Imaging, Expression Profiling, and Modeling: Systematic Approaches Integrated to Investigate BPC Regulation of the Circadian Clock

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This study investigates plant-specific GAGA-binding factors, BASIC PENTACYSTEINEs (BPCs), which are known to exhibit overlapping and antagonistic effects on various developmental phenotypes, including clock-mediated physiological activities. Nevertheless, their correlation with the Arabidopsis circadian oscillatory system, comprising interlocked transcriptional feedback loops, has remained unclear. To bridge knowledge gaps, I employed three methodologies: leaf movement monitoring offered intriguing insights into the multifaceted functions of class I and class II BPCs in orchestrating circadian rhythms; qRT-PCR experiments unveiled cryptic regulatory pathways; mathematical modeling enabled further elucidation of BPCs' roles in fine-tuning the circadian clock and ensuring optimal oscillations. In wet lab experiments, BPC mutant lines illustrated the precise control exerted by BPCs over key clock components, including CCA1, ELF4, GI, and PRRs, resulting in the attainment of distinct steady states. Additionally, BPC overexpression induction provided an alternative approach, bypassing salvage pathways within the BPC family. ChIP-seq evidence and analysis of clock gene profile alterations under disrupted BPC homeostasis facilitated the construction of a comprehensive simulated model to determine entry points and compare pathway efficacy. Overall, this research sheds light on how BPC proteins maintain homeostasis and choreograph the complex interplay of clock genes, with implications for potential agricultural applications in growth and development, thereby enhancing crop adaptability to environmental changes and increasing yield.

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