

Jasmonate Signaling and Stamen Development in *Arabidopsis*

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The plant hormone jasmonic acid (JA) is critical to defense signaling pathways and is essential for reproductive processes in some plant species. In *Arabidopsis*, JA is essential for three processes involved in male fertility: 1) filament elongation, 2) anther dehiscence, and 3) pollen viability. *Arabidopsis* mutants that are unable to synthesize JA, such as the *fad3-2 fad 7-2 fad8* and *opr3* mutants, are male sterile and flower development arrests at stage 12; however, fertility can be restored by exogenous application of JA. Mutations in the F-box protein COI1 also abolish JA responses. *coi1* mutant plants are male sterile but the phenotype cannot be rescued by application of JA. To identify JA-responsive genes that are critical to male fertility, we have carried out transcriptional profiling over the course of 22 hours in *Arabidopsis opr3* stamens using Affymetrix ATH1 arrays. From this investigation, we have identified a 15-member gene family without previously ascribed function, where 10 of these genes were rapidly induced by JA. The proteins encoded by these genes have conserved domains in common with the ZIM subfamily of zinc finger transcription factors, but no recognizable DNA binding domain, and we have named them JAsmonate Zim-domain (JAZ) proteins. JAZ-GFP fusion proteins were localized to the nucleus, following transient expression in onion epidermal cells. JAZ-GUS fusion proteins, expressed in *Arabidopsis* seedlings, were rapidly degraded after application of JA, but were stabilized by treatment with MG132, a 26S proteasome inhibitor. The JAZ-GUS fusion proteins were also stable in the *coi1-1* mutant background. Furthermore, overexpression of a construct containing a deletion of one conserved domain led to a dominant-negative phenotype that is similar to the phenotype of *coi1-1* – the plants are male sterile but cannot be rescued by application of JA. Given these data, we propose that the JAZ proteins are transcriptional repressors that are ubiquitinated by SCF^{COI1} and are degraded by the 26S proteasome to initiate transcription of jasmonate-responsive genes.