Predicting Target Binding Sites in Plant Immune Receptors

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Plants rely on repertoires of hundreds of NLR immune receptors to defend against diverse and rapidly evolving pathogens. Based on Arabidopsis and Brachypodium data, we have observed that a subset of highly variable NLRs (hvNLRs) show a high degree of intra-species diversity making them the likely source of novel specificities and, by extension, a species-wide pool of potentially adaptive variants. Recent expansion of available crop pan-genomes allowed extending this observation to rice, soy, and maize. Coupled with computational protein structure prediction, the observed sequence diversity is sufficient to predict target-binding sites in the hvNLRs of model species and crops. The resulting understanding will guide immune receptor engineering efforts aimed at improving plant health. It also provides clues to how our own innate immune receptors arose prior to the evolution of the adaptive immunity.