



SGN Database: From QTLs to Genomes

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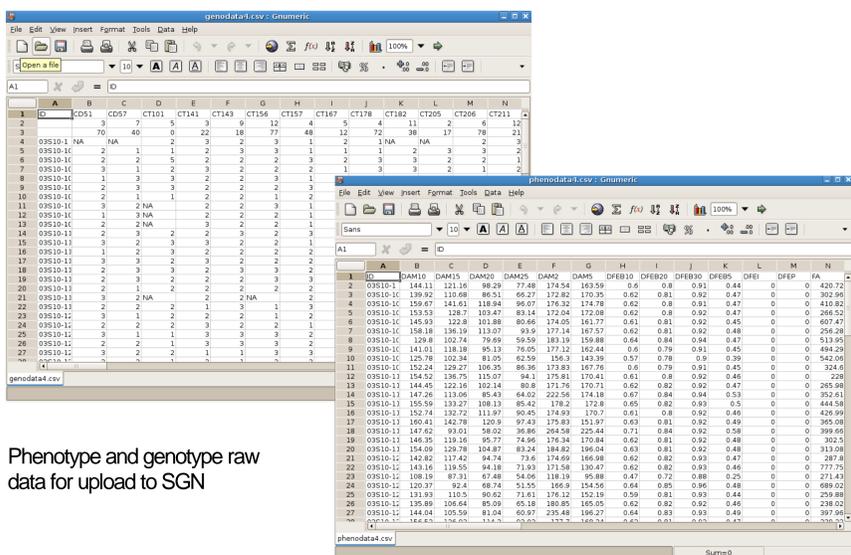
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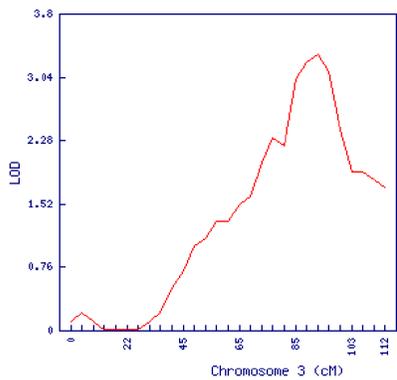
One of the major challenges of the post-genomic world is linking genomic variation to phenotypic variation of complex traits. Quantitative trait loci (QTL) analysis is used to dissect the genetic basis underlying polygenic traits. At the SOL Genomics Network (SGN) (<http://sgn.cornell.edu>), we have developed software tools and a database to store raw phenotype and genotype data from QTL studies, perform on the fly QTL analysis using R/QTL statistical software (<http://www.rqtl.org>), and visualize QTL map locations. Users can identify peaks and flanking markers for QTLs for traits of interest. The QTL software fully integrates with other analysis tools at SGN such as the Comparative Map Viewer (http://sgn.cornell.edu/cview/view_chromosome.pl), and is fully cross-referenced with other SGN-curated datasets (markers, BACs, and unigenes). For example, using the Comparative Map Viewer, users can compare predicted QTL regions to genetic maps of interest from the same or different Solanaceae species. Using the emerging tomato genome sequence, users can also identify corresponding BAC sequences or locations on the tomato physical map, which can yield candidate genes for a trait of interest.

Currently, QTL data from three F2 and two backcross population QTL studies on fruit morphology traits (up to 46 traits per population) is available at the SGN website for viewing.

QTL and Comparative Map Analysis

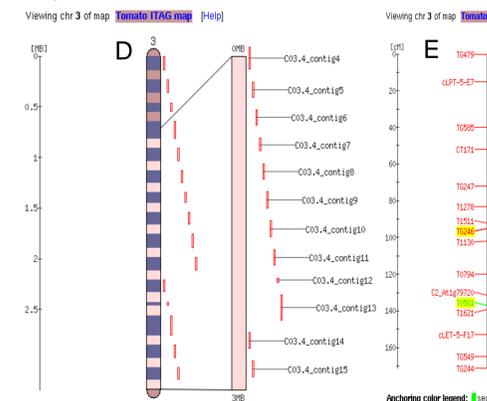
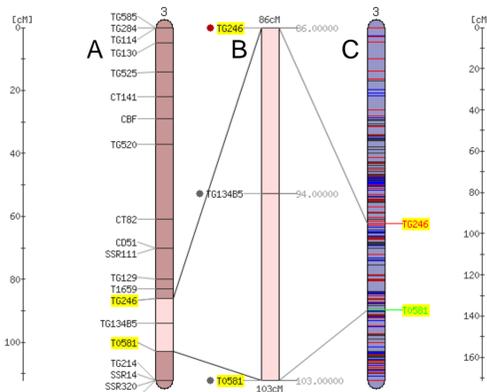


Phenotype and genotype raw data for upload to SGN



A QTL analysis with preset statistical parameters produces QTL map locations across the genome. Shown on the left is a QTL for a trait detected using a single QTL genome scan with a normal model and genotype probability of 0.01 calculated at every 5 cM.

Viewing chr 3 of map [Tomato-EXPIMP 2008](#) Comparing to chr 3 of map [Tomato-EXPEN 2000](#) [Help]



QTL map locations are cross-referenced to genetic maps of respective populations to indicate markers flanking a QTL. Using the Comparative Map Viewer, one can compare QTL map locations (A, B) to a variety of Solanaceae genetic maps (C) and tomato physical maps (D, E) including FingerPrint Contigs (FPC), Accessioned Golden Path (AGP) and International Tomato Annotation Group (ITAG) maps. ITAG maps are linked to Gbrowse where predicted genes, mRNA and CDS for contigs of interest are displayed.

Phenotype and Genotype Data Analysis

At the population level, basic statistics of phenotype data for traits are shown.

SGN population: QTL Tomato Howard German x LA1589 F2

Population details table with fields: Name, Description, Organism, Uploaded by.

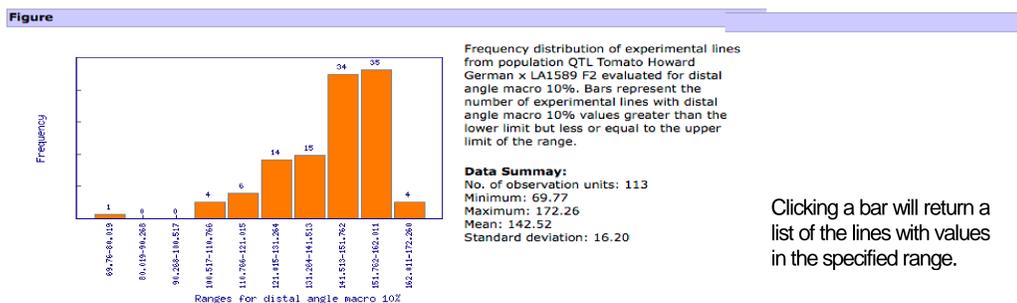
Phenotype Data table with columns: Trait, Minimum, Maximum, Average, No. of lines, Graph.

Clicking on the number of lines or graph icon (above) opens a page where phenotype data and QTL(s) for a trait are displayed (below).

Literature annotation: PMID: Morphological variation in tomato: a comprehensive study of quantitative trait loci controlling fruit shape and development. Show/hide abstract

SGN: distal angle macro 10% values in population QTL Tomato Howard German x LA1589 F2

Population details table for the specific trait.



Frequency distribution of experimental lines from population QTL Tomato Howard German x LA1589 F2 evaluated for distal angle macro 10%. Bars represent the number of experimental lines with distal angle macro 10% values greater than the lower limit but less or equal to the upper limit of the range.

Data Summary: No. of observation units: 113, Minimum: 69.77, Maximum: 172.26, Mean: 142.52, Standard deviation: 16.20

Clicking a bar will return a list of the lines with values in the specified range.

Phenotype Data table for the trait showing values for different plant accessions.

At the plant accession level, images, phenotype and mapping data are shown. Details such as map location and primer sets for a marker can be viewed by clicking on the chromosome and marker of interest.

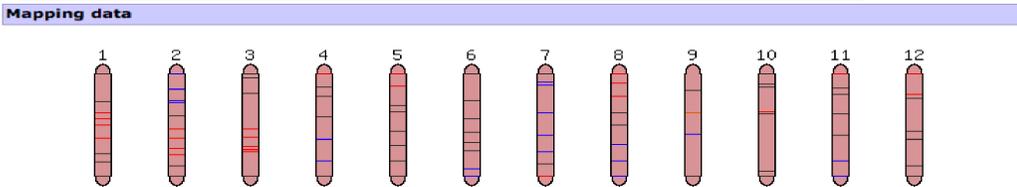
SGN accession: 03S10-90

Accession details table with fields: Accession, Description, Population, Organism, Uploaded by.

Associated loci: [Associate locus]



Phenotype data table for the accession showing trait values and population statistics.



Conclusion

QTL identification is an important approach in understanding the genetic basis of complex traits and development of marker assisted selection for faster, more reliable and cheaper improvement of polygenic traits in plants. The SGN QTL analyzer simplifies QTL detection and sharing data with the Solanaceae community. Through integration of user data with already existing genetic and physical maps at SGN, users are able to do comparative analysis, identify candidate genes and more.

References: Broman KW, Wu H, Sen, Churchil GA (2003) R/qtl: QTL mapping in experimental crosses. Bioinformatics 19:889-890. Mueller LA, Mills AA, Skwarecki B, Buels RM, Menda N, Tanksley SD (2008) The SGN comparative map viewer. Bioinformatics 24(3):422-3. Mueller LA, Solow TH, Taylor N, Skwarecki B, Buels R, Binns J, Lin C, Wright MH, Ahrens R, Wang Y, Herbst EV, Keyder ER, Menda N, Zamir D, Tanksley SD (2005) The SOL Genomics Network: A Comparative Resource for Solanaceae Biology and Beyond. Plant Physiol 136(3):1310-7.

Funding sources



<http://sgn.cornell.edu>

Contact SGN at: sgn-feedback@sgn.cornell.edu

SGN code and software <ftp://ftp.sgn.cornell.edu>