ABSTRACT

Xylem development is tightly regulated by hormones and other endogenous factors. The characterization of the acaulis5 (acl5) mutant in Arabidopsis thaliana, defective in thermospermine biosynthesis, led to the establishment of a role for this polyamine in the regulation of xylem maturation, preventing cell death before xylem differentiation has finished. Although the precise molecular mechanism is still unknown, a group of bHLH transcription factors has been identified (SAC51/AJAX1, AJAX2, AJAX3 and AJAX4) whose translation is promoted by thermospermine, and is indispensable for correct xylem maturation. They have been proposed to restrict the activity of another transcription factor, LONESOME HYGHWAY (LHW) to provide temporal control to xylem differentiation.

Although it is known that the degradation of DELLA proteins induced by gibberellins (GAs) is necessary for the increase in secondary growth that accompanies floral transition, the mechanism that directs this switch in vascular development has not been elucidated. In a yeast-two hybrid screening for the identification of transcription factors that mediate the activity of DELLA proteins, AJAX3 was isolated as an interactor of GAI, and the purpose of this Thesis has been to check if Gas regulate xylem maturation, and if they do it through this interaction. The combination of genetic, physiological and molecular analyses has shown that: (1) GA deficiency provokes a xylem phenotype similar to the one caused by loss of ACL5 function; (2) DELLA proteins accumulate in vasculature, overlapping with the expression of other elements necessary for xylem differentiation, such as ACL5 and LHW; and (3) forced accumulation of DELLAs in the ACL5 specific expression domain in the vasculature impairs xylem maturation. Moreover, AJAX3 inhibited the capacity of LHW to activate its targets in transient expression assays in Nicotiana benthamiana, while coexpression of GAI alleviated this repression.

Based on these results, we propose that GAs promote xylem maturation at least through the modulation of AJAX3 activity to accomodate the differentiation program to the increase in secondary growth during the transition to reproductive development.