From Genotype to Phenotype in the Mouse Genome Informatics (MGI) Database: Integrating Quantitative Trait Loci with the Annotated Mouse Genome

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The Mouse Genome Informatics (MGI) database is the community model organism database for the laboratory mouse. MGI supports access to integrated genetic, genomic, and comparative data for the mouse. The primary mission of MGI is to facilitate the use of the mouse as a model system for understanding the genetic basis of human biology and disease processes. MGI is freely available on the Web at http://www.informatics.jax.org/. With the availability of the nearly complete mouse genome sequence, MGI serves an important role as a source of highly curated biological data that can be integrated with the mouse genome sequence. The integration of biological data with annotated genome data presents new opportunities for *in silico* approaches for identifying potential candidate genes associated with genetically defined phenotypes (e.g., Quantitative Trait Loci or QTL). The MGI database contains over 2,250 records for QTL in the mouse. These data are obtained manually from peer-reviewed scientific literature. Data for each QTL record includes the genetic markers with which the phenotype is associated, the identification of the marker with the peak statistical score, the publication from which the data were derived, the strains of mice used in the study, and information about the extent (length) of the QTL region in the genome. The genetic markers used to define QTL were placed on the genome sequence using electronic PCR allowing the evaluation of genetically-defined phenotypes in the context of genes predicted in the genome and the biological attributes (e.g., expression, function, cellular location) of these genes. The QTL data from MGI that have been integrated with the genome are currently accessible via the Ensembl genome browser, the UCSC Genome Browser, and NCBI's Map Viewer.