

Identification of novel tryptophan-derived metabolites and associated genes of Arabidopsis by integrating PODIUM and mGWAS

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Project Goals: A better understanding of plant genomes and metabolism is necessary to discover valuable plant-based compounds, design abiotic and biotic stress-tolerant crops, and improve plant productivity. The difficulties in metabolite identification and associated gene discovery limit the progress to achieve these goals. We developed an approach to address these challenges by integrating the Pathway of Origin Determination in Untargeted Metabolomics (PODIUM) and metabolic genome-wide association studies (mGWAS). The combination of these tools provides origin information for metabolites and identifies metabolite-gene associations. In this project, metabolites generated from amino acids and the genes required for their synthesis or regulation will be identified in Arabidopsis and sorghum.

Tryptophan is a precursor for valuable compounds that play critical roles in plant growth and defense. Melatonin, a tryptophan-derived compound, is best known for its association with sleep-wake cycle control in mammals. In plants, melatonin has physiological effects on plant growth, photosynthesis, and responses to biotic and abiotic stressors. The biosynthetic route from tryptophan to melatonin in plants remains unclear. Arabidopsis produces other tryptophan-derived defense compounds to deal with herbivore attacks or pathogens, such as indole glucosinolates (IGs), camalexin, and indole-3-carboxylic acid (ICA). The biosynthesis of these compounds is relatively well characterized, but its regulation remains to be fully elucidated. Given the critical functions of these tryptophan-derived metabolites, we explored their biosynthesis and regulation by applying the PODIUM/mGWAS strategy on mutants disrupted in tryptophan metabolism. Differentially accumulated metabolite features (DAFs) generated from tryptophan were identified that may be intermediates in melatonin biosynthesis. By aligning tryptophan-derived DAFs with our mGWAS data, novel indole glucosinolate-gene associations were identified.

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