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# Identifying plant resistance pathways in *Arabidopsis thaliana*

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The destruction of plants by a pathogen results in millions of dollars lost in crop yield annually. Identifying the plant response pathway to the presence of a pathogen is key to combating plant disease. The gene-for-gene hypothesis suggests that for every pathogen avirulence gene (*avr*), there is a corresponding specific plant resistance (*R*) gene that recognizes it and elicits a defense response. One method for discovering resistance pathways is through the use of a suppressor screen in which the deletion or mutation of a negative regulator can reactivate a signaling pathway. Our *srfr* (suppressor of rps4-RLD) mutants were discovered to provide resistance to the *Pseudomonas syringae* pv. tomato DC3000 expressing *avrRps4* and thus is possibly a regulatory gene. The *srfr* mutants reactivated resistance to *avrRps4* in plants that have a non-functional *RPS4* gene. We are studying to see if the *srfr* gene signaling pathway reactivates *avr* responses dependent on R genes other than *RPS4*. We chose the well-studied *RPM1* gene, which functions in detecting bacteria expressing *avrRpm1*. After crossing *srfr3* and *rpm1-3* mutants and harvesting F1 seeds, we grow these F1 seeds to get the F2 generation population. We isolated genomic DNA from F2 plants and then applied PCR based markers to find homozygous double mutants using 2 genetic markers linked to the *srfr3* and *rpm1-3* mutation, respectively. The F3 generation plants will be available to test disease symptoms in these double mutants. Based on the results of disease symptoms of the F3 population against bacteria expressing *avrRpm1*, we will propose whether or not the *srfr3* gene is involved in the *RPM1* defense signaling pathway. If the F3 generation is susceptible to *avrRpm1*, then *srfr3* is not involved in the *RPM1* defense signaling pathway.