DIVERGENT RESPONSES OF AOA AND AOB IN REWETTED FEN PEATLANDS

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Rewetted peatlands will experience more frequent drought conditions as the climate changes, and therefore it is necessary to study how nutrient cycling (and corresponding greenhouse gas emission) will respond in these novel ecosystems. Thus far, the impact of drought on ammonia oxidizing microbes in peatlands is unclear, despite their role as a rate-limiting step in nitrification. This study aims to identify trends in archaeal and bacterial ammonia oxidizer abundances and their feedbacks with nitrogen-cycling genes in two rewetted fens in northeastern Germany (PW and CW). Drought conditions in the peat soils is neutrally defined via a k-means clustering algorithm, and AOA and AOB abundances are quantified with *amoA* gene copy numbers in both DNA and RNA samples from the soil at time points throughout a drought cycle. These results are supported by metatranscriptome analysis and phylogenetic-based clade assignment of AOA ASVs. Shifts in nitrifying communities were found to correlate with overall site hydrological stability, with AOB outnumbering AOA at both sites. Both AOA and AOB increased at the PW site during the drought, following a decrease in nitrogen fixation gene expression after drought onset and preceding an increase in ANRA-associated genes at the end of the drought cycle. In contrast, CW AOA and AOB showed limited dynamism in response to drought. The feedbacks between water table stability, drought and the prevalence of ammonia oxidation functional genes is crucial to understand how novel rewetted fen ecosystems will respond to climate change, as well as how these conditions will further affect the quality of the peat substrate and microbial-driven nutrient cycling.

**Keywords:** Rewetted fens; ammonia oxidizing microbes; drought; nitrogen cycling; climate change