Comprehensive RNA Profiling Identifies Novel Blackleg Resistance Genes in Canola

Drewnik, Dennis

The hemibiotrophic fungal pathogen Leptosphaeria maculans, the causative agent of blackleg disease, is the most devastating pathogen of canola (Brassica napus), causing $1.5 billion USD in worldwide crop loss annually. Although mitigation of crop loss relies heavily on molecular resistance breeding, there is currently little information available about the regulatory mechanisms underlying host resistance against L. maculans. This research aims to identify previously unknown genetic regulators and pathways contributing to host-incompatible interactions within this pathosystem. This research used complex computational analyses, performed on preexisting whole-leaf RNA sequencing data of resistant and susceptible canola plants, to identify 54 novel defense genes specifically activated in resistant plants across all infection stages. Furthermore, when gene deficient Arabidopsis mutants were challenged with the fungus, five of the 54 genes, including two transmembrane receptors of unknown biological function, showed to directly affect plant susceptibility. Gene expression was studied directly at the host-pathogen interface by dissecting tissues via laser microdissection and using qRT-PCR. Defense signaling hormones including Salicylic Acid and Jasmonic Acid, as well as antifungal metabolites such as Indole Glucosinolates, were discovered to accumulate in unique previously unknown spatial tissue gradients. Furthermore, mRNA abundances of novel genes coincided with known defense regulators, indicating new defense pathways. This research can assist plant scientists in the production of a more robust and prolific canola crop. Future application of this work can help increase worldwide crop yields to feed a growing population, estimated to reach 9 billion people by 2050.

Awards Won:

Intel ISEF Best of Category Award of $5,000

First Award of $5,000