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Mycorrhizal symbionts of *Populus* to be sequenced by the United States Department of Energy's Joint Genome Institute

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The US Department of Energy (DOE) has selected two soil fungi found in widespread beneficial symbioses with trees and plants for complete genomic DNA sequence analysis at the DOE's Joint Genome Institute in Walnut Creek, California. The organisms have been chosen in recognition of the significant role played by plant-fungal symbioses in sustainable agricultural/forestry ecosystems, and the global C and N cycles, and for new uses in environmental reclamation and clean up. The fungal projects are companions to the DOE's *Populus* genome sequence project (<http://www.ornl.gov/sci/ipgc/>). In addition to its agricultural and environmental significance, the project will provide the first ever look at the genome of a mushroom-forming ectomycorrhizal fungus. All three genome projects are scheduled for completion in 2004.

The work will be coordinated by Drs Gerald Tuskan and Stephen DiFazio, scientists at DOE's Oak Ridge National Laboratory, Tennessee, who already play a leading role in the poplar tree genome project. Drs Gopi Podila (University of Alabama, Huntsville, Alabama) and Francis Martin (INRA-Nancy) in France will lead the team analyzing the genome of an ectomycorrhizal (ECM) fungus, *Laccaria bicolor*, which colonizes many forest

tree species. Dr Peter Lammers from New Mexico State University will lead a team investigating the genome of an arbuscular mycorrhizal fungus, *Glomus intraradices*, which colonizes most major crop plants. Both teams will also work together on the comparative genomics of mycorrhizal symbiosis.

L. bicolor colonizes a wide variety of tree species including both pine and poplar. *Laccaria* has been used to study C metabolism, N and P acquisition and transport, and its ability to scavenge other micronutrients from soil. It has been used in large-scale commercial ECM inoculation programs in forest nurseries worldwide to enhance the growth of tree seedlings.

Arbuscular mycorrhizal fungi colonize the vast majority of all known plant species, yet unlike the ECM fungi are incapable of growth without a symbiotic host. *G. intraradices*, a widespread mycorrhizal fungus found in different ecosystems throughout the world, was chosen for sequence analysis because of its compact genome and the availability of dual-culture systems to produce pure fungal DNA free from host plant contamination. As a symbiont, *G. intraradices* is highly effective in mobilizing, taking up and transferring mineral nutrients from soils to plants. In addition to *Populus*, it readily colonizes most plant species including agriculturally important commodities such as maize, wheat, alfalfa, and rice.

The sequences of these fungi will facilitate the first comprehensive genomic analysis of plant-fungal interactions when combined with the sequence of the *Populus* tree genome. More specifically, *Populus trichocarpa* is the leading "model" tree species for scientific research because of its relatively modest genome size, extensive genetic resources, rapid early growth, ease of clonal propagation, and routine protocols for genetic transformation. Members of the *Populus* genus are also being harnessed for practical applications in pulp and paper manufacturing, biofuels' production, and phytoremediation, and are considered to play a significant and important role in global atmospheric CO₂ management via enhanced C sequestration in wood.

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The decision taken by the DOE to fund the sequencing of symbiotic fungal genomes reflects the importance of mycorrhizal fungi to the life and health of plants. Plants benefit from these associations by receiving substantially more nutrients, particularly P, N and trace metals, than uncolonized plants. The fungi explore a larger volume of soil than root systems at a lower cost to the plant. In addition, colonized plants are generally more resistant to diseases caused by microbial pathogens and are also more resistant to the effects of drought, although the biochemical mechanisms responsible for these economically important traits are largely unknown. On the other side of the symbiosis, both arbuscular mycorrhizal and ECM fungi benefit from the symbiosis primarily through continuous access to C resources from plant photosynthesis that are mobilized from leaves to root tissues and then to the symbiotic partners. However, the mechanism and regulation of plant-fungal C transfer remains largely unknown, despite the critical importance of these steps for modeling of the effects of mycorrhizal associations on global C cycling, C sequestration and phytoremediation.

We can now expect a wave of new studies to capitalize on the wealth of genetic information that will flow from the sequencing and post-genomics projects. Efforts will initially focus on determining the functions of the tens of thousands of new genes that will be discovered from these three genomes. Major areas of research/questions that will be addressed include:

1. How gene products from both partners interact to initiate the development of the symbiosis and move nutrients between partners.
2. The mechanisms by which mycorrhizal fungi improve plant productivity, disease and drought resistance.
3. The extent to which mycorrhizal fungi enhance CO₂-fixation from the atmosphere as the greenhouse effect continues to increase.
4. How the symbiosis can be harnessed to sequester more C underground in long-lasting chemical forms.
5. How the symbiosis might be utilized for inexpensive environmental clean-up.

This fungal sequencing project will facilitate the development of the emerging field of community genomics, a new initiative of the US DOE to move genomics from the realm of single organisms to the study of complex interactions among organisms in biological communities. This research will ultimately yield insights into the rules that govern ecosystem composition and function, thus enhancing our ability to remediate contaminated sites, produce bioenergy safely and cleanly with minimal disruption to natural systems or predict ecosystem responses to environmental disturbances.