

Genomic Encyclopedia of Fungi

The **Genomic Encyclopedia of Fungi** is the key project of the JGI Fungal Genomics Program to focus fungal genome sequencing,

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Plant Health

Plant health maintenance is critical for sustainable growth of biofuel feedstock and fungi, as symbionts, pathogens, and biocontrol agents, dramatically affect plant health.

Symbionts such as mycorrhizae can increase productivity of bioenergy feedstock plants. Mycorrhizae enter symbiotic relationships with plants and effectively extend the host root system towards regions of decaying organic matter to provide nutrients such as nitrogen and phosphorus. Optimizing feedstock plant growth therefore is dependent on understanding molecular mechanisms of interactions between plants and mycorrhizae.

Pathogens can have dramatic negative effects on bioenergy crops as witnessed with the 1970 epidemic of corn leaf blight. Understanding mechanisms of virulence and pathogenicity, host specificity and the life cycle of pathogenic fungi hold keys to developing methods to control growth of pathogenic fungi and protecting plants. Feedstock protection can also be achieved by biocontrol fungi, which kill fungi, nematodes, and insects pathogenic to plants and are attractive alternatives to the chemical treatments used now.

Comparing genomes of pathogenic and symbiotic fungi to closely related fungi that lack these features will help find specific traits from each group of fungi and will help to understand the mechanisms of their interaction with plants. Reference genomes of mycorrhiza and other soil-inhabiting fungi will also facilitate comprehensive metagenomics studies of the rhizosphere, studies which until now have been mostly limited to bacterial communities.

Biorefinery

Biorefinery methods convert biopolymers such as cellulose into simple sugars (eg, glucose and xylose) and then into biofuels employing fungal hosts optimized for large scale industrial processes. Knowing the enzymes and processes employed by diverse fungi in lignocellulose degradation and sugar fermentation as well as understanding the molecular biology of strains adopted by industry are essential for development robust platforms for biomass-to-biofuel production on an industrial scale. Genome sequencing in this area will provide a comprehensive catalog of enzymes, metabolic processes, and regulatory and secretory mechanisms. Resequencing of industrial strains should help to map desirable properties such as morphology, hyperproductivity, thermostability to genomic blueprints.

Fungal Diversity

Fungal diversity. Over a million species in the Kingdom Fungi have evolved over millions of years to occupy diverse ecological niches and have accumulated an enormous but yet undiscovered natural arsenal of potentially useful innovations. While the number of fungal genome sequencing projects continues to increase, the phylogenetic breadth of current sequencing targets is extremely limited. Exploration of phylogenetic and ecological diversity of fungi by genome sequencing is therefore a potentially rich source of valuable metabolic pathways and enzyme activities that will remain undiscovered and unexploited until a systematic survey of phylogenetically diverse genome sequences is undertaken.