Leveraging genetically diverse mice to identify host genes that affect tuberculosis susceptibility

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Quantitative genetics seeks to identify genes that contribute to phenotypic variation in populations. Recent development of multiparental mouse populations has renewed research interest in linkage mapping methods, such as quantitative trait locus (QTL) mapping. The *Mycobacterium tuberculosis* research community is uniquely positioned to leverage genetic and molecular trait data from diverse mouse populations. Multiple research teams have genotyped and phenotyped hundreds of mice from the Diversity Outbred and Collaborative Cross populations. We develop a QTL mapping framework for integrating genotypic and phenotypic data from these two mouse populations. We draw on genetic strengths of each population, high recombination counts and high heterozygosity levels in Diversity Outbred mice and reproducibility of Collaborative Cross mice, to examine the genetic underpinnings of tuberculosis susceptibility. Statistical power to detect QTL is greater with the combined (Diversity Outbred and Collaborative Cross) analysis and, thus, our methods refine and extend previous QTL mapping studies of tuberculosis-related traits.