Characterizing the role of epigenetic component ADA2 in *Brachypodium distachyon*

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Abstract

The SAGA complex is an important chromatin modification complex and activates nearly 10% of the *Saccharomyces cerevisiae* genome. SAGA (SPT-ADA2-GCN5-acetyltransferase) is a 1.8 mDa conglomeration of proteins composed of four separate but cooperative modules: the DUB (deubiquitination) module, the TAF module, the SPT module, and the HAT (histone acetyltransferase) module, all of which promote gene expression. This work focused on characterizing ADA2 in the model monocot *Brachypodium distachyon*. The major hypotheses were as follows: due to the conservation of SAGA across organisms, this complex also exists in *B. distachyon*; because ADA2 regulates a large portion of genes in other organisms, overexpressing ADA2 would alter development and provide clues regarding its function; and that these phenotypes would be related to the regulation of meristems in tillering and flowering in *B. distachyon*, as has been demonstrated in model dicot *Arabidopsis thaliana*. We generated three independently transformed transgenic lines (*UBI:ADA2-eGFP*) that overexpress ADA2. ADA2 protein accumulation and SAGA-targeted histone modifications correlated with the development of primary tillers in *B. distachyon* plants. Several genes involved in tiller regulation exhibited altered expression in the *UBI:ADA2-eGFP* lines, and ChIP-qPCR analysis revealed that ADA2 binds to the promoters of genes involved in axillary meristem development, such as *KN1* (*KNOTTED1*) and *FON1* (*FLORAL ORGAN NUMBER1*). Immunoblot analysis revealed that ADA2 protein accumulated in the inflorescence structures prior to grain development and flowering time was significantly delayed in the *UBI:ADA2-eGFP* lines. Emergence of the flag leaf was delayed in the *UBI:ADA2-eGFP* lines, suggesting that the delay in flowering results from delayed pseudostem development. Plants collected at this stage also demonstrated binding of ADA2 to the promoters of *FON1* and *KN1*. Overall these observations suggest that there is a common mechanism regulating both tiller development and flowering in *B. distachyon*, and that regulation of these processes is facilitated by ADA2.

About the Candidate

Jordan holds an Honours Bachelor of Medical Sciences in Biochemistry (with a minor in Genetics) from Western University. She also completed a Masters degree in the lab of Dr Jean-Benoit Charron at McGill University. Her doctoral work examined the role of chromatin modifiers in the model monocot, *Brachypodum distachyon*.