

Resource Summary Report

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POWERMARKER

RRID:SCR_009332

Type: Tool

Proper Citation

POWERMARKER (RRID:SCR_009332)

Resource Information

URL: <http://statgen.ncsu.edu/powermarker/>

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Description: A comprehensive set of statistical methods for genetic marker data analysis, designed especially for SSR/SNP data analysis. PowerMarker builds a powerful user interface around both new and traditional statistical methods for population genetic analysis. See analysis to check out the versatility of PowerMarker. PowerMarker is also a 2D Viewer - which was used intensively for visualizing linkage disequilibria results. (entry from Genetic Analysis Software)

Abbreviations: POWERMARKER

Resource Type: software resource, software application

Keywords: gene, genetic, genomic

Resource Name: POWERMARKER

Resource ID: SCR_009332

Alternate IDs: nlx_154544

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260801T191059+0000

Ratings and Alerts

No rating or validation information has been found for POWERMARKER.

No alerts have been found for POWERMARKER.

Data and Source Information

Usage and Citation Metrics

We found 623 mentions in open access literature.

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

Galal AA, et al. (2025) Molecular diversity and genetic potential of new maize inbred lines across varying sowing conditions in arid environment. Scientific reports, 15(1), 2809.

Niu M, et al. (2025) Microsatellite and Mitochondrial COI Provide Novel Insights Into the Population Genetic Structure of White Prunicola Scale (*Pseudaulacaspis prunicola*) in China. Ecology and evolution, 15(1), e70865.

Laribi M, et al. (2025) Genetic diversity and population structure of a core collection of Mediterranean durum wheat accessions using DArTseq markers. BMC genomics, 26(1), 1130.

Huang M, et al. (2025) Genetic diversity, population structure and quality-trait associations in *Blumea balsamifera* revealed by EST-SSR markers. PloS one, 20(7), e0328403.

Li Y, et al. (2025) Migration of wheat stripe rust from the primary overwintering region to neighboring regions in China. Communications biology, 8(1), 350.

Wang F, et al. (2025) Phenotypic Characterization and Marker-Trait Association Analysis Using SCoT Markers in Chrysanthemum (*Chrysanthemum morifolium* Ramat.) Germplasm. Genes, 16(6).

Ruan X, et al. (2025) Core collection construction and genetic diversity analysis of tea plant (*Camellia sinensis* [L.] O. Kuntze) accessions in Huangshan city using SSR markers. PloS one, 20(4), e0322209.

Zeng H, et al. (2025) Phenotypic Traits, SSR Core Primer Screening, and Genetic Diversity Analysis of *Toxicodendron vernicifluum* From Different Seed Sources in Yunnan, China. Ecology and evolution, 15(7), e71794.

Siamey J, et al. (2025) Agro-morphological and molecular characterization of *Amaranthus* genotypes. PloS one, 20(9), e0328567.

Lei X, et al. (2025) Genetic structure and designing a preliminary core collection of *Zizania latifolia* in China based on 12 microsatellites markers. PeerJ, 13, e18909.

Kulkarni KP, et al. (2025) Generation and characterization of novel transcriptome-derived SSR markers for genetic applications in blueberry. Scientific reports, 15(1), 25050.

Shahid I, et al. (2025) Phylogenetic analysis of the enigmatic Kalash population in Pakistan. Scientific reports, 15(1), 18101.

Ofem NP, et al. (2025) Genetic diversity and structure of Asian cowpea germplasm. Scientific reports, 15(1), 27909.

Kim KC, et al. (2025) Development of Simple Sequence Repeat (SSR) Markers from a Genome Survey of a *Cymbidium kanran* Makino Population in Jeju Island, Republic of Korea. *Journal of microbiology and biotechnology*, 35, e2501013.

Islam MZ, et al. (2025) Genetic variability, correlation and path coefficient analysis of phenotypic traits and genetic diversity of Aman rice landraces (*Oryza sativa* L.). *Scientific reports*, 15(1), 18606.

Mekapogu M, et al. (2025) Evaluation of Genetic Diversity and Identification of Cultivars in Spray-Type Chrysanthemum Based on SSR Markers. *Genes*, 16(1).

Lun X, et al. (2025) Cell surface Toll-like receptor polymorphisms influence *Bartonella* and ectoparasite infections in striped hamsters. *iScience*, 28(7), 112883.

Yi ZH, et al. (2025) A novel EST-SSR fingerprint database development strategy for accurate identification of asparagus cultivars. *BMC plant biology*, 25(1), 1691.

Ghazy AI, et al. (2025) Selection of heat stress tolerant wheat genotypes for desert environments. *Scientific reports*, 15(1), 36672.

Sehgal D, et al. (2024) Genomic wide association study and selective sweep analysis identify genes associated with improved yield under drought in Turkish winter wheat germplasm. *Scientific reports*, 14(1), 8431.