Understanding Parasitism: Plant Transcription Factor Is Regulated in a Strain-Dependent Manner by Root-Knot Nematode

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One major challenge in the 21st century is increasing crop yield to feed the world's growing population on diminishing arable land. Plant parasitic nematodes, including the Root-Knot Nematode (RKN), cause nearly US $100 billion dollars in annual global crop damage. Previous attempts in nematode control have yielded little success partly due to lack of understanding pathogenicity by distinct nematode strains at the phenotypic and molecular levels. Recent studies have shown that RKN strains, VW9 and LM, trigger distinct plant host response. In particular, the expression of AGAMOUS, a key plant transcription factor, is highly suppressed in VW9-infected but not in LM-infected roots. To elucidate the role of AGAMOUS in host-parasite interactions, it is imperative to identify the target genes of AGAMOUS and their respective biological processes. To this end, I conducted computational sequence search to identify candidate AGAMOUS target genes and then performed quantitative gene expression analysis to validate conserved targets. For the first time, three AGAMOUS target genes upon RKN infection were revealed: glycoside hydrolase 3 which is involved in cell wall remodeling, energy metabolism and pathogen defense; ß-ketoacyl-coa synthase which catalyzes fatty acyl-CoA elongation; and phosphoenolpyruvate carboxylase which plays a key role in nitrogen fixation. This provides molecular evidence for the phenotypic results that plant growth and root development were severely damaged by VW9 but not LM. The discovery of these target genes and their biological processes has shed new light on the mechanisms of the host-parasite interaction and developing a novel strategy to engineer nematode resistant crops.

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