Resource Summary Report

Generated by NIF on Apr 22, 2025

CARTHAGENE

RRID:SCR_009013
Type: Tool

Proper Citation

CARTHAGENE (RRID:SCR_009013)

Resource Information

URL: http://www.inra.fr/mia/T/CarthaGene/

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Description: A genetic/radiation hybrid mapping software that looks for multiple populations maximum likelihood consensus maps using a fast EM algorithm for maximum likelihood estimation and powerful ordering algorithms inspired from TSP (Traveling Salesman Problem) technology. It can handle large data sets made up of different populations (either F2 backcross, recombinant inbred lines, F2 intercross, phase known outbreds, haploid/diploid radiation hybrids). It can also exploit existing syntenic relationships between the organism mapped and a reference (sequenced) organism for accurate dense RH mapping. (entry from Genetic Analysis Software)

Abbreviations: CARTHAGENE

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, c++, tcl/tk, ms-windows, unix, solaris, linux, sources are available for other operating systems (gpl/qpl).

Funding:

Resource Name: CARTHAGENE

Resource ID: SCR_009013

Alternate IDs: nlx_154008

Record Creation Time: 20220129T080250+0000

Record Last Update: 20250421T053709+0000

Ratings and Alerts

No rating or validation information has been found for CARTHAGENE.

No alerts have been found for CARTHAGENE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 41 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Qu K, et al. (2024) Identification of quantitative trait loci and candidate genes for grain superoxide dismutase activity in wheat. BMC plant biology, 24(1), 716.

Lee HE, et al. (2021) Chromosome Level Assembly of Homozygous Inbred Line 'Wongyo 3115' Facilitates the Construction of a High-Density Linkage Map and Identification of QTLs Associated With Fruit Firmness in Octoploid Strawberry (Fragaria × ananassa). Frontiers in plant science, 12, 696229.

Istace B, et al. (2021) Sequencing and Chromosome-Scale Assembly of Plant Genomes, Brassica rapa as a Use Case. Biology, 10(8).

El Hage F, et al. (2021) Responses of Maize Internode to Water Deficit Are Different at the Biochemical and Histological Levels. Frontiers in plant science, 12, 628960.

Boideau F, et al. (2021) A Modified Meiotic Recombination in Brassica napus Largely Improves Its Breeding Efficiency. Biology, 10(8).

Zhang X, et al. (2021) Genetic analysis of three maize husk traits by QTL mapping in a maize-teosinte population. BMC genomics, 22(1), 386.

Kishor DS, et al. (2021) Identification of an Allelic Variant of the CsOr Gene Controlling Fruit Endocarp Color in Cucumber (Cucumis sativus L.) Using Genotyping-By-Sequencing (GBS) and Whole-Genome Sequencing. Frontiers in plant science, 12, 802864.

Guillaumie S, et al. (2020) Dissecting the control of shoot development in grapevine: genetics and genomics identify potential regulators. BMC plant biology, 20(1), 43.

Ollier M, et al. (2020) QTL mapping and successful introgression of the spring wheat-derived

QTL Fhb1 for Fusarium head blight resistance in three European triticale populations. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 133(2), 457.

Lee HY, et al. (2020) Uncovering Candidate Genes Controlling Major Fruit-Related Traits in Pepper via Genotype-by-Sequencing Based QTL Mapping and Genome-Wide Association Study. Frontiers in plant science, 11, 1100.

Pecrix Y, et al. (2019) Sunflower resistance to multiple downy mildew pathotypes revealed by recognition of conserved effectors of the oomycete Plasmopara halstedii. The Plant journal : for cell and molecular biology, 97(4), 730.

Siddique MI, et al. (2019) Identifying candidate genes for Phytophthora capsici resistance in pepper (Capsicum annuum) via genotyping-by-sequencing-based QTL mapping and genome-wide association study. Scientific reports, 9(1), 9962.

Gill HS, et al. (2019) Fine Mapping of the Wheat Leaf Rust Resistance Gene Lr42. International journal of molecular sciences, 20(10).

Virlouvet L, et al. (2019) Water Deficit-Responsive QTLs for Cell Wall Degradability and Composition in Maize at Silage Stage. Frontiers in plant science, 10, 488.

Desiderio F, et al. (2019) Genomic Regions From an Iranian Landrace Increase Kernel Size in Durum Wheat. Frontiers in plant science, 10, 448.

Termolino P, et al. (2019) Recombination suppression in heterozygotes for a pericentric inversion induces the interchromosomal effect on crossovers in Arabidopsis. The Plant journal : for cell and molecular biology, 100(6), 1163.

Choi S, et al. (2018) Identification of Cucumber mosaic resistance 2 (cmr2) That Confers Resistance to a New Cucumber mosaic virus Isolate P1 (CMV-P1) in Pepper (Capsicum spp.). Frontiers in plant science, 9, 1106.

Yang N, et al. (2017) Contributions of Zea mays subspecies mexicana haplotypes to modern maize. Nature communications, 8(1), 1874.

Chao H, et al. (2017) Genetic dissection of seed oil and protein content and identification of networks associated with oil content in Brassica napus. Scientific reports, 7, 46295.

Yoshitsu Y, et al. (2017) QTL-seq analysis identifies two genomic regions determining the heading date of foxtail millet, Setaria italica (L.) P.Beauv. Breeding science, 67(5), 518.