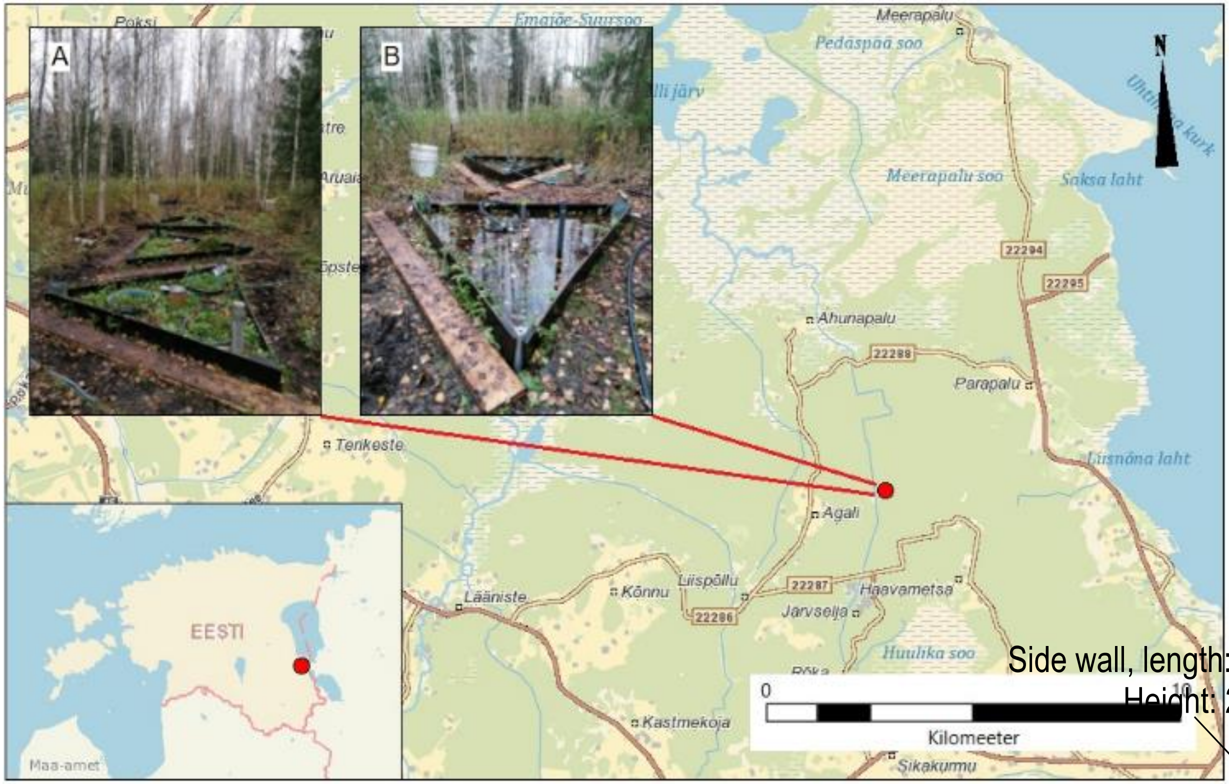
Peatlands under pressure

- Managed peatlands - source of nitrous oxide (N_2O) emissions
- N_2O – greenhouse gas
- The management of changed peatlands is economically, ecologically and environmentally critical

This study examined

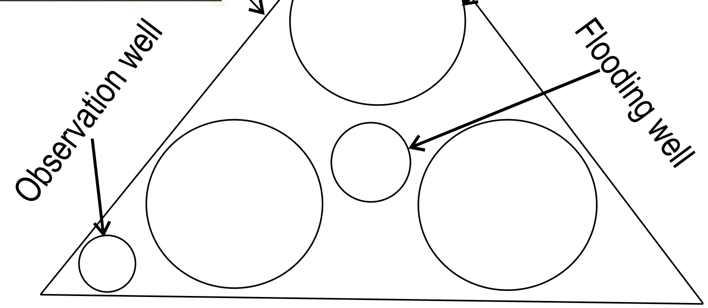
- processes responsible for N_2O emissions in peatlands by analysing relationships of isotope signatures and abundances of genes with N_2O production and consumption in soils of drained and rewetted peatland forest.

Study sites



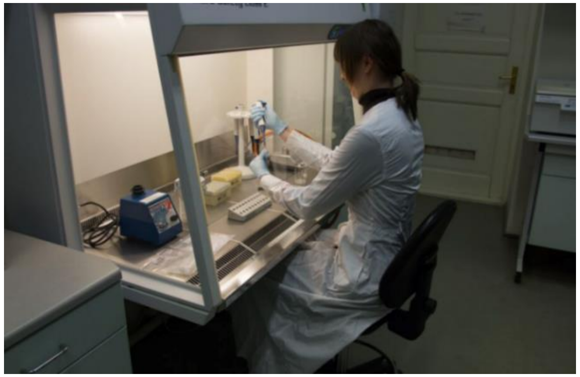
Geographical location with onsite photos of the study site.

Schematic diagram of the design of the study site.



- Dominated by spruce and birch trees
- Autumn in 2020

Methods



- Peat samples were taken for chemical analyses (pH, organic matter, total N, NH_4-N, NO_3-N, total P, Ca, K, Mg)
- **Microbial analyses**
  - DNA extraction from peat samples
  - The bacterial and archaeal 16S rRNA genes and key functional genes involved in nitrogen cycling in soil were quantified by using quantitative PCR method
    - Denitrification: *nirS*, *nirK*, *nosZI*, *nosZII* genes
    - Nitrification: bacterial and archaeal *amoA* genes

- **Gas analyses**
  - Closed chamber technique
- **Isotopic analyses**
  - Tracer amendments: NH_4^+ and NO_3^-
  - N_2O isotopic composition
  - Site preference ($SP = \delta^{15}N^{\alpha} - \delta^{15}N^{\beta}$) (Toyoda et al., 1999)

NH_4-N & NO_3-N & N_2O

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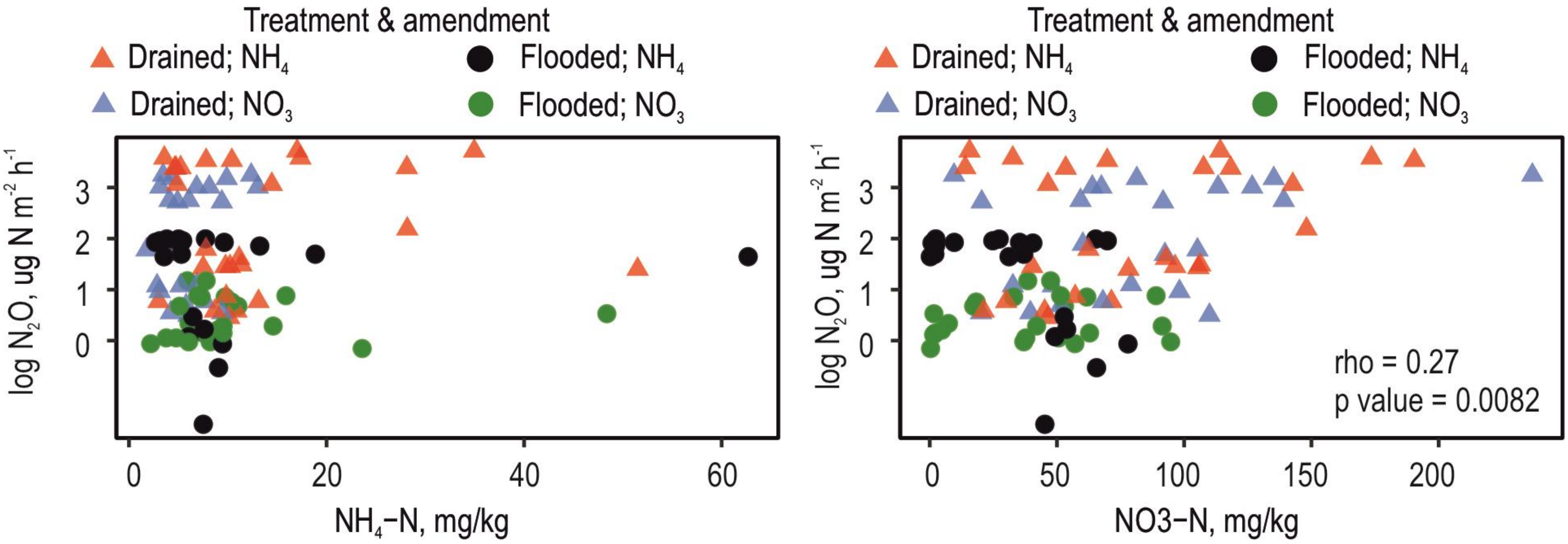

Soil nitrate and ammonia concentrations over the course of experiment

Nitrification genes

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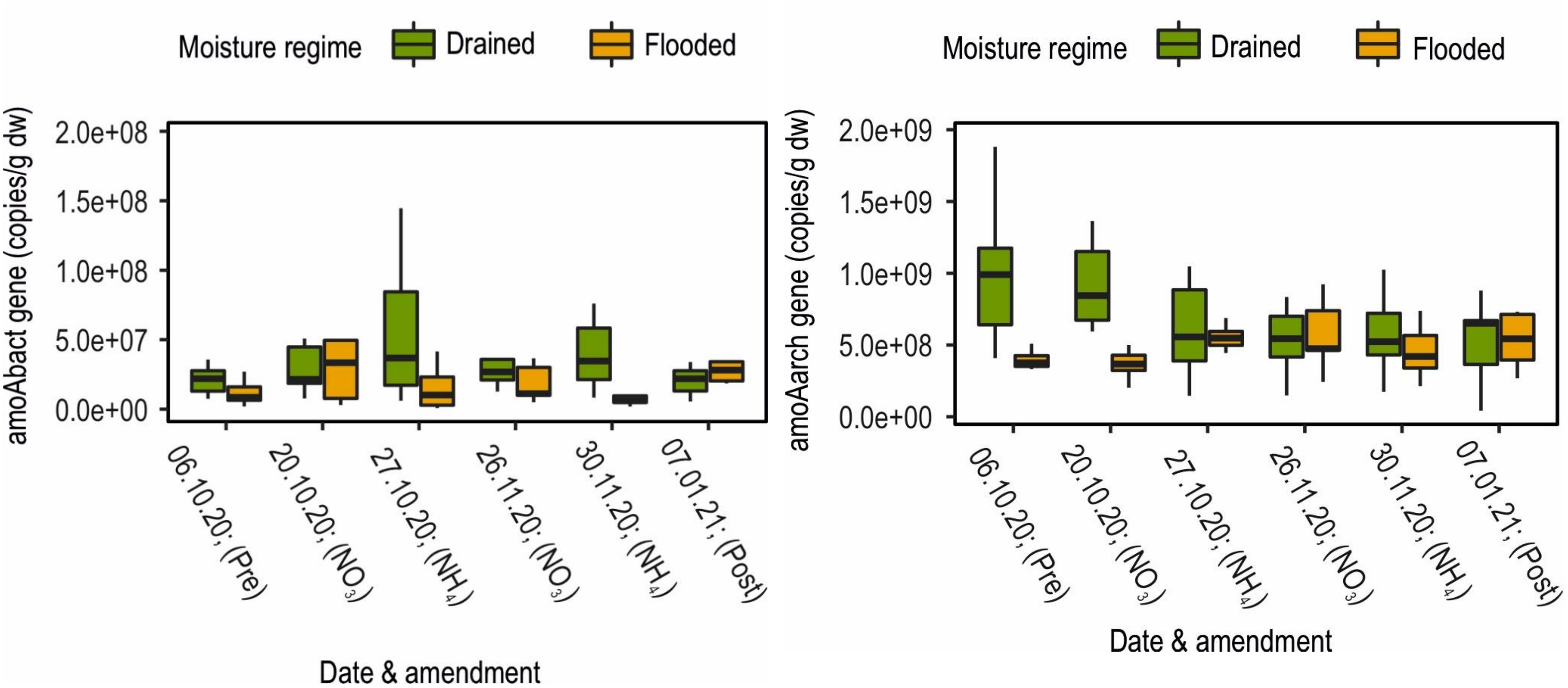
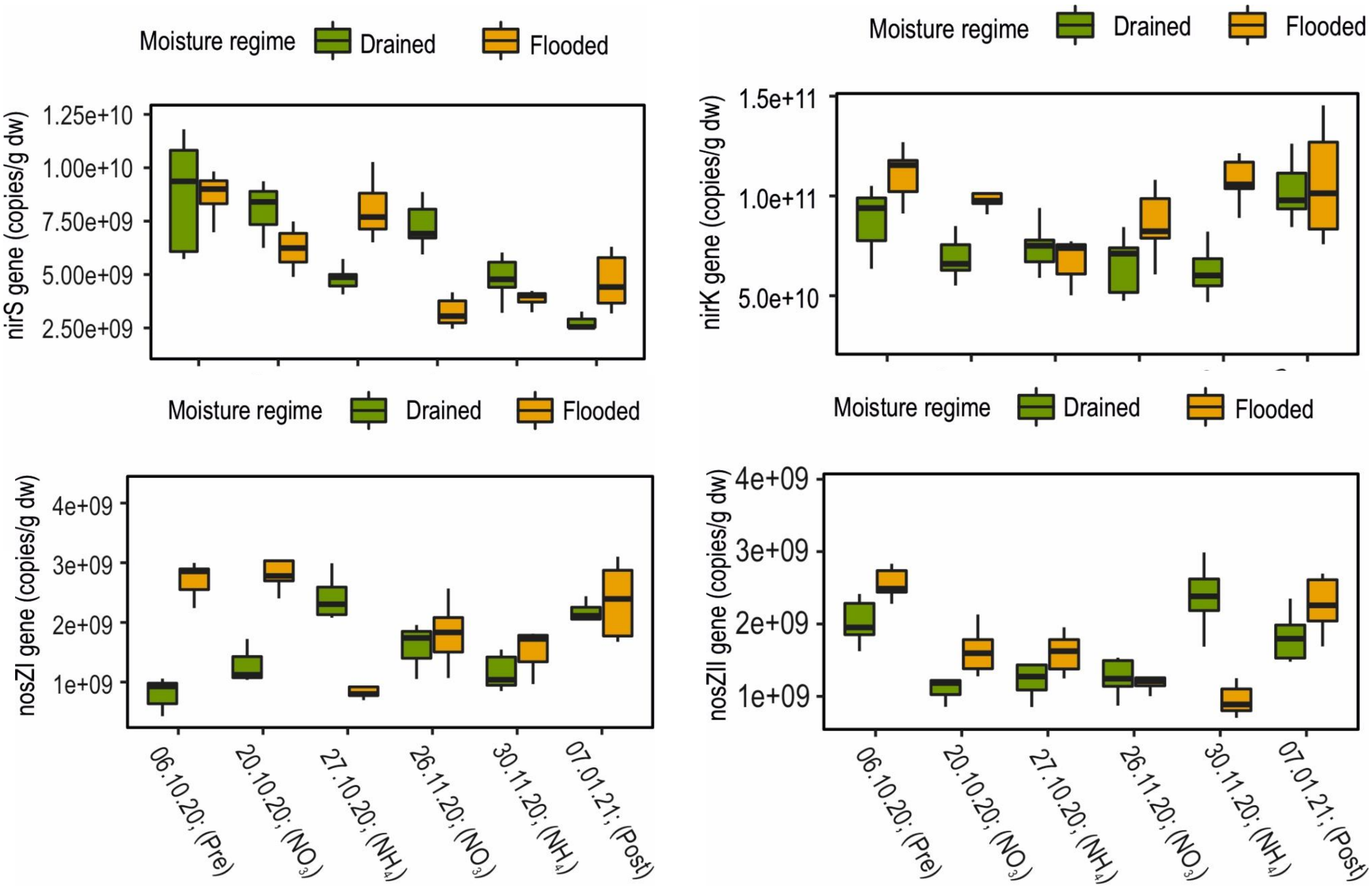


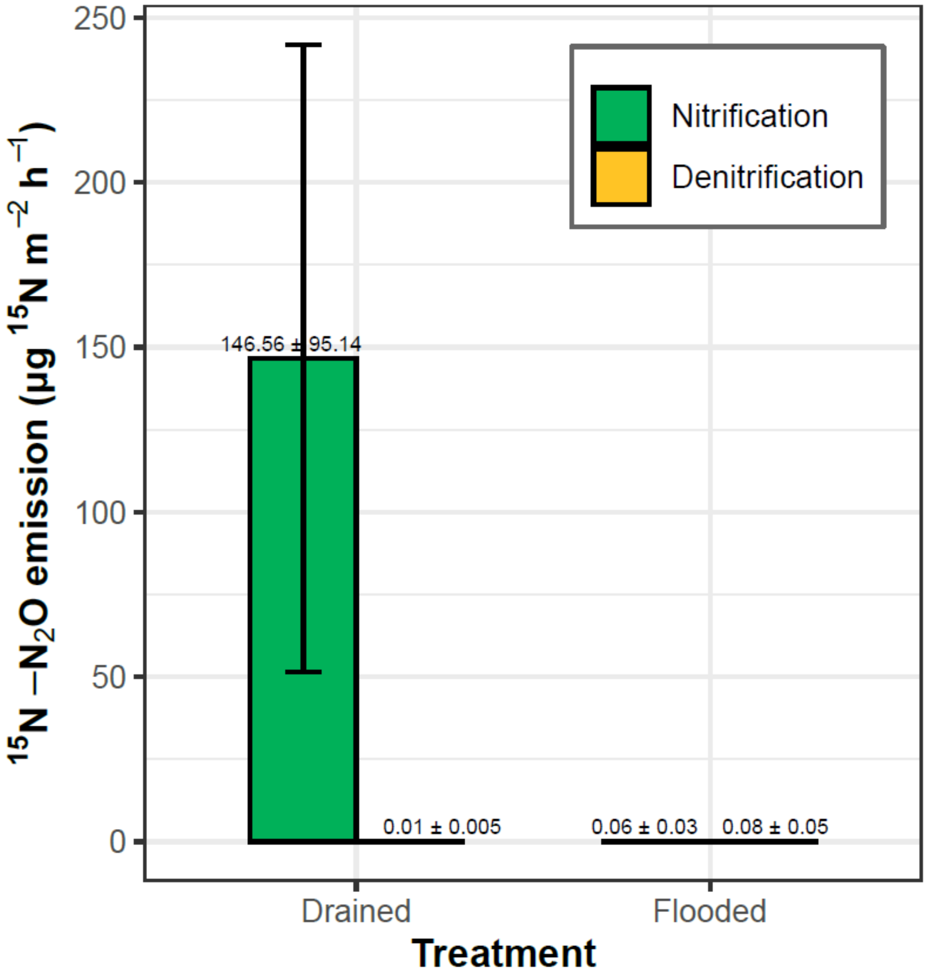
Number of gene copy numbers for bacteria *amoA* and archaea *amoA* under drained and flooded conditions during the experiment.

Denitrification genes



nirS, *nirK*, *nosZI*, *nosZII* gene copy numbers under drained and flooded conditions.

^{15}N-N_2O emissions



^{15}N-N_2O emissions from drained and flooded treatments.

Site preference (SP) & $\delta^{18}O$ & genes & N_2O

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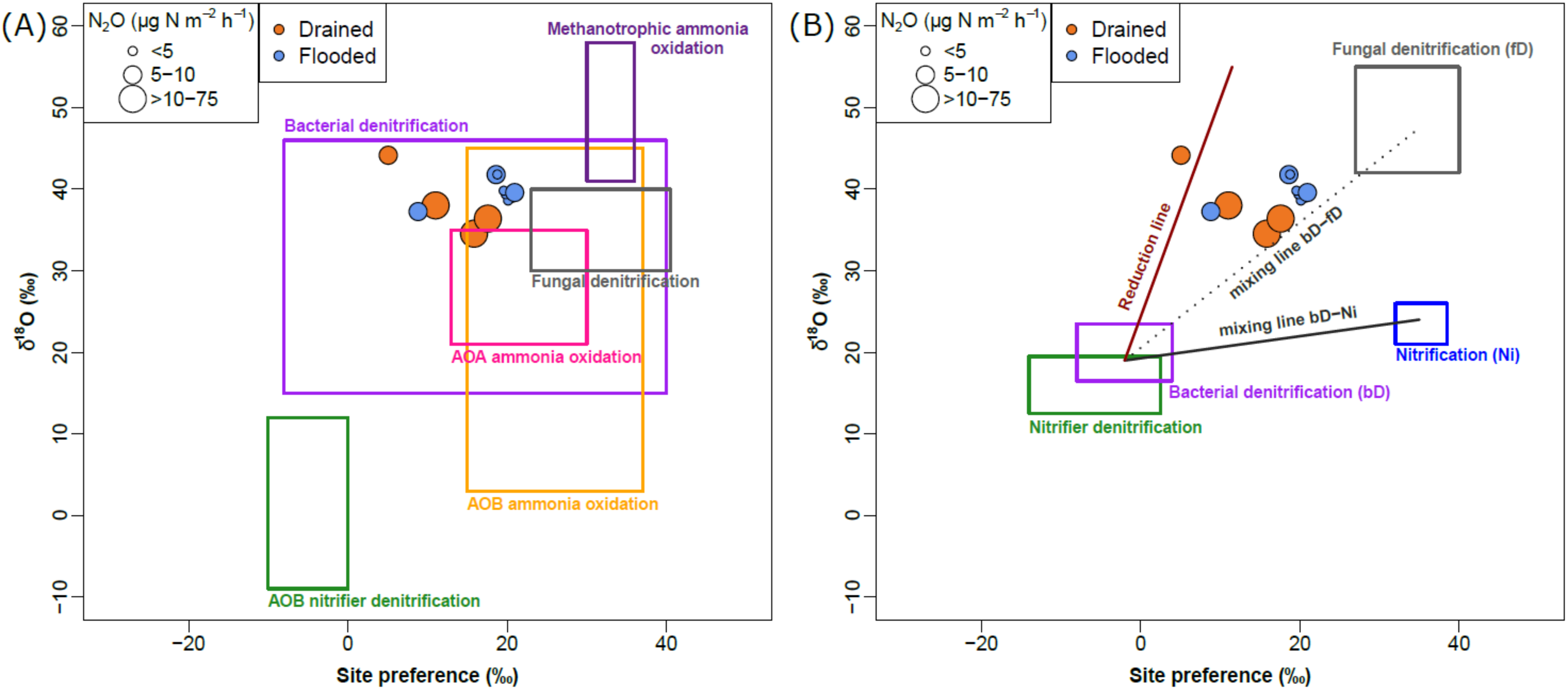

N_2O gas site preference values versus $\delta^{18}O$ for pre-treatment conditions

(A) Hu et al (2015)

(B) Yu et al (2020)

Site preference (SP) & $\delta^{18}O$ & genes & N_2O

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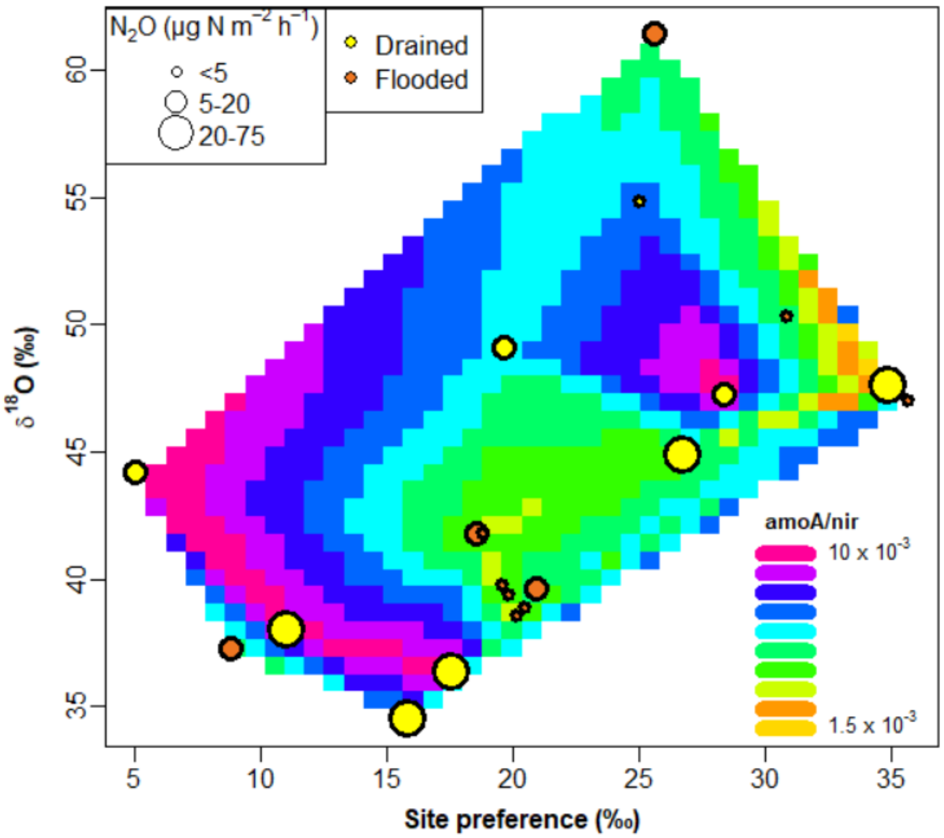
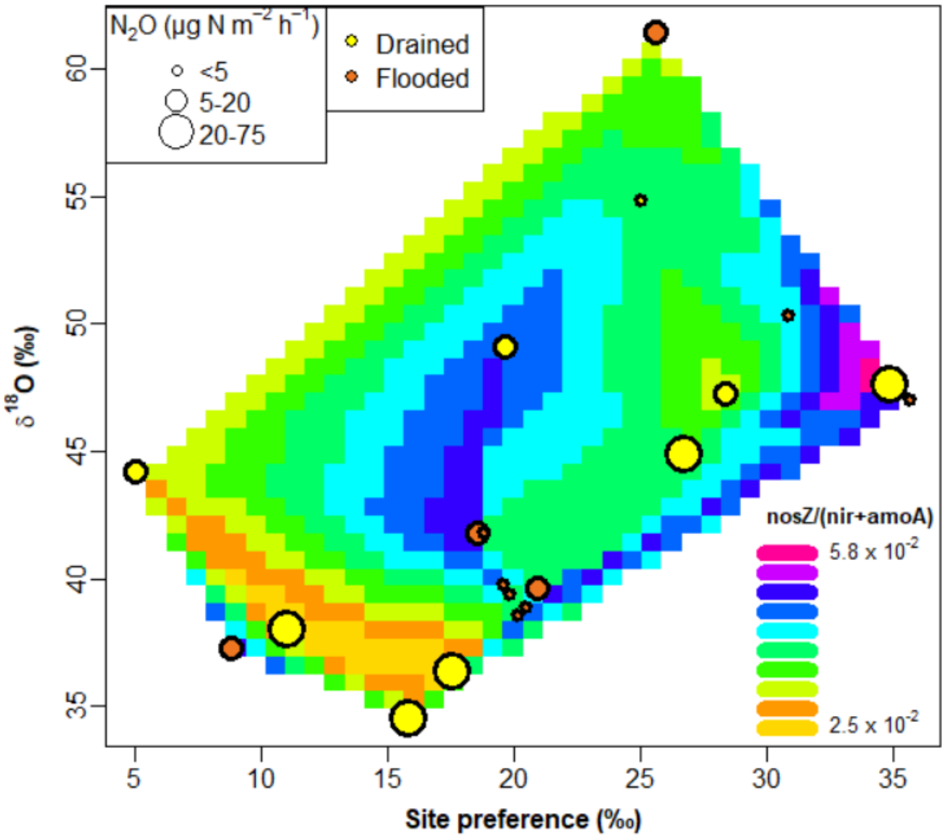


Nitrification vs denitrification (*amoA*/*nir*)



Consumers vs producers (*nosZ*/(*nir*+*amoA*))

Conclusions

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- **Drained peatland forest** sites emit **N_2O** the most.

- Denitrification genes ***nirK*** and ***nirS*** react in different conditions and are affected by **moisture and temperature**.

- Deciding the processes according to site preference (SP) & $\delta^{18}O$ is problematic – microbial analyses show that it is more complex. **Microbial and isotopic analyses complement each other.**

- In drained peatland forest sites, **most of the N_2O emissions come through the nitrification process**.

Acknowledgements

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