

# Association Mapping in Structured Populations

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Inference in molecular population genetics. <i>Journal of the Royal Statistical Society Series B: Statistical Methodology</i> , 2000, 62, 605-635.	1.1	258
2	Pharmacogenetics and the serotonin system: initial studies and future directions. <i>European Journal of Pharmacology</i> , 2000, 410, 165-181.	1.7	236
3	Family-based association studies. <i>Statistical Methods in Medical Research</i> , 2000, 9, 563-587.	0.7	55
4	Consistent Long-Range Linkage Disequilibrium Generated by Admixture in a Bantu-Semitic Hybrid Population. <i>American Journal of Human Genetics</i> , 2000, 67, 926-935.	2.6	72
5	Linkage Disequilibrium Analysis of Biallelic DNA Markers, Human Quantitative Trait Loci, and Threshold-Defined Case and Control Subjects. <i>American Journal of Human Genetics</i> , 2000, 67, 1208-1218.	2.6	84
6	Variation of serotonergic gene expression: neurodevelopment and the complexity of response to psychopharmacologic drugs. <i>European Neuropsychopharmacology</i> , 2001, 11, 457-474.	0.3	60
7	Map-based cloning of quantitative trait loci: progress and prospects. <i>Genetical Research</i> , 2001, 78, 213-218.	0.3	76
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10	Accounting for Unmeasured Population Substructure in Case-Control Studies of Genetic Association Using a Novel Latent-Class Model. <i>American Journal of Human Genetics</i> , 2001, 68, 466-477.	2.6	231
11	Quantitative Similarity-Based Association Tests Using Population Samples. <i>American Journal of Human Genetics</i> , 2001, 69, 601-614.	2.6	24
12	Pathophysiology of sickle cell disease: Role of cellular and genetic modifiers. <i>Seminars in Hematology</i> , 2001, 38, 299-306.	1.8	103
13	Epidemiological methods for studying genes and environmental factors in complex diseases. <i>Lancet, The</i> , 2001, 358, 1356-1360.	6.3	442
14	Candidate gene studies of bipolar disorder. <i>Annals of Medicine</i> , 2001, 33, 248-256.	1.5	41
15	Genetic Case-Control Association Studies in Neuropsychiatry. <i>Archives of General Psychiatry</i> , 2001, 58, 1015-1024.	13.8	113
16	Introduction: Bayesian Models and Markov Chain Monte Carlo Methods. <i>Genetic Epidemiology</i> , 2001, 21, S660-1.	0.6	4
17	Bayesian Association Mapping for Quantitative Traits in a Mixture of Two Populations. <i>Genetic Epidemiology</i> , 2001, 21, S692-9.	0.6	18
18	Joint Modeling of Genetic Association and Population Stratification Using Latent Class Models. <i>Genetic Epidemiology</i> , 2001, 21, S409-S414.	0.6	8

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19	Fine-scale mapping using Hardy-Weinberg disequilibrium. <i>Annals of Human Genetics</i> , 2001, 65, 207-219.	0.3	32
20	LOD score exclusion analyses for candidate genes using random population samples. <i>Annals of Human Genetics</i> , 2001, 65, 313-329.	0.3	11
21	Family-based tests of association and/or linkage. <i>Annals of Human Genetics</i> , 2001, 65, 407-419.	0.3	25
22	Unbiased methods for population-based association studies. <i>Genetic Epidemiology</i> , 2001, 21, 273-284.	0.6	132
23	Caught in the trio trap? Potential selection bias inherent to association studies using parent-offspring trios. <i>American Journal of Medical Genetics Part A</i> , 2001, 105, 351-353.	2.4	21
24	Association study designs for complex diseases. <i>Nature Reviews Genetics</i> , 2001, 2, 91-99.	7.7	1,247
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42	Ascertainment Bias in Family-based Case-Control Studies. <i>American Journal of Epidemiology</i> , 2002, 155, 875-880.	1.6	10
43	Genetic Epidemiology and Congenital Malformations. <i>JAMA Pediatrics</i> , 2002, 156, 315.	3.6	41
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56	Enabling Population and Quantitative Genomics. <i>Genetical Research</i> , 2002, 80, 1-6.	0.3	20
57	Pharmacogenomics of Asthma Treatment. , 0, , 215-234.		2
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103	Functional markers in plants. <i>Trends in Plant Science</i> , 2003, 8, 554-560.	4.3	640
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1030	Association mapping of caffeine content with TCS1 in tea plant and its related species. <i>Plant Physiology and Biochemistry</i> , 2016, 105, 251-259.	2.8	28
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1033	New QTLs for lint percentage and boll weight mined in introgression lines from two feral landraces into <i>Gossypium hirsutum</i> acc TM. <i>Plant Breeding</i> , 2016, 135, 90-101.	1.0	19
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1044	Assessing the genetic diversity in onion ( <i>Allium cepa</i> L.) landraces from northwest Spain and comparison with the European variability. <i>New Zealand Journal of Crop and Horticultural Science</i> , 2016, 44, 103-120.	0.7	19
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1049	Population structure, linkage disequilibrium and association mapping for morphological traits in sunflower ( <i>Helianthus annuus</i> L.). <i>Biotechnology and Biotechnological Equipment</i> , 2016, 30, 236-246.	0.5	7
1050	Dissection of QTL alleles for blast resistance based on linkage and linkage disequilibrium mapping in japonica rice seedlings. <i>Australasian Plant Pathology</i> , 2016, 45, 209-218.	0.5	6
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1055	Brazilian multicenter study of association between polymorphisms in <i>CRISPLD2</i> and <i>JARID2</i> and non-syndromic oral clefts. <i>Journal of Oral Pathology and Medicine</i> , 2017, 46, 232-239.	1.4	20
1056	Molecular genetic diversity and association mapping of nut and kernel traits in Slovenian hazelnut ( <i>Corylus avellana</i> ) germplasm. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	25
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1059	Genome-wide population structure and evolutionary history of the Frizarta dairy sheep. <i>Animal</i> , 2017, 11, 1680-1688.	1.3	10
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1070	Genetic Association Studies and Next Generation Sequencing in Stroke: Methods. , 2017, , 21-52.		0
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1077	Microsatellite based linkage disequilibrium analyses reveal Saltol haplotype fragmentation and identify novel QTLs for seedling stage salinity tolerance in rice ( <i>Oryza sativa</i> L.). <i>Journal of Plant Biochemistry and Biotechnology</i> , 2017, 26, 310-320.	0.9	12
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1103	A Novel QTL for Powdery Mildew Resistance in Nordic Spring Barley ( <i>Hordeum vulgare</i> L. ssp. <i>vulgare</i> ) Revealed by Genome-Wide Association Study. <i>Frontiers in Plant Science</i> , 2017, 8, 1954.	1.7	16
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1107	Genome-wide association mapping of black point reaction in common wheat ( <i>Triticum aestivum</i> L.). <i>BMC Plant Biology</i> , 2017, 17, 220.	1.6	141
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1120	Mapping association of molecular markers and sheath blight ( <i>Rhizoctonia solani</i> ) disease resistance and identification of novel resistance sources and loci in rice. <i>Euphytica</i> , 2018, 214, 1.	0.6	5
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1136	Genome-wide association analysis of kernel morphology in breeding lines derived from synthetic hexaploid wheat in Qinghai Province, China. <i>Cereal Research Communications</i> , 2018, 46, 399-411.	0.8	0
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1150	Development and Characterization of Novel Genic-SSR Markers in Apple-Juniper Rust Pathogen <i>Gymnosporangium yamadae</i> (Pucciniales: Pucciniaceae) Using Next-Generation Sequencing. <i>International Journal of Molecular Sciences</i> , 2018, 19, 1178.	1.8	10
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1161	Genome-wide mapping of quantitative trait loci in admixed populations using mixed linear model and Bayesian multiple regression analysis. <i>Genetics Selection Evolution</i> , 2018, 50, 32.	1.2	20
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1168	Association of yield-related traits in founder genotypes and derivatives of common wheat ( <i>Triticum</i> ) Tj ETQq1 1 0.784314 rgBT /Overl	1.6	28
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1175	Fast and powerful genome wide association of dense genetic data with high dimensional imaging phenotypes. <i>Nature Communications</i> , 2018, 9, 3254.	5.8	6
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1177	Genetic diversity and association mapping of Ethiopian and exotic finger millet accessions. <i>Crop and Pasture Science</i> , 2018, 69, 879.	0.7	19
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1181	Detection of QTL (quantitative trait loci) associated with wood density by evaluating genetic structure and linkage disequilibrium of teak. <i>Journal of Forestry Research</i> , 2019, 30, 2247-2258.	1.7	6
1182	Genome-wide association study for frost tolerance in canola ( <i>Brassica napus</i> L.) under field conditions. <i>Journal of Plant Biochemistry and Biotechnology</i> , 2019, 28, 211-222.	0.9	7
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1198	Genetic variability in a population of Letelle sheep in South Africa. <i>South African Journal of Animal Sciences</i> , 2019, 49, 281.	0.2	2
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1200	Conservation genomics in the fight to help the recovery of the critically endangered Siamese crocodile <i>Crocodylus siamensis</i> . <i>Molecular Ecology</i> , 2019, 28, 936-950.	2.0	21
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1206	Genome-wide association study reveals E2F3 as the candidate gene for scallop growth. <i>Aquaculture</i> , 2019, 511, 734216.	1.7	22
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1208	Characterization of strawberry ( <i>Fragaria</i> spp.) accessions by genotyping with SSR markers and phenotyping by leaf antioxidant and trichome analysis. <i>Scientia Horticulturae</i> , 2019, 256, 108561.	1.7	8
1209	Using the RTM-GWAS procedure to detect the drought tolerance QTL-allele system at the seedling stage under sand culture in a half-sib population of soybean [ <i>Glycine max</i> (L.) Merr.]. <i>Canadian Journal of Plant Science</i> , 2019, 99, 801-814.	0.3	7
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1213	Natural variation in the <i>THICK TASSEL DWARF1</i> ( <i>TD1</i> ) gene in the regulation of maize ( <i>Zea mays</i> L.) ear-related traits. <i>Breeding Science</i> , 2019, 69, 323-331.	0.9	7
1214	Insights into the Population Structure and Association Mapping in Globe Artichoke. <i>Compendium of Plant Genomes</i> , 2019, , 129-143.	0.3	0
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1222	Characterization of molecular diversity and genome-wide association study of stripe rust resistance at the adult plant stage in Northern Chinese wheat landraces. <i>BMC Genetics</i> , 2019, 20, 38.	2.7	56
1223	Genetic diversity and demography of the critically endangered Roberts' false brook salamander ( <i>Pseudoeurycea robertsi</i> ) in Central Mexico. <i>Genetica</i> , 2019, 147, 149-164.	0.5	8
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1240	Multifactorial Inheritance and Complex Diseases. , 2019, , 323-358.		3
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1258	Genome-Wide DNA Methylation Analysis Reveals a Conserved Epigenetic Response to Seasonal Environmental Variation in the Staghorn Coral <i>Acropora cervicornis</i> . <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	27
1259	Genome-Wide Association Study Reveals Genomic Regions Associated With Ten Agronomical Traits in Wheat Under Late-Sown Conditions. <i>Frontiers in Plant Science</i> , 2020, 11, 549743.	1.7	16
1260	Genome-Wide Association Mapping through 90K SNP Array for Quality and Yield Attributes in Bread Wheat against Water-Deficit Conditions. <i>Agriculture (Switzerland)</i> , 2020, 10, 392.	1.4	29
1261	Genome-wide association mapping reveals putative candidate genes for drought tolerance in barley. <i>Environmental and Experimental Botany</i> , 2020, 180, 104237.	2.0	14
1262	Genetic diversity of pinto and fresh bean ( <i>Phaseolus vulgaris</i> L.) germplasm collected from Erzincan province of Turkey by inter-primer binding site (iPBS) retrotransposon markers. <i>Türk Tarım Ve Ormancılık Dergisi/Turkish Journal of Agriculture and Forestry</i> , 2020, 44, 417-427.	0.8	11
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1264	<i>OsSYL2<sup>AA</sup></i> , an allele identified by gene-based association, increases style length in rice ( <i>Oryza sativa</i> L.). <i>Plant Journal</i> , 2020, 104, 1491-1503.	2.8	17
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1271	Mixed logistic regression in genome-wide association studies. <i>BMC Bioinformatics</i> , 2020, 21, 536.	1.2	3
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1273	Multi-locus genome-wide association studies reveal novel genomic regions associated with vegetative stage salt tolerance in bread wheat ( <i>Triticum aestivum</i> L.). <i>Genomics</i> , 2020, 112, 4608-4621.	1.3	32
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1277	Molecular characterization of QTL-allele system for drought tolerance at seedling stage and optimal genotype design using multi-locus multi-allele genome-wide association analysis in a half-sib population of soybean ( <i>Glycine max</i> (L.) Merr.). <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2020, 18, 295-306.	0.4	3
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1297	Genome-Wide Mapping of Loci Associated With Resistance to Clubroot in <i>Brassica napus</i> ssp. <i>napobrassica</i> (Rutabaga) Accessions From Nordic Countries. <i>Frontiers in Plant Science</i> , 2020, 11, 742.	1.7	14
1298	Genome-Wide Association Mapping of Adult-Plant Resistance to Stripe Rust in Common Wheat ( <i>Triticum aestivum</i> ). <i>Plant Disease</i> , 2020, 104, 2174-2180.	0.7	6
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1306	Genetic diversity analysis of <i>Rhanterium eppaposum</i> Oliv. by ISSRs reveals a weak population structure. <i>Current Plant Biology</i> , 2020, 21, 100138.	2.3	15
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1312	Genetic diversity, SNP-trait associations and genomic selection accuracy in a west African collection of Kersting's groundnut [ <i>Macrotyloma geocarpum</i> (Harms) MarÃ©chal & Baudet]. <i>PLoS ONE</i> , 2020, 15, e0234769.	1.1	24
1313	Adjusting for Spatial Effects in Genomic Prediction. <i>Journal of Agricultural, Biological, and Environmental Statistics</i> , 2020, 25, 699-718.	0.7	10
1314	Identification of QTL and genes for pod number in soybean by linkage analysis and genome-wide association studies. <i>Molecular Breeding</i> , 2020, 40, 1.	1.0	14
1315	Assessment of Genetic Diversity of the 'Acquaviva Red Onion'(Allium cepa L.) Apulian Landrace. <i>Plants</i> , 2020, 9, 260.	1.6	16
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1317	Diversity analysis of provitamin A maize inbred lines using single nucleotide polymorphism markers. <i>Acta Agriculturae Scandinavica - Section B Soil and Plant Science</i> , 2020, 70, 265-271.	0.3	6
1318	Genome-wide association mapping revealed syntenic loci QFhb-4AL and QFhb-5DL for Fusarium head blight resistance in common wheat ( <i>Triticum aestivum</i> L.). <i>BMC Plant Biology</i> , 2020, 20, 29.	1.6	21
1319	Phylogeography, genetic stocks, and conservation implications for an Australian endemic marine turtle. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2020, 30, 440-460.	0.9	23
1320	Drought response of flax accessions and identification of quantitative trait nucleotides (QTNs) governing agronomic and root traits by genome-wide association analysis. <i>Molecular Breeding</i> , 2020, 40, 1.	1.0	12
1322	Panmictic population genetic structure of northern British Columbia mountain goats ( <i>Oreamnos</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.8	9
1323	Analysis of genetic variation and population structure among of oregano ( <i>Origanum acutidens</i> L.) accessions revealed by agro-morphological traits, oil constituents and retrotransposon-based inter-primer binding sites (iPBS) markers. <i>Genetic Resources and Crop Evolution</i> , 2020, 67, 1367-1384.	0.8	13
1324	<i>Mycobacterium tuberculosis</i> associated with severe tuberculosis evades cytosolic surveillance systems and modulates IL-1 $\beta$ production. <i>Nature Communications</i> , 2020, 11, 1949.	5.8	52
1325	Genome-wide association studies for resistance to viral nervous necrosis in three populations of European sea bass ( <i>Dicentrarchus labrax</i> ) using a novel 57k SNP array DlabChip. <i>Aquaculture</i> , 2021, 530, 735930.	1.7	39
1326	Genetic diversity and population structure of bread wheat genotypes determined via phenotypic and SSR marker analyses under drought-stress conditions. <i>Journal of Crop Improvement</i> , 2021, 35, 303-325.	0.9	16
1327	Population genetic structure and classification of cultivated and wild pea ( <i>Pisum</i> sp.) based on morphological traits and SSR markers. <i>Journal of Systematics and Evolution</i> , 2021, , .	1.6	3
1328	Innovative approach to identify multigenomic and environmental interactions associated with birth defects in family-based hybrid designs. <i>Genetic Epidemiology</i> , 2021, 45, 171-189.	0.6	1
1329	locStra: Fast analysis of regional/global stratification in whole-genome sequencing studies. <i>Genetic Epidemiology</i> , 2021, 45, 82-98.	0.6	8

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1331	Genome-Wide Association Study (GWAS) to Identify Salt-Tolerance QTLs Carrying Novel Candidate Genes in Rice During Early Vegetative Stage. <i>Rice</i> , 2021, 14, 9.	1.7	40
1332	Genetic characterization and association mapping in near-isogenic lines of waxy maize using seed characteristics and SSR markers. <i>Genes and Genomics</i> , 2021, 43, 79-90.	0.5	10
1333	Detection of QTNs for kernel moisture concentration and kernel dehydration rate before physiological maturity in maize using multi-locus GWAS. <i>Scientific Reports</i> , 2021, 11, 1764.	1.6	12
1334	Functional gene assessment of bread wheat: breeding implications in Ningxia Province. <i>BMC Plant Biology</i> , 2021, 21, 103.	1.6	4
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1336	Performance of model-based multifactor dimensionality reduction methods for epistasis detection by controlling population structure. <i>BioData Mining</i> , 2021, 14, 16.	2.2	2
1339	Detection of breeding signatures in wheat using a linkage disequilibrium-corrected mapping approach. <i>Scientific Reports</i> , 2021, 11, 5527.	1.6	18
1340	Assessment of phenotypic and molecular diversity in soybean [ <i>Glycine max</i> (L.) Merr.] germplasm using morpho-biochemical attributes and SSR markers. <i>Genetic Resources and Crop Evolution</i> , 2021, 68, 2827-2847.	0.8	7
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1350	Penalized linear mixed models for structured genetic data. <i>Genetic Epidemiology</i> , 2021, 45, 427-444.	0.6	3

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1353	Genome-Wide Association Study on Reproduction-Related Body-Shape Traits of Chinese Holstein Cows. <i>Animals</i> , 2021, 11, 1927.	1.0	17
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1553	Evaluating the Diversity of Ecotypes of Red Clover ( <i>Trifolium pratense</i> L.) from Northwestern Spain by Phenotypic Traits and Microsatellites. <i>Agronomy</i> , 2021, 11, 2275.	1.3	4
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1717	SSR-Based Molecular Identification and Population Structure Analysis for Forage Pea ( <i>Pisum sativum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.0	8
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1728	Elucidating a history of invasion: population genetics of pirarucu ( <i>Arapaima gigas</i> , Actinopterygii.) <i>Tj ETQq1 1 0.784314 rgBT<sub>2</sub>Overlo</i>	1.0	2
1729	Determining Genetic Diversity and Population Structure of Common Bean ( <i>Phaseolus vulgaris</i> L.) Landraces from TÃ¼rkiye Using SSR Markers. <i>Genes</i> , 2022, 13, 1410.	1.0	17
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