

**AN INTEGRATED APPROACH TO MANAGING AND DISPLAYING QUANTITATIVE  
TRAIT LOCI DATA**

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Recent efforts in gene mapping research have identified a substantial number of quantitative trait loci (QTL) relating to alcohol-related behaviors in mice. In order to utilize complex trait data spanning multiple data sets most effectively, it is necessary to address issues of data integration, storage and display. We have developed an integrated application for management of QTL data. This application has two main components: a custom database of QTL results and metadata, and the open source genetic mapping program, CMap (<http://www.gmod.org/cmap/>) for graphical display. Both components use a web interface and an underlying MySQL database. The CMap mapping output can be customized and configured to display QTL as well as genetic markers and candidate genes on a scale model of the chromosome. The QTL database stores additional details on each locus, such as the significance estimates, strain populations used in mapping and the associated references. The resulting application can be used to browse by chromosome through sets of QTL data, create figures for publication, or retrieve experimental details on particular loci. Currently the database contains information on 60 alcohol-related quantitative trait loci, and will soon be expanded to incorporate other drug-related QTLs as well. Supported by a grant from the Department of Veterans Affairs and NIH grants AA10760 and AA13519.