Mechanistic Characterization of a Transcription Factor bZIP16 in Regulating Arabidopsis Flowering Pathways

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bZIP transcription factors exist in all eukaryotes. In plants, they are master regulators of many central developmental and physiological processes. In 2012. bZIP16 was reported to promote seed germination and hypocotyl elongation during the early seedling development by repressing RGL2 and PIL5. Interestingly, a previous study has indicated that RGA and RGL2 both negatively regulate the floral transition. It inspired us to pursue whether bZIP16 also functions in Arabidopsis flowering time control. By counting the rosette leaf numbers at bolting, we found that bzip16 mutants showed late-flowering phenotypes under long-day and short-day conditions in Arabidopsis. To clarify how the floral transition is regulated by bZIP16, we performed a transcriptomic study and qRT-PCR to analyze the expressions of genes regulating flowering time in both wild-type and bzip16 mutant. Those results revealed that bZIP16 does not affect the expressions of genes in photoperiodic, gibberellin, autonomous and vernalization pathway. In contrast, bZIP16 significantly represses the expression of FLC and promotes the expressions of SOC1 and FT. Our chromatin-immunoprecipitation assay indicated that bZIP16 directly binds to the FLC promoter harboring G-box motif. The expression repression of FLC by bZIP16 will de-repress the expressions of SOC1 and FT to promote flowering. Our studies demonstrated that bZIP16 not only promotes seed germination and hypocotyl elongation in early seedling development but also plays a positive role in floral induction. Our research also revealed bZIP16 as a new floral regulator in controlling flowering time.

Awards Won:

Intel ISEF Best of Category Award of $5,000

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