Elucidation and Validation of Genes Associated with Biological Nitrification Inhibition in Populus

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To provide crops with the nitrogen they require for robust growth, nitrogen fertilizer is added to the soil to increase yields. However, nitrogen use efficiency (NUE) in bioenergy crops such as poplar is low, which may result in pollution of waterways by nitrate runoff, emissions of the potent greenhouse gas nitrous oxide, and reduced carbon dioxide sequestration in soils. One of the main reasons for this low NUE is the activity of microbes that convert soil nitrogen into nitrate and nitrous oxide in a process called nitrification. Plant roots exudate chemicals (biological nitrification inhibitors or BNIs) that reduce microbial nitrification. Thus, controlling the production of BNIs by roots can help mitigate nitrogen loss and improve NUE in bioenergy crops. Despite substantial research in this area, little is known about the genes and pathways involved in root BNI production. Furthermore, the current methodologies used to analyze BNI-related traits in plant populations are inefficient. This project will use genome-wide association analysis of a large poplar population to discover and characterize genes involved in the production of BNIs and, therefore, understand their role affecting NUE. A high-throughput mass spectrometry approach will be developed to analyze nitrification and mineralization in samples from the soil surrounding poplar roots at an unprecedented scale, while metabolomics and soil nitrification studies of root exudates will help identify BNI-associated genes. This knowledge will provide avenues to increase NUE in bioenergy crops with the concomitant increase in carbon sequestration, given the tight connection between the carbon and nitrogen cycles. Furthermore, the outcomes of this project will contribute to our understanding of ecosystem function and to inform the design and engineering of more efficient bioenergy crops.

This research was selected for funding by the Office of Biological and Environmental Research.