Analysis of Gene Interaction Between the Transcription Factor SPT6L and Genes that Regulates Flowering of Arabidopsis Thaliana

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The flowering of plants is necessary for their further reproduction. Flowering is regulated by hundreds of genes encoding proteins. The goal of my academic work is to find out how AGO binding domain of the SPT6L protein affects flowering. I proceed from the hypothesis that a plant, mutated in the AGO binding domain of the SPT6L gene, will flower earlier. Finding a mechanism of flower gene SPT6L regulation paves the way for explaining the function of SPT6L. AGO proteins along with small RNAs are important regulators of gene activity and elucidation of their function would allow a better understanding of some inherited diseases and mostly to further develop in breeding technologies. In order to identify the main SPT6L's regulatory pathways, I analyzed the genetic interactions between single mutants of three key and well-described flowering regulatory genes and a mutant in the transcriptional gene named SPT6L. I crossed the mutant in SPT6L, which is mutated in the AGO binding domain with plants mutant in the flc (flowering inhibitor) and soc1 (signaling pathway integrator) genes. The FT gene (florigen) is in a strong genetic linkage to the SPT6L gene, so a double mutant cannot be obtained by crossing. Because of that, I have chosen an innovative CRISPR/Cas9 gene editing method to excise the AGO domain of the SPT6L gene. I successfully obtained mutant offspring selected by genotyping, I performed a phenotypic study and concluded that the action of the SPT6L gene is probably indirect, has inhibitory effects on FT and FLC, and apparently involved in more regulatory pathways.

Awards Won:

Second Award of $2,000