

Natural resistance variations among *Arabidopsis thaliana* populations against oomycete pathogen *Hyaloperonospora arabidopsidis*

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ABSTRACT

Oomycetes are a group of plant pathogens that is responsible for numerous plant diseases, such as the late potato blight, sudden oak death, and downy mildew, which have led to economic losses and environmental impacts. Although oomycetes are destructive, there are currently no methods that are cost-efficient or effective enough for control in agriculture. However, researchers have discovered ecotypes of the small plant *Arabidopsis thaliana* have evolved multiple resistance genes against oomycete *Hyaloperonospora arabidopsidis* in the wild. These resistance genes are able to detect effector proteins released by oomycete *Hyaloperonospora arabidopsidis* and elicit the hypersensitive cell death (HR) immune response to prevent further spread of pathogen within the plant cell. But in the evolutionary battle for survival, the oomycete has also evolved new effector proteins to avoid detection by these resistance genes. Although the interaction between a specific resistance gene and its corresponding effector protein has been studied extensively, there is a lack of knowledge regarding interactions of multiple resistance genes against multiple pathogens. My research focused on the phenotypic resistance variations in *A. thaliana* ecotypes as a result of multiple resistance genes. Spray inoculation of the 96 *A. thaliana* ecotypes with the five variations of *H. arabidopsidis* pathogen showed that ecotypes from the same geographic origin do not display similar patterns of resistance against the pathogens, despite facing similar selection pressures. Trypan blue staining of ecotypes infected with *H. arabidopsidis* Emco revealed that developmental regulation of resistance response is present throughout *A. thaliana* species, not just in ecotype Col-0. Comparison between syringe inoculation of ATR1 effector protein into the *A. thaliana* ecotypes and whole-pathogen spray inoculation showed that resistance gene RPP1 alone is not able to stop pathogen growth and proliferation in all ecotypes. Understanding how resistance genes work in combination in *A. thaliana* may potentially help in development of more resilient crop varieties and sustainable pest management tactics.

KEYWORDS

Geography, developmental, regulation, RPP1, ATR1