

The Role of ERF Transcription Factors in Defenses Against Specialist and Generalist Herbivores
in *Arabidopsis thaliana*

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Abstract

Plant responses to herbivory are complex, involving differential perception, multiple signaling pathways, and the transcription of defense-responsive genes. Using a whole-genome microarray and bioinformatics tools, we identified transcription factors and *cis*-elements important in differential responses in *Arabidopsis thaliana* after attack by aphids, the specialist caterpillar, *Pieris rapae*, and the generalist caterpillar, *Spodoptera exigua*. Insect-specific changes in gene expression were observed and involved the fine-tuning of the stress-related hormones, jasmonate, salicylate, and ethylene. Ethylene was produced in response to both insect species, although the amounts and timing of production differed. Additionally, rapid and increased jasmonate and jasmonate-isoleucine elicitation in *Arabidopsis* after attack by both insects confirmed these signals as general herbivore-related responses. Using RT-PCR, we found members of the *ERF* (Ethylene Response Factor) transcription factor family and *AtMYC2* to be differentially regulated in response to the two caterpillars. We assessed the feeding behavior of *S. exigua* and *P. rapae* in wild-type and *ERF* mutant plants (*erf5*, *erf6*, *erf104*, and *erf105*) using a novel digital phenotyping technique. *S. exigua* maintained similar growth rates despite consuming less mutant tissue. Although induced aliphatic and indolyl glucosinolate (GS) levels were significantly higher in *erf104* plants after *S. exigua* feeding, no consistent relationships between GS and tissue consumption by insects were found. Our results demonstrate clear insect resistance phenotypes in *erf* mutants, suggesting a role for ERFs in the negative regulation of a defense mechanism other than glucosinolate production.