

Investigating the roles of WRKY transcription factors in commensal bacteria root colonization

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Roots are continuously exposed to a wide range of microorganisms, including commensals, beneficials, and pathogens. To defend against pathogens, plants evolved two defense strategies: microbe-associated molecular pattern-triggered immunity (MTI) and microbial effector-triggered immunity (ETI), based on the extracellular perception of common molecular patterns or the intracellular perception of virulence-associated effectors, respectively. However, it is not understood how plants can distinguish between pathogen and commensal, allowing only commensal microbes to colonize the root while keeping pathogens at bay. Teixeira et al. (2021) and Ma et al. (2021) demonstrated that plant-associated commensal bacteria modulate a specific and evolutionarily conserved sector of Arabidopsis MTI during root colonization. We postulate that this sector contains genes whose downregulation is required for successful root colonization and community assembly. WRKY transcription factors are enriched in the immune-responsive genes that are downregulated by a single commensal strain or a group of commensal strains from various bacterial taxa.

Therefore, we are investigating the underlying molecular mechanisms of WRKYs by using dexamethasone (Dex)-inducible overexpression lines and mutant lines of the most highly flg22-induced WRKY28 and WRKY30 genes, assessing their MTI responses to flg22, and evaluating their roles in root colonization by commensal bacteria. In response to flg22, preliminary results show that WRKY28/WRKY30 Dex-inducible overexpression lines display a shorter-root phenotype compared to Col-0. In contrast, WRKY28/WRKY30-SRDX (SUPERMAN Repression Domain X) dominant-repressor lines display a longer-root phenotype, suggesting that WRKY28 and WRKY30 modulate flg22-triggered root growth inhibition.