Genome sequencing reveal structural and nucleotide-level divergence among immunosuppressing G-type Lectin Receptor kinases across multiple *Salix* species.

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Project goals: This project seeks to elucidate the molecular basis of host immunosuppression during endophyte recruitment in the genus *Salix* and access speciation-driven divergence of these molecular process at the genome level.

In revealing a novel role for self-immunosuppression in plants during host-cell invasion by microbes, Plasminogen-Apple-Nematode (PAN) domain proteins, D-mannose lectin receptor kinases (G-LecRKs), were shown to function as negative regulators of defense signaling during pathogenesis by the fungal pathogen *Sphaerulina musiva*[1], parasitism of *Arabidopsis* by nematodes[2], and engineering of *Arabidopsis* into a host of the fungal symbiont *Laccaria bicolor*[3]. Moreover, PAN domain carrying S-locus kinases, reported to mediate self-incompatibility during pollination, fall under the same class of G-LecRKs[4]. Across eukaryotes, immunosuppression is an essential biological phenomenon for gamete fertilization, cell growth and proliferation during organismal development. Here, we propose that the PAN domain, comprised of a core of highly conserved cysteine residues, is a unifying feature that is found in association with proteins involved in immunosuppression across highly divergent organisms. Further, we reveal that PAN domain proteins are used or targeted by pathogens, parasites and symbionts during host-cell invasion. As such, the PAN domain is a reliable biomarker for the host-cell invasion machinery. Species divergence in the PAN domain-containing G-LecRKs was evaluated using Nanopore assemblies of 11 genomes sampled to represent diverse speciation events in the genus *Salix* and implications on species-level differences in endosphere microbial community diversity will be illustrated.

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