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Genomic Exploration of Plant Pathogens and Host Resistance

Crop diseases cause yield losses and affect food security. Genetically understanding pathogens and plant resistance is critical for disease management and crop improvement. Next-generation sequencing (NGS) technologies provide unprecedented tools to study the plant-pathogen system. In this talk, first, the cloning of the wheat leaf rust resistant gene *Lr42* will be presented. The identification of the gene will promote use of *Lr42* in wheat breeding programs. The cloning was facilitated by adaptation of bulked RNA sequencing analysis to wheat, which represents a labor- and cost-efficient approach. The second topic is about the genetic dissection of host resistance to a maize disease Goss's wilt, which has spread throughout the Great Plains in the US in recent years. Specifically, a locus associated with Goss's wilt resistance was identified through examining copy number variation between resistant and susceptible maize lines. Third, the construction of a reference genome sequence of the wheat blast fungus will be presented. Wheat blast is a devastating new fungal disease, originally identified in South America and spread to South Asia recently. Availability of the reference genome sequence and comparison of genomes from multiple strains led to the finding of dispensable mini-chromosomes. The results showed that the mini-chromosome harbors effector genes and, remarkably, different wheat blast isolates contain distinct sequences from ends of indispensable core chromosomes. Collectively, three projects to be presented demonstrate the value of NGS and represent new strategies in genetic studies of crop diseases.