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Phakopsora pachyrhizi (soybean rust) effector candidates that alter plant immune responses

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Previous sequencing of the haustorial transcriptome of the soybean rust fungus, *Phakopsora pachyrhizi*, led to prediction of at least 150 putatively secreted proteins. These proteins were termed *P. pachyrhizi* effector candidates (*PpECs*), and 82 of the longest full-length coding sequences were cloned into various vectors that enabled bacterial delivery via the Type III secretion system, viral delivery, transient expression via *Agrobacterium* infiltration, or expression in yeast. Given the challenges of investigating effector functions directly in an obligate, biotrophic fungus, we used these systems as surrogates to identify *PpECs* that have abilities to suppress and/or activate defense or defense-like responses in host and non-hosts. The *PpECs* were also tagged with GFP so that their possible localizations within plant cells could be determined. The main categories of localization were cytoplasmic, nuclear, cytoplasmic + nuclear, and sub-nuclear. We have further characterized a few of the *PpECs* including *PpEC15*, a predicted protease that attenuated basal defense in tobacco and *Arabidopsis* and was localized to the nucleus when transiently expressed in *Nicotiana benthamiana*. The results suggest that *PpEC15* cleaves one or more nuclear plant proteins that positively regulate basal immunity.