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Identification of differentially expressed genes: A step closer towards cloning the root-knot nematode resistance genes in upland cotton

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The southern root-knot nematode (*Meloidogyne incognita*; RKN) is one of the most important endoparasitic pests of Upland cotton (*Gossypium hirsutum* L.). RKN management through host plant resistance is the most economical, practical, and environmentally sound method to provide protection against this pest. High level of nematode resistance found in a germplasm line 'Auburn 623RNR' was transferred to line M-120 through backcrossing Auburn 623RNR to an agronomically adapted cultivar C-201. The resistant line M-120 displays a high degree of resistance to both galling and egg production. Prior genetic analysis of line M-120 has identified two epistatically interacting RKN resistance QTLs, *qMi-C11* and *qMi-C14*, affecting gall formation and RKN reproduction, respectively. Root tissues of RKN resistant and susceptible plants infected with nematodes were obtained at two intervals after inoculation for transcriptome sequencing using RNA-seq approach. Preliminary analysis shows that over 1400 genes display differential expression (DE) between resistant and susceptible lines. Further functional characterization of DE genes at previously marked QTL intervals will offer clues toward the identification of the causal genes conferring RKN resistance in Upland cotton.

Biography

Peng W Chee has completed his M S in Plant Breeding & Genetics from Montana State University in 1994, PhD in Plant Breeding & Genetics from North Dakota State University 1998 and currently working as a Professor of Crop & Soil Sciences at National Environmentally Sound Production Agriculture Laboratory (NESPAL). His lab conducts research on the development and application of biotechnology tools for crop improvement, focusing primarily on cotton. We work closely with the cotton breeding (Dr. May's lab) and genomic (Dr. Paterson's lab) research groups to solve practical problems in, and enhance efficiency of cotton breeding by using DNA marker technology. Projects that are currently in progress include introgression of genes conferring fiber quality from Pima into Upland cotton with the aid of molecular markers and exploration to uncover novel genes or gene combinations from non-cultivated *Gossypium* species for cotton improvement. In addition to molecular markers, his lab also utilizes plant transformation technology to introduce value-added traits for cotton improvement.

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