

Improved Biofuel Production through Discovery and Engineering of Terpene Metabolism in Switchgrass

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Project Goals:

Of the myriad specialized metabolites that plants form to adapt to environmental challenges, terpenoids form the largest group. In many major crops, unique terpenoid blends serve as key stress defenses that directly impact plant fitness and yield. In addition, select terpenoids are used for biofuel manufacture. Thus, engineering of terpenoid metabolism can provide a versatile resource for advancing biofuel feedstock production, but requires a system-wide knowledge of the diverse biosynthetic machinery and defensive potential of often species-specific terpenoids. This project merges genome-wide enzyme discovery with comparative –omics, protein structural and plant microbiome studies to define the biosynthesis and stress-defensive functions of switchgrass (*Panicum virgatum*) terpenoid metabolism. These insights will be combined with the development of genome editing tools to design plants with desirable terpene blends for improved biofuel production on marginal lands.

Abstract:

Diterpenoids constitute a diverse class of metabolites with critical functions in plant development, defense, and ecological adaptation. Major monocot crops, such as maize (*Zea mays*) and rice (*Oryza sativa*), deploy diverse blends of specialized diterpenoids as core components of biotic and abiotic stress resilience. This study reports the genome-wide discovery and functional characterization of terpenoid-metabolic genes, enzymes and pathways toward a diverse range of diterpenoids in the bioenergy crop switchgrass (*Panicum virgatum*). Biochemical analysis of several dozen enzymes revealed a modular metabolic network producing a diverse array of diterpenoid metabolites several of which perhaps uniquely occurring in switchgrass. Structure-guided protein mutagenesis of select enzymes identified active site determinants that may resemble neo-functionalization events that occurred during diversification of the switchgrass diTPS family and offer resources for engineering of bioactive metabolites. Combined transcriptomics and metabolomics studies identified multiple enzyme products in switchgrass root and leaf tissue with, albeit moderate, accumulation in response to oxidative and drought stress, thus supporting a possible physiological functions in the plants adaptation to abiotic stressors. Cultivation and analysis of switchgrass in small controlled environment devices (EcoFABs) now enabled a precise analysis of the role of switchgrass root diterpenoids in plant-environment interactions.

References:

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