

CSB DEPARTMENTAL SEMINAR

An atypical NLR confers bacterial wilt resistance in a wild *Solanum* specie



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Ralstonia solanacearum is a devastating pathogen that causes bacterial wilt disease in many plant hosts and causes severe yield loss in the field. However, only a few numbers of resistance genes were identified to induce immunity against *R. solanacearum*. *Solanum americanum* is a close relative of economically important solanaceous crops, and it is diploid with a 1.1Gb genome and harbors around 500 nucleotide-binding leucine-rich repeat receptors (NLRs), which makes *S. americanum* desirable for finding novel resistance genes. To identify novel bacterial wilt resistance genes, natural accessions of *Solanum americanum* were tested for bacterial wilt resistance. *R. solanacearum* type III-secreted effector RipAZ1 from Pe_26 strain was previously shown to trigger immune responses in *S. americanum* SP2273 accession but not in SP2275. Using bulk segregant analysis, we mapped the resistance gene locus at the upper arm of chromosome 5. Among 19 candidate NLRs, Resistance to *R. solanacearum* 1a (Rrs-amr1a) and Rrs-amr1b are shown to be required as pair NLRs for RipAZ1 recognition. Interestingly, Rrs-amr1a has an atypical NLR architecture with an additional nucleotide-binding leucine-rich repeat domain in its C-terminal. Taken together, identifying the novel pair NLRs that recognize RipAZ1 will help develop bacterial wilt-resistant solanaceous crops. Future studies on the function of integrated domains of Rrs-amr1a and how the pair NLRs triggers immunity will elucidate the mechanism of bacterial wilt resistance in *S. americanum*.

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