

PublisherInfo		
PublisherName	:	BioMed Central
PublisherLocation	:	London
PublisherImprintName	:	BioMed Central

Finding promise in white rot

ArticleInfo		
ArticleID	:	4950
ArticleDOI	:	10.1186/gb-spotlight-20040506-02
ArticleCitationID	:	spotlight-20040606-02
ArticleSequenceNumber	:	302
ArticleCategory	:	Research news
ArticleFirstPage	:	1
ArticleLastPage	:	3
ArticleHistory	:	RegistrationDate : 2004-5-6 OnlineDate : 2004-5-6
ArticleCopyright	:	BioMed Central Ltd2004
ArticleGrants	:	
ArticleContext	:	130594411

The complete genome sequence of a white rot fungus, reported in the May 2 [Nature Biotechnology](#), reveals an impressive array of enzymes with potential for biotechnological exploitation, according to Diego Martinez and colleagues at the United States Department of Energy (DoE) [Joint Genome Institute](#).

Martinez's team sequenced the 30-MB genome of *Phanerochaete chrysosporium* strain RP78 by a whole-genome shotgun approach. The genome contains 11,777 protein-coding genes, including secreted oxidases, peroxidases, and hydrolytic enzymes that cooperate in wood decay.

The white rot fungi are the only microbes known to efficiently degrade all the components of wood, including lignin, the most significant aromatic polymer on Earth, according to Dan Cullen, research scientist with the [US Department of Agriculture Forest Products Lab](#) and coauthor of the paper. "They're found everywhere, in dead and down trees. Only a handful of organisms are able to degrade lignin, its very recalcitrant to decay, and these fungi are able to do that... so they're believed to be important - pivotal, in fact - to the carbon cycle," said Cullen.

P. chrysosporium is also used extensively in industry, for instance, for the bleaching of pulp from paper and textiles and the degradation of an array of organo-pollutants, Cullen said. "The DoE's decision to sequence it was based in part on those biotech angles, but they're also very interested in the biomass utilization and some related issues," he said.

"Among the new genes is a huge number - over 240 genes - encoding extracellular enzymes involved in carbohydrate degradation," said Cullen, "so this fungus has a really impressive amount of genetic diversity."

Until now, when looking for industrial enzymes, research was aimed at enzymatic screening from culture filtrates from the fungus, said [Tuula Teeri](#), professor in the Laboratory of Wood Biotechnology, Royal Institute for Technology, Sweden. "This means that what you come up with is the kind of enzymes that you have an assay for, and also those ones that are most abundantly produced - but you miss a lot of the interesting compounds," she said. "What the genomics actually can give is that we can get our hands on the minor components."

These enzymes nevertheless play a very important role in lignocellulose degradation and could constitute very interesting tools for looking at modification of the lignocellulose degradation process for industrial purposes, said Teeri, who was not involved in the study.

According to Teeri, another important finding is that while other filamentous fungi respond to chemical stimuli with coordinated expression of groups of genes, "*P. chrysosporium* doesn't do that; it individually regulates individual enzyme component. You can almost use the fungus as a biosensor," she said.

"The paper looks at sequence, but unlike some other sequenced genomes where DNA comes before any understanding of what it might mean, this paper captures a genome sequence, and then functionality

and understanding of the relevance to the functioning of the organism in its ecosystem," said [Roberta Farrell](#), professor in the Department of Biological Sciences at Waikato University, New Zealand.

Farrell said the authors establish mycology as a discipline that can contribute to ecosystem functioning. "This paper really does the right analysis of the genome sequence and takes it way beyond just a bunch of As and Ts and Cs and Gs," Farrell, who was not involved in the study, told us.

References

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