Goldschmidt 2026 Abstract
https://doi.org/10.46427/gold2026.34781

Land use largely affects N_2O emissions than flooding by modifying nir*S*- and nir*K*- containing communities in reservoir riparian zone

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Denitrification is an important biological process for nitrogen balance in riparian zones, an aquatic-terrestrial ecotones, which are hotspots for nitrous oxide (N_2O) emission. However, we know little about the effect of riparian land use on the aggregate associated denitrifier communities and N_2O emissions along a flooding gradient, along with how these microbes are associated with N_2O emissions. In this study, the abundance, diversity and community of nir*S* and nir*K* genes and N_2O flux were investigated in three flooding conditions (waterward sediment, interface soil and landward soil) within three land-use types (woodland, sparse woodland and grassland) of the reservoir riparian zone. The results showed the lowest N_2O flux was observed in interface soil, and the highest flux was under woodland. Ammonium nitrogen (NH_4^+) and total nitrogen (TN) were driven factors influencing the flux. The abundance of both nir*S* and nir*K* genes had strong positive associations with nitrite (NO_3^-) and clearly varied among land-use types. Variations in nir*S*- and nir*K*-containing communities existed across sampling sites from each land-use type in terms of β-diversity. Soil NO_3^-, TN and NH_4^+ significantly affected communities of nir*S* and nir*K* genes. Network analysis revealed that all flooding conditions and land-use types had similar keystone taxa like *Azospira* and *Bradyrhizobium*, which were significantly related to N_2O emissions. Taken together, land-use type but not flooding significantly influence soil denitrifier in the reservoir riparian zone. This study also highlighted soil NO_3^- content affect N_2O emissions by modifying nir*S* and nir*K*-containing communities in riparian zones.