

Resource Summary Report

Generated by [NIF](#) on Sep 1, 2026

MCQTL

RRID:SCR_009285

Type: Tool

Proper Citation

MCQTL (RRID:SCR_009285)

Resource Information

URL: <http://carlit.toulouse.inra.fr/MCQTL/>

Proper Citation: MCQTL (RRID:SCR_009285)

Description: Software package to perform QTL mapping in multi-cross designs that allows the analysis of the usual populations derived from inbred lines and can link the families by assuming that the QTL locations are the same in all them. Moreover, a diallel modelling of the QTL genotypic effects is allowed in multiple related families. Obviously, the analysis of a single cross is also feasible. (entry from Genetic Analysis Software)

Abbreviations: MCQTL

Synonyms: Multi-Cross QTL mapping

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, java, c++, unix, linux

Resource Name: MCQTL

Resource ID: SCR_009285

Alternate IDs: nlx_154470

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260829T183058+0000

Ratings and Alerts

No rating or validation information has been found for MCQTL.

No alerts have been found for MCQTL.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Li W, et al. (2024) Modeling QTL-by-environment interactions for multi-parent populations. *Frontiers in plant science*, 15, 1410851.

Klein A, et al. (2020) Meta-analysis of QTL reveals the genetic control of yield-related traits and seed protein content in pea. *Scientific reports*, 10(1), 15925.

Marchadier E, et al. (2019) The complex genetic architecture of shoot growth natural variation in *Arabidopsis thaliana*. *PLoS genetics*, 15(4), e1007954.

Bordat A, et al. (2017) Different genetic architectures underlie crop responses to the same pathogen: the {*Helianthus annuus* * *Phoma macdonaldii*} interaction case for black stem disease and premature ripening. *BMC plant biology*, 17(1), 167.

Frey FP, et al. (2016) First steps to understand heat tolerance of temperate maize at adult stage: identification of QTL across multiple environments with connected segregating populations. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 129(5), 945.

Bajgain P, et al. (2016) Nested Association Mapping of Stem Rust Resistance in Wheat Using Genotyping by Sequencing. *PloS one*, 11(5), e0155760.

Horn F, et al. (2015) Linkage mapping of Barley yellow dwarf virus resistance in connected populations of maize. *BMC plant biology*, 15, 29.

Leroux D, et al. (2014) Clusthaplo: a plug-in for MCQTL to enhance QTL detection using ancestral alleles in multi-cross design. *TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik*, 127(4), 921.

Adiredjo AL, et al. (2014) Genetic control of water use efficiency and leaf carbon isotope discrimination in sunflower (*Helianthus annuus* L.) subjected to two drought scenarios. *PloS one*, 9(7), e101218.

Bohra A, et al. (2013) Emerging paradigms in genomics-based crop improvement. *TheScientificWorldJournal*, 2013, 585467.