

# Mapping tuberculosis-related traits in multiparental mouse populations

*Frederick J. Boehm, Clare M. Smith, Daniel M. Gatti, Michael Kiritsy, Sherry Kurtz, Karen Elkins, Gillian Beamer, Christopher M. Sasseti*

*11/26/2019*

One aim of quantitative genetics is to identify genetic variants that influence phenotypic variations in disease-related traits. Recent development of multiparental mouse populations, which incorporate DNA from more than two founders, has renewed research interest in quantitative trait locus (QTL) mapping for complex phenotypes. We are uniquely positioned to leverage genetic and molecular trait data from diverse mouse populations. We have genotyped and phenotyped hundreds of mice from the Diversity Outbred and Collaborative Cross populations. We present a QTL mapping framework for integrating genotypic and phenotypic data from these two mouse populations. We draw on strengths of each population, high recombination counts and high heterozygosity levels in Diversity Outbred mice and genetic reproducibility of Collaborative Cross mice, to examine genetic underpinnings of tuberculosis susceptibility.