Transcriptome analysis of root-knot nematode (Meloidogyne incognita)-infected tomato (Solanum lycopersicum) roots reveals complex gene expression profiles and metabolic networks of both host and nematode during susceptible and resistance responses - DTU Orbit (30/08/2017)

Transcriptome analysis of root-knot nematode (Meloidogyne incognita)-infected tomato (Solanum lycopersicum) roots reveals complex gene expression profiles and metabolic networks of both host and nematode during susceptible and resistance responses

Root knot nematodes (RKNs, Meloidogyne incognita) are economically important endoparasites having a wide-host range. We have taken a comprehensive transcriptomic approach to investigate the expression of both tomato and RKN genes in tomato roots at five infection time intervals from susceptible plants and two infection time intervals from resistant plants, grown under soil conditions. Differentially expressed genes during susceptible (1827-tomato, 462-RKN) and resistance (25-tomato, 160-RKN) interactions were identified. In susceptible responses, tomato genes involved in cell wall structure, development, primary and secondary metabolites and defense signalling pathways along with RKN genes involved in host parasitism, development and defense are discussed. In resistance responses, tomato genes involved in secondary metabolite and hormone-mediated defense responses along with RKN genes involved in starvation stress-induced apoptosis are discussed. Also, forty novel differentially expressed RKN genes encoding secretory proteins were identified. Our findings, for the first time, provide novel insights into temporal regulation of genes involved in various biological processes from tomato and RKN simultaneously during susceptible and resistance responses, and reveals involvement of a complex network of biosynthetic pathways during disease development.

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