Immune-suppressing pattern recognition receptors mediate host-driven recruitment of microbes

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Project Goals: Identify and characterize species-divergence of immune-suppressing pattern recognition receptors in *Salix spp*.

Unlike models which posit that microbe-associated molecular patterns (MAMPs) are responsible for evasion of innate host immunity during colonization by microbes, we provide evidence of active host-driven recruitment of microbes by specific membrane-bound pattern recognition receptors (PRRs), which recognize carbohydrate moieties in microbial cell walls leading to global suppression of the host's own immune response to facilitate colonization. A hallmark feature of these PRRs is that they have conserved protein domain architecture which includes lectin-binding, S-locus, Plasminogen-Apple-Nematode (PAN), transmembrane (TM) and kinase domains. We hypothesize that upon recognition of microbial MAMPs, the intracellular kinase domain initiates signaling cascades which results in suppression of host defense mechanism to facilitate colonization. However, there is currently no knowledge of which specific domain is responsible for suppression of host immunity to facilitate invasion by microbes. Using comparative genomics across seven *Salix* species (, *S. purpurea*, *S. viminalis*, *S. udensis*, *S. integra*, *S. koriyanagi*, *S. alberti*, and *S. suchowensis*) coupled with molecular genetic approaches including heterologous transgenesis, transient assays and transcriptome profiling, we provide evidence that a key domain encompassing twenty amino acids is essential for suppression of host defense mechanisms. Mutating as few as six of these amino acids resulted in successful induction of defense response based on observed increases in expression of canonical defense marker-genes, including WRKY40, WRKY72 and NPR1. Implications of genomic variation in this domain across the *Salix* species will be illustrated by differential abundance of microbial symbionts in the root tissue as determined by 16S and fungal ITS sequencing. This discovery provides opportunities for engineering novel symbiotic interactions for sustainable production of plant-based industrial feedstocks.

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