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Dynamics of Microbial Communities and Greenhouse Gas Flux 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 nutrient quantity and distribution relies on complicated biogeochemical processes. Yet, our understanding of the microbial processes governing carbon and nitrogen cycling needs improvement, 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 microbial processes with greenhouse gas (GHG) emissions in riparian alder forests. Topsoil peat samples were collected from riparian alder forests and analyzed with quantitative polymerase chain reaction (qPCR), and sequencing techniques were employed to assess processes and communities, while physicochemical parameters and in-situ GHG emissions were concurrently measured.

Floods exert a substantial influence on the intricate biogeochemical cycles within soil ecosystems. The flooding event led to a change in bacterial 16S rRNA abundances and a noticeable expansion in the size of *Bryobacter* and *Candidatus Solibacter* communities associated with the breakdown of organic carbon. Several aerobic genera like *Arthrobacter*, *Ferruginibacter*, *Lacunisphaera*, and *Novosphingobium*, which were identifiable before short-term flooding, became undetectable. Many of these organisms were known for their role in breaking down carbon compounds, highlighting the transformative impact of short-term flooding on the composition and functions of soil microbial communities and GHG emissions.

In the examined sites, a diverse array of arbuscular mycorrhizal (AM) fungal genera were identified, including *Acaulospora*, *Archaeospora*, *Claroideoglossum*, *Diversispora*, and *Paraglossum*. One pivotal aspect of these fungal communities is their role in establishing arbuscular mycorrhiza, a beneficial symbiotic association between plant roots and fungi. AM fungi contribute significantly to enhancing plant nutrition, stress resistance, and shaping soil structure and fertility.

Nitrifiers, particularly those associated with archaeal *amoA*, experienced notable shifts. Denitrifiers, identified through the *nosZII* gene, were also significantly impacted. Moreover, microorganisms engaged in the n-damo process displayed alterations. The flooding event was

observed to augment the community size of denitrifying and nitrogen-fixing genera such as *Rhodanobacter*, *Pseudolabrys*, and RB41. In contrast, a decrease was noted in the abundance of nitrifiers, exemplified by the decline of *Nitrospira*. Furthermore, several associations were observed between marker genes of the nitrogen cycle and N₂O emissions.