

Microbial community dynamics and N₂O-related genes responses to short-term flooding in riparian forest soil

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The growing interest in the impact of short-term floods on various ecosystems is driven by climate change and the increasing occurrence of extreme rainfall events. The control of nitrogen quantity and distribution relies on complicated biogeochemical processes. Yet, our understanding of the microbial processes governing nitrogen cycling needs to be improved, hindering our ability to estimate the effects of climate change on forests.

This study aimed to evaluate the influence of short-term flooding on bacterial, archaeal and fungal communities and nitrogen cycle processes with nitrous oxide (N₂O) emissions in riparian alder forests.

Topsoil peat samples were collected from riparian alder forests in 2017 and 2018. Real-time polymerase chain reaction (qPCR) and sequencing techniques were employed to assess processes and communities, while physicochemical parameters and in-situ N₂O emissions were concurrently measured. 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* (N₂ fixation); *nrfA* (dissimilatory nitrate reduction to ammonium, DNRA); bacterial, archaeal and COMAMMOX (complete ammonia oxidation) *amoA* (nitrification); and n-damo(nitrate/nitrite-dependent anaerobic methane oxidation)-specific 16S rRNA.

The results indicated a significant impact of short-term flooding on the abundance of bacteria, particularly those harbouring archaeal *amoA*, n-damo-specific 16S rRNA, and *nosZII* genes. Furthermore, several associations were observed between marker genes of the nitrogen cycle and N₂O emissions. The bacterial and fungal communities showed a shift in the community because of the short-term flooding. Sudden changes in soil moisture influenced the patterns of marker genes of nitrogen cycle processes and microbial communities.