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Title: A genome-wide association study reveals cytokinin as a major component in the root defense

responses against Ralstonia solanacearum

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Keywords: Bacterial wilt

cytokinin defense GWAS hormones immune system

Issue Date: 2021

Publisher: Oxford Academic

Citation: Journal of Experimental Botany, 72(7), 2727-2740.

Abstract: Bact

Bacterial wilt caused by the soil-borne pathogen Ralstonia solancearum is economically devastating, with no effective methods to fight the disease. This pathogen invades plants through their roots and colonizes their xylem, clogging the vasculature and causing rapid wilting. Key to preventing colonization are the early defense responses triggered in the host's root upon infection, which remain mostly unknown. Here, we have taken advantage of a high-throughput in vitro infection system to screen natural variability associated with the root growth inhibition phenotype caused by R. solanacearum in Arabidopsis during the first hours of infection. To analyze the genetic determinants of this trait, we have performed a genome-wide association study, identifying allelic variation at several loci related to cytokinin metabolism, including genes responsible for biosynthesis and degradation of cytokinin. Further, our data clearly demonstrate that cytokinin signaling is induced early during the infection process and cytokinin contributes to immunity against R. solanacearum. This study highlights a new role for cytokinin in root immunity, paving the way for future research that will help in understanding the mechanisms underpinning root defenses

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URI: https://doi.org/10.1093/jxb/eraa610 (https://doi.org/10.1093/jxb/eraa610)

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