

76. Land management alters N-cycling metabolic potential in Pacific Northwest soils

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Project Goals: The impact of an expanded bioenergy industry on soil and atmospheric chemistry remain unknown. Reduced nitrogen (R-Nr) application is required for enhanced plant growth. Nitrifying microorganisms in soil convert R-Nr to more mobile and biologically less favorable oxidized forms, reducing crop yields and increasing production of detrimental fugitive gases. Ammonia oxidizing Archaea (AOA) are often observed in high abundances in soils, and are implicated as the dominant assemblage responsible for the first step of nitrification, ammonia oxidation to nitrite. However, little information regarding their role in nitrification in soils of biofuels cultivars is available. To that end, the goal of this project was to assess whether differing soil types and nitrogen delivery strategies: 1) impacted the abundance, distribution, and diversity of nitrifying assemblages, 2) altered the release of different fugitive gases, and 3) altered broader components of microbial diversity and metabolic activities associated with the nitrogen cycle.

Abstract: Cellulosic ethanol production from switchgrass has gained interest as an economically and environmentally sustainable alternative to fossil fuels. Successful plant propagation requires the application of inorganic nutrients, of which nitrogen-based fertilizers are the most expensive, and often converted to energetically and environmentally less favorable forms by nitrifying microorganisms. To assess whether alternative land-management practices associated with biofuels crop production differentially impact nitrogen transformations, metagenomes were generated from several soils in Eastern and Western Washington associated with different soil chemistries and agricultural histories. We focused on genes for nitrification (ammonia monooxygenase), general nitrogen cycling processes (including denitrification, dissimilatory nitrate reduction to ammonia, assimilatory nitrite/nitrate reduction, and urea utilization), and genes implicated in archaeal ammonia oxidation (e.g., the copper containing nitrite reductase). Abundances of ammonia monooxygenase genes were highest in long-term agricultural field plots in Eastern Washington, and mainly affiliated with *Thaumarchaeota*. Comparisons of short metagenomic fragments with full-length amoA gene sequences in clone libraries developed from the same sites revealed good consistency in diversity and rank abundance patterns, with *Nitrososphaera* and *Nitrosotalea* comprising the majority of the AOA ecotypes. Western Washington forest soils displayed lower levels of thaumarchaeal amoA, yet bacterial variants displayed similar abundance patterns in both eastern and western soils. Gene variants involved in canonical denitrification (*nirS*, *nosZ*) were elevated levels in some, but not all, agricultural soils. Notably, *nosZ* variants affiliated with the recently described 'atypical', non-denitrifier pathway were abundant in most soils, in some instances in numbers ten-fold greater than the *nosZ* of typical denitrifiers. Thus, emissions of N₂O from soils may be attenuated under condition favoring the expression of this novel reductase. The demonstration that AOA are the dominant ammonia-oxidizing population in these intensively managed soil systems now provides a framework for associating key transformation of nitrogen, including the production of atmospherically reactive oxides, with patterns of AOA species distribution and activity.

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