

Secrets of cooperation between trees and fungi revealed

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Plants gained their ancestral toehold on dry land with considerable help from their fungal friends. Now, millennia later, that partnership is being exploited as a strategy to bolster biomass production for next generation biofuels. The genetic mechanism of this kind of symbiosis, which contributes to the delicate ecological balance in healthy forests, also provides insights into plant health that may enable more efficient carbon sequestration and enhanced phytoremediation, using plants to clean up environmental contaminants.

These prospects stem from the genome analysis of the symbiotic fungus *Laccaria bicolor*, generated by the U.S. Department of Energy Joint Genome Institute (DOE JGI) and collaborators from INRA, the National Institute for Agricultural Research in Nancy, France, and published March 6 in the journal *Nature*.

This international team effort also involved contributions from 16 institutions, including Oak Ridge National Laboratory; Ghent University, Belgium; Lund University, Sweden; Goettingen University, Germany; CNRS-Aix-Marseille University, France; Nancy University, France; and the University of Alabama, Huntsville.

Trees' ability to generate large amounts of biomass or store carbon is underpinned by their interactions with soil microbes known as mycorrhizal fungi, which excel at procuring necessary, but scarce, nutrients such as phosphate and nitrogen. Most of these nutrients are transferred to the growing tree. When *Laccaria bicolor* establishes a

partnership with plant roots, a mycorrhizal root is created. The fungus within the root is protected from competition with other soil microbes and gains preferential access to carbohydrates within the plant. Thus, the mutualistic relationship is established.

"Forests around the world rely on the partnership between plant roots and soil fungi and the environment they create, the rhizosphere," said Eddy Rubin, DOE JGI Director. "The *Laccaria* genome represents a valuable resource, the first of a series of tree community genomics projects to have passed through our production sequencing line. These community resources promise to advance a systems approach to forest genomics."

Rubin indicates that by using DNA sequence to survey the forest ecosystem, from the plants to symbiotic and pathogenic fungi, researchers can ultimately optimize the conditions under which a biomass plantation would thrive. "We now have the opportunity to gain fundamental insights into plant development and growth as related to their intimate interaction with symbiotic fungi. These insights will lead to bolstered biomass productivity and improved forests."

Laccaria bicolor occurs frequently in the birch, fir, and pine forests of North America and is a common symbiont of *Populus*, the poplar tree whose genome was determined by the JGI in 2006. The analysis of the 65-million-base *Laccaria* genome, the largest fungal genome sequenced to date, yielded 20,000 predicted protein-encoding genes, almost as many as in the human genome. In sifting through these data, researchers have discovered many unexpected features, including an arsenal of small secreted proteins (SSPs), several of which are only expressed in tissues associated with symbiosis. The most prominent SSP accumulates in the extending hyphae, the tips of the fungus that colonize the roots of the host plant.

"We believe that the proteins specific to this host/fungus interface play a decisive role in the establishment of symbiosis," said Francis Martin, the *Nature* study's lead author. This genome exploration led Martin and his CNRS-Marseille University and DOE JGI colleagues to the unexpected observation that the genome of *Laccaria* lacks the enzymes involved in degradation of the carbohydrate polymers of plant cell walls but maintains the ability to degrade non-plant cell walls, which may account for *Laccaria*'s protective capacity. These observations point towards the dual life that mycorrhizal fungi like *Laccaria* possess, that is, the ability to grow in soil fending off pathogens and using decaying organic matter while serving as a custodian of living plant roots.

The genome, Martin said, shows a large number of new and expanded gene families compared with other fungi. Many of these families are involved in signaling and other processes that drive the complex transition between two distinct lifestyles of *Laccaria*: the benign saprotroph, able to use decaying matter of animal and bacterial origins, versus the symbiont, living in mutually profitable harmony with plant roots.

The team also discovered new classes of genes that may be candidates for the complex communication that must occur between the players in the host/plant subsoil arena during fungal development. They report that fungi play a critical role in plant nutrient use efficiency by translocating nutrients and water captured in soil pores inaccessible to roots of the host plant.

"The *Laccaria* genome sequence, its analysis, associated genomics, and bioinformatics tools provide an unprecedented opportunity to identify the key components of organism-environment interactions that modulate ecosystem responses to global change and increased nutrient input needed for faster growth, said Martin. "By examining and manipulating patterns of gene expression, we can identify the genetic control points

that regulate plant growth and plant-mutualist response in an effort to better understand how these interactions control ecosystem function."

Mycorrhizae are critical elements of the terrestrial ecosystems, Martin said, since approximately 85 percent of all plant species, including trees, are dependent on such interactions to thrive. Mycorrhizae significantly improve photosynthetic carbon assimilation by plants.

"Host trees like *Populus* are able to harness this formidable web of mycorrhizal hyphae that permeates the soil and leaf litter and coax a relationship for their mutual nutritional benefit," said co-author DOE JGI and Oak Ridge National Laboratory researcher Jerry Tuskan. "This process is absolutely critical to the success of the interactions between the fungi and the roots of the host plant so that an equitable exchange of nutrients can be achieved." The DOE JGI and its collaborators have now embarked on characterizing several other poplar community symbionts that will provide a more comprehensive understanding of the biological community of the poplar forest. These include *Glomus*, a second plant symbiotic fungus, *Melampsora*, a leaf pathogen, and several plant endophytes, bacteria and fungi that live inside the poplar tree.

"DOE JGI's expanding portfolio of community genomes provides the researchers with a set of resources that can be used to map out the processes by which fungi colonize wood and soil litter. These fungi interact with living plants within their ecosystem in order to perform vital functions in the carbon and nitrogen cycles that are so fundamental to sustainable plant growth," said Tuskan.

Source: DOE's Joint Genome Institute

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