

## Sequencing of the *Populus* Rhizosphere

### [The Plant Genome Group](#)

Environmental Sciences Division  
Oak Ridge National Laboratory  
Oak Ridge, TN 37931-6422

There is growing evidence that microorganisms associated with the soil-root interface or rhizosphere influence the response of plants to fluctuations in their chemical, physical, and biological surroundings. The same may be true for the hundreds of as yet unclassified endophytes: symbiotic, commensal, and parasitic microorganisms that are continuously being discovered in the leaves, roots, and stems of *Populus*. When viewed in total, a single large perennial plant, *i.e.*, a tree, may be considered as an ecosystem unto itself, where organisms interact beneficially or antagonistically over time, creating structure and function for further interactions to occur. Indeed, unlike ephemeral herbaceous annuals, it is the perennial nature of *Populus* and other tree species that evolutionarily facilitates the development of consortia of microorganisms that help shape responses to global climate change or perturbations due to environmental contaminants. The response of these systems to elevated CO<sub>2</sub> and temperature, for example, is virtually unknown, and could be an important component of overall ecosystem responses to climate change. Characterization of the *Populus* rhizosphere would allow in-depth exploration of the coordinated community response to these perturbations, thus adding a needed dimension to climate change research and providing another step in the quest for mechanistic modeling of ecosystem responses.

We therefore propose random shotgun profiling of those organisms which occupy the plant rhizosphere. This community is likely composed of hundreds to thousands of bacteria and fungi, many of which perform vital biological functions that ensure the optimal functioning of the *Populus* ecosystem. However, the biodiversity of these communities is just now being revealed by preliminary, small-scale sequencing studies. In total, these symbionts and associates extend the genome of *Populus* by orders of magnitude, yet the ecological implications of these interactions are completely unknown, yet could hold significant consequences for how global change might impact ecosystem function and/or rates and magnitudes of carbon sequestration in soils. DOE has an opportunity to open these black boxes with moderate shotgun sequencing efforts through their Joint Genome Institute, thus revealing the rich diversity of interactions that shape biotic responses and determine ecological function.



Environmental Sciences Division, Oak Ridge National Laboratory, Oak Ridge, TN 37831  
<http://www.esd.ornl.gov/>