HD-Zip II transcription factors in auxin-regulated plant development

The homeodomain-leucine zipper (HD-Zip) class of transcription factors is unique to plants. HD-Zip proteins bind to DNA exclusively as dimers recognizing dyad symmetric sequences and act as positive or negative regulators of gene expression. On the basis of sequence homology in the HD-Zip DNA-binding domain, HD-Zip proteins have been grouped into four families (HD-Zip I-IV). Each HD-Zip family can be further divided into subfamilies containing paralogous genes that have arisen through genome duplication. Remarkably, all the members of the HD-Zip II γ and -δ clades are regulated by light quality changes that induce in the majority of the angiosperms the shade-avoidance response, a process regulated at multiple levels by auxin. Intriguingly, it has recently emerged that, apart from their function in shade avoidance (Sessa et al. 2018; Carabelli et al. 2018), the HD-Zip II γ and -δ transcription factors control, in a white-light environment, several auxin-regulated developmental processes (Turchi et al. 2013). Among them, we focused our attention on gynoecium and columella development.

In the gynoecium of the hat3 athb4 mutant, the valves appear severely splitted, insted of being tightly fused. This phenotype is resembling the loss of function of the SPATULA (SPT) gene, which is indeed involved in the formation of the style and stigma, the upper part of the gynoecium. In the wild type, the apical style region undergoes a transition from a bilaterally symmetric stage to a radially symmetric structure during gynoecium development. Two transcription factors, INDEHISCENT and SPT, are both necessary and sufficient for the radIALIZATION process and control style symmetry by directly regulating auxin distribution. We are studying the genetic interactions between HAT3/ATHB4 and SPT, by crossing the respective mutant lines and analyzing the expression of HAT3 and SPT marker lines in the spt and hat3 athb4 mutants, respectively. Indeed, HAT3 and ATHB4 expression is strongly reduced in the spt-12 mutant, and the overexpression of HAT3 and/or ATHB4 rescues the spt-12 phenotype. These data, together with the previous observation that HAT3 and ATHB4 are direct and positive target of SP, strongly suggest that HAT3 and ATHB4 are downstream effectors of SPT in the control of auxin distribution that brings to the bilateral-to-radial transition in the apical part of the gynoecium.

Columella is composed of 5-6 tier of cells located at the root apex with a role in physical protection of the root meristem and gravity sensing. As it contains stem cells (CSC) and differentiated cell (DC) in a regular and stable arrangement, columella is an excellent model system to study molecular mechanisms to balance cell proliferation and differentiation, a process profoundly affected by auxin. Loss of function HD-Zip II (hat3 athb4 athb2) mutant shows a reduced number of CSC layer and reduced CSC division rate, in an auxin dependent manner. Moreover, a molecular-genetic approach highlights an interaction between HD-Zip II proteins and two plant-specific transcription factors, FEZ and SOMBRERO (SMB), that form a regulatory circuit required for the correct columella developmental program. Taken together the data suggest that HDZIP II factors, in concert with FEZ/SMB, contribute to the columella stem cell maintenance interfering with auxin pathway.

References:

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