Genomics update

Is the hope for a cellulosic biofuel a lot of rot?

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Compared with the small amount of fermentable sugars in corn kernels, lignocellulose obtained from agricultural waste products or non-food crops is an abundant natural resource that can be used for the production of ethanol-based biofuel. However, the rigid structure linking cellulose and hemicellulose to lignin, while rather handy for plants, restricts the availability of fermentable sugars necessary to produce ethanol. As a result, current biofuel production relies on expensive and toxic pretreatment to detach the cellulose from lignin and render it susceptible to hydrolysis (Scharf and Tartar, 2008). But alternative approaches recently have been deduced from the genomes of organisms that naturally convert lignocellulose into fermentable sugars.

Several animals, such as termites and ruminant mammals, use symbiotic microbes to degrade lignin and cellulose. In all termites, this occurs in the digestive tract, but involves different types of symbionts in ‘lower’ and ‘higher’ termites: lower termites harbour both protozoa and bacteria, whereas higher termites only contain bacterial symbionts (Scharf and Tartar, 2008). To find lignin-degrading enzymes, researchers examined the microbiota metagenome of the wood-feeding higher termite Nasutitermes sp. and characterized a diverse bacterial community inhabiting a portion of the hindgut where the lignin breakdown occurs (Warnecke et al., 2007). This study identified a large set of bacterial genes for cellulose and xylan hydrolysis, thus providing a direct link between bacterial symbionts and lignocellulose degradation (Warnecke et al., 2007). In contrast, a recent metagenomic survey of unculturableView Termite Group I bacteria, which inhabit the protozoan symbionts of lower termites, demonstrated that the bacteria provide essential nitrogenous compounds to their host protists and termites but do not directly produce enzymes that break down wood (Hongoh et al., 2008). But because the microbial community in termites is complex and the relative contribution of host and symbiont genes in lignocellulose degradation is unknown (Scharf and Tartar, 2008), the genomes of other lignin-degrading organisms also are being investigated.

Basidiomycete white-rot fungi degrade lignocellulose through the secretion of oxidative and hydrolytic enzymes and are the only microbes capable of completely degrading lignin and converting it to CO₂ and H₂O (Ward et al., 2004). Although many species of white-rot fungi exist, Phanerochaete chrysosporium has been studied extensively because it decays lignin while leaving a large proportion of the cellulose undisturbed (Volk, 2004). In contrast to some ascomycete fungi that have few duplicated genes (e.g. Neurospora crassa), the genome sequence of P. chrysosporium revealed that lignin depolymerization genes are assembled in complex and diverse gene families (Martinez et al., 2004). The P. chrysosporium genome also harbours a novel peroxidase with similarity to previously recognized lignin and manganese peroxidases (Martinez et al., 2004). At least six other genes are predicted to encode copper radical oxidases, as well as four predicted aryl alcohol oxidases, which provide H₂O₂ necessary for the peroxidase catalytic breakdown of lignocellulose. Moreover, the P. chrysosporium genome also harbours large gene families of glycoside hydrolases that degrade cellulose and hemicellulose (Martinez et al., 2004).

Unfortunately, white-rot fungi use a fairly large amount of energy to completely degrade lignin, so recent work has focused on closely related brown-rot fungi, which can gain access to cellulosic hemicelluloses without completely breaking down lignin (Martinez et al., 2009). The recent transcriptome, secretome and genome sequence of the brown-rot fungus Postia placenta (Basidiomycota, Polyporales) has shed light on the mechanism that this organism employs to obtain plant nutrients (Martinez et al., 2009). In contrast to P. chrysosporium, the P. placenta genome lacks genes for lignin depolymerization as well as all conventional cellulose-binding domains, indicating that P. placenta has lost the energetically expensive lignocellulose-degrading enzymes seen in the white-rotting P. chrysosporium (Martinez et al., 2009). The P. placenta genome also harbours relatively few cellulolytic enzymes, such as endoglucanases and

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β-glucosidases. Instead, expression data indicate that the fungus depolymerizes cellulose using highly reactive oxidant molecules, and then deploys multiple hemicellulases and a single putative β-1,4-endoglucanase to release cellobiose for hydrolysis (Martinez et al., 2009). This simplified decay process has evolved independently in multiple clades of basidiomycete fungi (Hibbett and Donoghue, 2001) and is characterized by the loss or reduction of gene families commonly found in white-rot fungi (Martinez et al., 2009).

To further enhance the knowledge of fungal lignocellulose breakdown and its applications in biotechnology, current efforts are afoot to sequence other fungal genomes, including the white-rot fungus *Schizophyllum commune* and the wood-decaying oyster mushroom *Pleurotus ostreatus* (Stajich, 2009). Although exploiting fungal processes for commercial biofuel production may seem a distant goal, discovering the enzymatic arsenal of phylogenetically diverse wood-rotting fungi might one day enable a more cost-effective and environmentally friendly method for producing biofuel.

**References**


