Cross-species genetic network inference by reverse engineering

-- Understanding the crosstalk between plants and parasitic nematodes

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Abstract

Root-knot nematodes (RKN) are widespread plant parasites that cause substantial loss to agricultural production. RKN invade their host plant at the root tip, and then migrate through the root to their eventual feeding site. Intercellular movement is facilitated by the secretion of enzymes and proteins that degrade the structure of the plant cell wall. Feeding sites are formed through massive physiological and morphological modifications of plant root cells triggered by the injection of nematode effector proteins. While it is clear that understanding how host plant defenses against nematode invasion is crucial to control nematode infection, little is currently known about these signaling networks.

In this project, a model plant-pathogen system, \textit{Medicago truncatula} infected with the RKN \textit{Meloidogyne hapla}, was adopted to examine cross species genetic networks. \textit{M. truncatula} plants were infected by \textit{M. hapla} lines genetically similar to recombinant inbred lines. RNA samples for plant and RKN were collected simultaneously from feeding sites, and were sequenced to derive the expression profiles and \textit{M. hapla} genotypes using Illumina sequencing. Candidate genes that appear to be involved in plant-nematode interactions were identified by within species eQTL analysis for \textit{M. hapla}, and cross species eQTL mapping for \textit{M. truncatula}.

A complex regulatory network involving candidate plant and pathogen genes will be constructed based on 1) pathogen marker genotypes, 2) pathogen expression profiles and 3) plant expression profiles. This will format testable hypotheses for plant-nematode interactions and help gain insight into the complex signaling network.