

POSTER PRESENTATION

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Linking genotype to phenotype with Bayesian network modeling of *Chlamydia* infection

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Background

Understanding the causal pathways that link genotypes with gene expression and higher order phenotypes, such as disease susceptibility, has been a recent goal of systems genetic studies. Pairwise correlations can select genes and phenotypes that are associated with a common genetic locus; however, the directions of these links are more difficult to determine. We propose a method in which Bayesian networks are used to establish causal pathways from genotype to gene expression to phenotype and apply it to mice infected with *Chlamydia psittaci*.

Results

Recombinant inbred BXD mice strains have been previously used to study the genetic differences that cause a much greater resistance to *Chlamydia psittaci* infection in C57BL/6J mice compared with DBA/2J mice [1].

Gene expression levels and higher order phenotypes, such as pathogen load and survival, were collected for 44 BXD strains. Directed graphs linking SNPs [2] in the BXD genomes to this data were created with QTL mapping and the Bayesian network method. Figure 1 shows a selection of the resulting causal pathways; many of the genes in these pathways are known to be associated with immune response or GTPase activity, which has been linked to *Chlamydia psittaci* infection [1].

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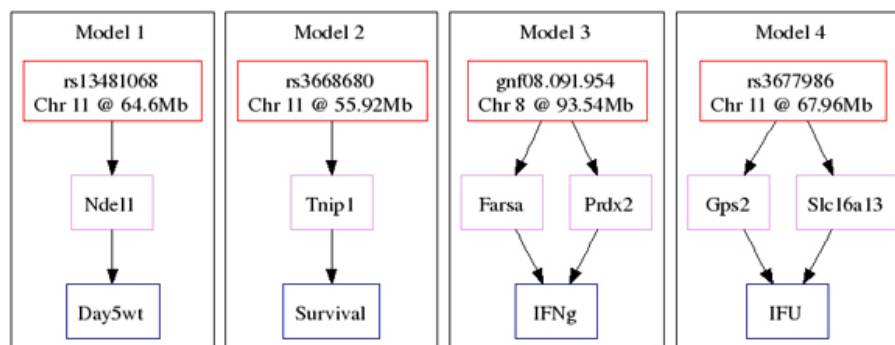


Figure 1 Causal pathways linking genotype SNPs to gene expression levels to phenotypes in BXD mice infected with *Chlamydia psittaci*

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