

72. Agricultural land-usage completely reshapes nitrifier diversity

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Project Goals: This abstract represents ongoing work that is part of the DOE-BER funded project entitled “Archaeal Influence on Nitrogen Transformations in Soil and Root Systems of Bioenergy Crop Species”. The most general objectives are to resolve the relative contributions of ammonia oxidizing archaea and ammonia oxidizing bacteria to nitrification and production of atmospherically active gases, evaluate biotic and abiotic variables that determine their distribution and activity, and identify control methods through amendment with selective inhibitors or land management practices within the context of bioenergy cultivars.

The transition of marginalized lands into agricultural usage significantly changes terrestrial systems, altering the biological, physical and chemical properties of soil ecosystems. However, it remains uncertain as to whether these changes have broader consequences on the underlying genetic diversity of microbial communities that facilitate specific biogeochemical cycles. Aerobic ammonia and nitrite oxidizing organisms are responsible for nitrification in terrestrial environments. This process has significant consequences on the distribution and form of nitrogen in soils, as well as the release of fugitive nitrogen oxide gases. Thus, controlling the environmental impacts of nitrogen fertilizer application is essential to achieving sustainable agriculture methods. To assess whether long-term management practices associated with cropping of potential bioenergy feedstocks (switchgrass cultivars) were associated with different nitrifying populations, amplicon sequencing (i.e., tag sequencing) was applied to biomarkers associated with aerobic ammonia and nitrite oxidation (ammonia monooxygenase-*amoA*, nitrite- oxidoreductase-*nxB*, respectively) from long-term managed and native soils in eastern Washington, USA. These data indicated that aerobic ammonia-oxidizing archaea and bacteria (AOB and AOA, respectively) associated with soils under managed conditions were significantly different from native soils. At both broad and fine phylogenetic resolution (i.e., genus and sub-cluster), specific groups of AOA and AOB were identified that contributed either exclusively with managed or native lands, perhaps indicating different life strategies that maybe intimately related to the net-input of carbon and other nutrients associated with switchgrass cultivation. Nitrite oxidizing Bacteria (NOB) also displayed significant differences associated with management. However, *nxB* genes observed in this study were highly diverse, displaying low nucleotide identity to previously observed sequences from environmental surveys, indicating tremendous unrecognized breadth of phylogenetic diversity within this group. Taken together, these results suggest that management practices associated with propagating soils of bioenergy cultivars select for specific taxonomic groups of aerobic nitrifiers.