Dissecting the genetic and molecular basis of plant-pathogen interaction in wheat stem rust pathosystem

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The identification of genetic factors that define the outcome of host-pathogen interaction (virulence vs. avirulence) is critical for developing crop varieties with long lasting resistance. Plants recognize pathogen colonization in part using resistance (R) genes, which mostly belong to a class of NBS-LRR-encoding (NLR) genes, which serve as the immune receptors of protein ligands (effectors) secreted by pathogens into host cells. The R gene - mediated sensing of effectors initiates an effector-triggered immunity pathway resulting in cell death preventing further spread of infection. In our projects, we have identified and characterized the first R gene (referred to as Sr35) that confers resistance against one of the major devastating wheat diseases, stem rust, caused by Puccinia graminis f. sp. tritici (Pgt). This gene was used as an entry point to unravel the molecular bases of resistance to Pgt in wheat, especially to its recently emerged broadly virulent Pgt race Ug99. We have used the whole genome sequencing of multiple Sr35-virulent and –avirulent Pgt strains including natural field isolates and chemically mutagenized strains to identify fungal ligand (AvrSr35) that is recognized by Sr35. By combining comparative genome analyses, microscopic imaging, bimolecular fluorescence complementation, co-immunoprecipitation and transient expression in planta, we demonstrated that AvrSr35 is a protein with the N-terminal secretion signal peptide that interacts with Sr35 protein and triggers defense responses. To accelerate identification of R genes and matching effectors, we also conduct re-sequencing of wheat and Pgt populations. Combined with large-scale phenotyping, these resources allow for the joint mapping of genetic factors in the populations of host and pathogen. These efforts are aimed at constructing the detailed map of wheat-Pgt interaction that captures the complexity of interactions between the plant’s numerous immune receptors and diverse virulence proteins secreted by pathogens.