



Articles of Significant Interest in This Issue

Diverse Hydroxylations of Fatty Compounds by a Class III Cytochrome P450 in a White-Rot Fungus

Phanerochaete chrysosporium is a white-rot fungus whose metabolism of lignin, aromatic pollutants, and lipids has been most extensively studied; it harbors 154 cytochrome P450-encoding genes in its genome. Sakai et al. (e01091-18) show that *P. chrysosporium* CYP505D6, a fused protein consisting of P450 and its reductase, hydroxylates fatty alcohols and acids with a carbon chain length of 9 to 15 at the ω -1 to ω -7 or ω -1 to ω -6 positions, respectively. Aromatic compounds, such as naphthalene and 1-naphthol, were also hydroxylated by CYP505D6. These findings highlight the unique substrate spectrum of CYP505D6, rendering it an attractive candidate enzyme for the biotechnological industry.

Rapid Identification of Catabolic Pathways in a Nonmodel Bacterium

Nonmodel microbes have diverse catabolic potentials, with applications including industrial bioconversions and environmental bioremediation. Cecil et al. (e01185-18) show that techniques for barcoded transposon insertion sequencing can be used to rapidly identify and organize the full catabolic network of a nonmodel bacterium. When applied to *Novosphingobium aromaticivorans*, this approach highlighted pathway interactions and led to the elucidation of previously unknown genes involved in degradation of the lignin-derived aromatic compound syringate. This technique has the potential for broad application to accelerate pathway discovery in nonmodel microbes.

Delineation of a Common Thiosulfate Assimilation Pathway in the Yeast *Saccharomyces cerevisiae*

Saccharomyces cerevisiae can produce more ethanol when using thiosulfate than when sulfate is used, as less energy is required to reduce thiosulfate to H₂S for assimilation. Using both genetic and biochemical approaches, Chen et al. (e01241-18) have elucidated the complete thiosulfate assimilation pathway in *S. cerevisiae*, which employs several enzymes of the sulfate assimilation pathway plus only one additional enzyme, rhodanese. Since rhodanese is present in most organisms, including bacteria and plants, thiosulfate is likely a common sulfur source for most organisms with the sulfate assimilation system.

Pesticide Metabolites Are Often More Toxic to Soil Microbes than Are Their Parent Compounds

The toxicity of pesticides to soil microorganisms has been attributed primarily to the parent compounds, while the potential effects of their metabolic products have attracted little attention. Vasileiadis et al. (e01536-18) showed, using iprodione and 3,5-dichloraniline (its soil derivative) as model compounds, that pesticide metabolites could be the main drivers of adverse effects on the structure and function of the soil microbial community, and ammonia-oxidizing microorganisms were found to be the most sensitive endpoint in soil and *in vitro* tests. These findings provide significant advances in pesticide environmental risk assessment.

Redirecting Siderophore Biosynthesis in *Myxococcus xanthus*

Myxochelins are well-known siderophores from myxobacteria. Using a novel plasmid-based expression system for the heterologous reconstitution of a biosynthetic pathway in the myxobacterium *Myxococcus xanthus*, Korp et al. (e01789-18) showed that a single enzyme, a hitherto-undescribed member of the amidohydrolase superfamily, is sufficient to convert myxochelins into previously described, structurally distinctive siderophores from the marine bacterium *Pseudoalteromonas piscicida*.

Regulatory Networks Governing Methionine Catabolism

Methionine (Met) shuttles organic nitrogen and plays a central role in nitrogen metabolism. Exogenous Met strongly induces the expression of its catabolic genes and generates volatile organic sulfur-containing compounds (VOSCs) via the Ehrlich and demethiolation pathways. Xu et al. (e01840-18) have found that in addition to the Ehrlich pathway, the demethiolation pathway is also regulated by a nitrogen catabolite repression-sensitive pathway that controls the transcription of genes required to catabolize poor nitrogen sources. This work advances our understanding of nitrogen catabolite repression-sensitive transcriptional regulation of sulfur-containing amino acid catabolism and provides a basis for fuel and valuable flavor alcohol production.