

GDCB SEMINAR

4:10 p.m. • Tuesday, Nov. 30, 2021 • 1414 Molecular Biology Building

“Interspecies transfer of *RAMOSA1* orthologs and *cis* regulation of grass inflorescence architecture”

Abstract — A key objective in biology is to understand the genetic basis of morphological diversity between and within species. In grasses including cereal crops such as maize, rice and sorghum and a plethora of wild grasses, grains are borne in reproductive shoots that are called inflorescences. There is tremendous intra- and interspecific variation among inflorescence morphology in the grasses. These similarities and differences provide an effective model for studying genetic mechanisms that underly evolutionary change in plant architecture including variation in inflorescence morphology impacting yield in cereal crops and weedy grass species. Despite such agronomical and ecological significance, the genes that underlie diverse inflorescence forms in the grasses have not been fully elucidated, and tests of functional conservation of syntenic orthologous genes are limited.

Using genetic approaches in maize, our lab has identified plant developmental mechanisms that regulate the architecture of both vegetative shoots and inflorescence shoots. For example, the *ramosa1* (*RA1*) transcription factor gene is central to a genetic network regulating floral shoot (inflorescence) branching. To better understand unique and conserved aspects of that network we carried out a cross-species investigation of *ramosa1* function. We performed genetic tests for functional conservation of syntenic orthologous

RA1 genes from maize, sorghum and a wild grass called setaria. In sorghum and setaria inflorescences, *RA1* expression marked meristem boundary domains in concordance with *RA1* transcript accumulation in maize. To directly test function, *RA1* transgene constructs from maize (Zm), sorghum (Sb) and setaria (Sv) were transformed into maize and introgressed into a common inbred genetic background containing the strong *ra1-R* mutant, so that the only functional *RA1* came from the transgene. The Zm*RA1*, Sb*RA1* and Sv*RA1* transgenes showed differential complementation and effects on the regulation of branching in maize tassels and ears. Through examining two different Sb*RA1* constructs and a maize-setaria promoter swap construct we identified *cis*-regulatory differences that impact ear and tassel morphology, and correlations with open chromatin signatures and conserved upstream sequences including known transcription factor binding motifs, as potential drivers of inflorescence diversity in the grasses.



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