VIP1 and its family members are not important for Agrobacterium-mediated transformation

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Arabidopsis VIP1 was first identified as a protein interacting in yeast with the Agrobacterium virulence protein VirE2. Several reports indicated the importance of VIP1 in Agrobacterium-mediated transformation. As a plant bZIP transcription factor, VIP1 has been implicated in innate immunity in response to the PAMP flg22. VIP1 may also regulate responses to sulfur deficiency and hypo-osmotic stress. In 2014, after carefully analyzing the transformation susceptibility of numerous vip1-1 mutant and VIP1 overexpressing transgenic plants, our lab concluded that VIP1 is not important for Agrobacterium-mediated transformation. However, the T-DNA insertion in the vip1-1 mutant permits expression of the first 244 VIP1 amino acids, including the crucial bZIP DNA binding domain. We used CRISPR/Cas9 to generate the vip1-2 mutant, which expresses the first 145 VIP1 amino acids but lacks the bZIP domain. Homozygous vip1-2 plants show transformation susceptibility similar to that of wild-type plants. VIP1 belongs to Group I, subgroup 1 of the Arabidopsis bZIP transcription factor family. This subgroup contains five additional VIP1 homologs: PosF21, bZIP29, bZIP52, bZIP69, and bZIP30. Because these homologs may function redundantly with VIP1, we obtained transgenic Arabidopsis lines expressing a VIP1-SRDX fusion protein (Tsugama et al, 2016). Mitsuda et al. (2006) showed that overexpression of a transcription factor-SRDX fusion protein can dominantly repress expression of genes normally activated by the transcription factor and its homologs. All VIP1-SRDX transgenic lines showed wild-type levels of both transient and stable transformation susceptibility. We are currently determining whether VirE2 interacts with VIP1 subgroup 1 homologs, and whether expression of VirE2 alters their subcellular localization. Taken together, these results confirm and extend our original observations that neither VIP1 nor its close homologs is important for Agrobacterium-mediated transformation.