The development of economical viable bioenergy source is important to a sustainable industrial society and to the control of greenhouse emission. Among all the bioenergy substrates, lignocellulosic biomass has recently gained high interests, because it does not compete with the food production and animal feed. However, the extraction of lignocellulosic biomass for biofuel is hindered by lignin, one of the major components of plant cell wall. Lignin is mainly composed of three monomers, H, G, and S-lignins. Modification of lignin biosynthesis has been widely studied. Plants with down regulated lignin biosynthesis often show undesired growth retardation and abnormal development. The underlying mechanism of the lignin modification induced dwarfism (LMID), however, is still unclear. Taking advantage of the rich genetic, genomic, and molecular resources in the model plant Arabidopsis thaliana, we chose to use an Arabidopsis lignin mutant ref8 for study LMID. The ref8 was treated with a chemical mutagen to create random mutations and screened for suppressor lines that grow bigger than the original mutant. The suppressor lines show significant changes in the soluble metabolic profiles, compared to both WT and ref8. The ability to bolt and to flower is also recovered in some suppressor lines.

Identification of a growth inhibition relieved gene, GIR1

The leaf rosette of the representative suppressor lines are significantly bigger than those of ref8. The ability to bolt and to flower is also recovered in some suppressor lines.

Metabolic analysis of different suppressor lines suggests more GIR genes are involved in LMID

PCA analysis indicates that the suppressor lines have distinct metabolic profiles, compared to those of WT and ref8. Total 417 m/z features are included in this analysis. Suppressor 71-12, 8-1, and 97-1 have different alleles of the same gir1 gene.

DFRC lignin analysis of representative suppressor lines show predominant H-lignin content

Summary

1. Multiple homozygous suppressor lines with GIR phenotypes have been generated. Metabolic analysis suggests different GIR genes are involved in the underlying mechanisms of LMID.
2. All the analyzed suppressor lines show predominant H-lignin composition, which leads to lower biomass recalcitrance.

Future Work

LMID is a major barrier for developing lignocellulose biomass as efficient biofuel substrate. The identification of GIR1 suggests that the growth retardation in lignin-modified plants can be reverted through plant genetic engineering. The metabolic profiles of different suppressors indicate more GIR genes are involved in the underlying mechanisms of LMID. Identifying these GIR genes will provide information for developing and optimizing lignin-modified plants for efficient biofuel production.