

Development of a 63K SNP Array for Cotton and High-D Interspecific Populations of *Gossypium* spp.

G3: Genes, Genomes, Genetics

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Citation Report

#	ARTICLE	IF	CITATIONS
1	The Utilization of Translocation Lines and Microsatellite Markers for the Identification of Unknown Cotton Monosomic Lines. , 0, , .		1
2	Bioinformatics Tools and Genomic Resources Available in Understanding the Structure and Function of <i>Gossypium</i> . , 2016, , .		4
3	SNP-Based MAS in Cotton under Depressed Recombination for <i>Ren</i> ^{lon} Flanking Recombinants: Results and Inferences on Wide Cross Breeding Strategies. <i>Crop Science</i> , 2016, 56, 1526-1539.	1.8	7
4	High-density linkage map construction and QTL analysis for earliness-related traits in <i>Gossypium hirsutum</i> L. <i>BMC Genomics</i> , 2016, 17, 909.	2.8	51
5	A MAGIC population-based genome-wide association study reveals functional association of <i>ChRBB1_A07</i> gene with superior fiber quality in cotton. <i>BMC Genomics</i> , 2016, 17, 903.	2.8	113
6	RNA-Seq-Mediated Transcriptome Analysis of a Fiberless Mutant Cotton and Its Possible Origin Based on SNP Markers. <i>PLoS ONE</i> , 2016, 11, e0151994.	2.5	28
7	Genome-Wide SNP Linkage Mapping and QTL Analysis for Fiber Quality and Yield Traits in the Upland Cotton Recombinant Inbred Lines Population. <i>Frontiers in Plant Science</i> , 2016, 7, 1356.	3.6	105
8	Introductory Chapter: Introduction to Cotton Research Highlights. , 0, , .		3
9	argyle: An R Package for Analysis of Illumina Genotyping Arrays. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 281-286.	1.8	36
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11	Progress in genome sequencing will accelerate molecular breeding in cotton (<i>Gossypium</i> spp.). <i>3 Biotech</i> , 2016, 6, 217.	2.2	15
12	A HapMap leads to a <i>Capsicum annuum</i> SNP infinium array: a new tool for pepper breeding. <i>Horticulture Research</i> , 2016, 3, 16036.	6.3	47
13	Molecular mapping of bunchy top disease resistance in <i>Gossypium hirsutum</i> L.. <i>Euphytica</i> , 2016, 210, 135-142.	1.2	17
14	A Genetic Map Between <i>Gossypium hirsutum</i> and the Brazilian Endemic <i>G. mustelinum</i> and Its Application to QTL Mapping. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1673-1685.	1.8	19
15	Development, genetic mapping and QTL association of cotton <i>PHYA</i> , <i>PHYB</i> , and <i>HY5</i> -specific CAPS and dCAPS markers. <i>BMC Genetics</i> , 2016, 17, 141.	2.7	15
16	The Immature Fiber Mutant Phenotype of Cotton (<i>Gossypium hirsutum</i>) Is Linked to a 22-bp Frame-Shift Deletion in a Mitochondria Targeted Pentatricopeptide Repeat Gene. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1627-1633.	1.8	24
17	SNP Marker Discovery in Pima Cotton (<i>Gossypium barbadense</i> L.) Leaf Transcriptomes. <i>Genomics Insights</i> , 2016, 9, GEI.S40377.	3.0	8
18	Development and validation of the Axiom [®] Apple480K SNP genotyping array. <i>Plant Journal</i> , 2016, 86, 62-74.	5.7	156

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20	Development and Evaluation of a High Density Genotyping <i>Axiom_Arachis</i> ™ Array with 58%K SNPs for Accelerating Genetics and Breeding in Groundnut. Scientific Reports, 2017, 7, 40577.	3.3	144
21	Genome-wide association study of yield components and fibre quality traits in a cotton germplasm diversity panel. Euphytica, 2017, 213, 1.	1.2	42
22	Genome-wide association study discovered genetic variation and candidate genes of fibre quality traits in <i>Gossypium hirsutum</i> L.. Plant Biotechnology Journal, 2017, 15, 982-996.	8.3	199
23	Population structure and genetic basis of the agronomic traits of upland cotton in China revealed by a genome-wide association study using high-density <i>SNP</i> s. Plant Biotechnology Journal, 2017, 15, 1374-1386.	8.3	196
24	Genome-wide SNP Genotyping Resolves Signatures of Selection and Tetrasomic Recombination in Peanut. Molecular Plant, 2017, 10, 309-322.	8.3	114
25	Association mapping for seed cotton yield, yield components and fibre quality traits in upland cotton (<i>Gossypium hirsutum</i> L.) genotypes. Plant Breeding, 2017, 136, 958-968.	1.9	10
26	Genetic Diversity and Population Structure in the Landrace Accessions of <i>Gossypium hirsutum</i> . Crop Science, 2017, 57, 2457-2470.	1.8	12
27	Sub genome anchored physical frameworks of the allotetraploid Upland cotton (<i>Gossypium hirsutum</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tj 7, 15274.	3.3	23
28	Diversity analysis of cotton (<i>Gossypium hirsutum</i> L.) germplasm using the CottonSNP63K Array. BMC Plant Biology, 2017, 17, 37.	3.6	56
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31	Identification and Characterization of Segregation Distortion Loci on Cotton Chromosome 18. Frontiers in Plant Science, 2016, 7, 2037.	3.6	24
32	Identification of Marker-Trait Associations for Lint Traits in Cotton. Frontiers in Plant Science, 2017, 8, 86.	3.6	37
33	Quantitative Trait Locus Mapping for Verticillium wilt Resistance in an Upland Cotton Recombinant Inbred Line Using SNP-Based High Density Genetic Map. Frontiers in Plant Science, 2017, 8, 382.	3.6	49
34	QTL Analysis of Transgressive Nematode Resistance in Tetraploid Cotton Reveals Complex Interactions in Chromosome 11 Regions. Frontiers in Plant Science, 2017, 8, 1979.	3.6	17
35	QTLs Analysis and Validation for Fiber Quality Traits Using Maternal Backcross Population in Upland Cotton. Frontiers in Plant Science, 2017, 8, 2168.	3.6	47
36	High-density 80K SNP array is a powerful tool for genotyping <i>G. hirsutum</i> accessions and genome analysis. BMC Genomics, 2017, 18, 654.	2.8	122

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38	Historical Datasets Support Genomic Selection Models for the Prediction of Cotton Fiber Quality Phenotypes Across Multiple Environments. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1721-1732.	1.8	30
39	Genetic dissection of the fuzzless seed trait in <i>Gossypium barbadense</i> . <i>Journal of Experimental Botany</i> , 2018, 69, 997-1009.	4.8	34
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45	Single-Locus and Multi-Locus Genome-Wide Association Studies in the Genetic Dissection of Fiber Quality Traits in Upland Cotton (<i>Gossypium hirsutum</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 1083.	3.6	74
46	Identification of SNPs and Candidate Genes Associated With Salt Tolerance at the Seedling Stage in Cotton (<i>Gossypium hirsutum</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 1011.	3.6	50
47	Genome-Wide Association Studies Reveal Genetic Variation and Candidate Genes of Drought Stress Related Traits in Cotton (<i>Gossypium hirsutum</i> L.). <i>Frontiers in Plant Science</i> , 2018, 9, 1276.	3.6	91
48	Identification of molecular markers associated with genic male sterility in tetraploid cotton (<i>Gossypium hirsutum</i> L.) through bulk segregant analysis using a cotton SNP 63K array. <i>Czech Journal of Genetics and Plant Breeding</i> , 2018, 54, 154-160.	0.8	5
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51	Tools for Genetic Studies in Experimental Populations of Polyploids. <i>Frontiers in Plant Science</i> , 2018, 9, 513.	3.6	175
52	Wild Relatives of Maize, Rice, Cotton, and Soybean: Treasure Troves for Tolerance to Biotic and Abiotic Stresses. <i>Frontiers in Plant Science</i> , 2018, 9, 886.	3.6	211
53	QTL Mapping for Fiber Quality and Yield Traits Based on Introgression Lines Derived from <i>Gossypium hirsutum</i> Å— <i>G. tomentosum</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 243.	4.1	49
54	Dissection of complicate genetic architecture and breeding perspective of cottonseed traits by genome-wide association study. <i>BMC Genomics</i> , 2018, 19, 451.	2.8	22

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56	Genome-wide association study of <i>Gossypium arboreum</i> resistance to reniform nematode. <i>BMC Genetics</i> , 2018, 19, 52.	2.7	7
57	A genome-wide association study of early-maturation traits in upland cotton based on the CottonSNP80K array. <i>Journal of Integrative Plant Biology</i> , 2018, 60, 970-985.	8.5	28
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61	Genome mapping and molecular markers identification for yield, yield component and fibre quality traits in tetraploid cotton. <i>Plant Breeding</i> , 2019, 138, 880-896.	1.9	3
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66	Genome-wide variation patterns between landraces and cultivars uncover divergent selection during modern wheat breeding. <i>Theoretical and Applied Genetics</i> , 2019, 132, 2509-2523.	3.6	56
67	Genome-wide association study of the oil content in upland cotton (<i>Gossypium hirsutum</i> L.) and identification of GhPRXR1, a candidate gene for a stable QTLqOC-Dt5-1. <i>Plant Science</i> , 2019, 286, 89-97.	3.6	35
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74	Ramularia leaf spot: an emergent disease of cotton in Brazil. <i>Tropical Plant Pathology</i> , 2019, 44, 473-482.	1.5	6
75	High-density linkage map construction and QTL analyses for fiber quality, yield and morphological traits using CottonSNP63K array in upland cotton (<i>Gossypium hirsutum</i> L.). <i>BMC Genomics</i> , 2019, 20, 889.	2.8	32
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77	Genome-wide association mapping of stress-tolerance traits in cotton. <i>Crop Journal</i> , 2019, 7, 77-88.	5.2	26
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92	QTL mapping for plant height and fruit branch number based on RIL population of upland cotton. <i>Journal of Cotton Research</i> , 2020, 3, .	2.5	6
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103	Genome-wide association study of micronaire using a natural population of representative upland cotton (<i>Gossypium hirsutum</i> L.). <i>Journal of Cotton Research</i> , 2021, 4, .	2.5	6
104	Finding Needles in a Haystack: Using Geo-References to Enhance the Selection and Utilization of Landraces in Breeding for Climate-Resilient Cultivars of Upland Cotton (<i>Gossypium hirsutum</i> L.). <i>Plants</i> , 2021, 10, 1300.	3.5	3
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106	Genome-Wide Association Analysis Reveals Loci and Candidate Genes Involved in Fiber Quality Traits Under Multiple Field Environments in Cotton (<i>Gossypium hirsutum</i>). <i>Frontiers in Plant Science</i> , 2021, 12, 695503.	3.6	12
107	GBS-SNP and SSR based genetic mapping and QTL analysis for drought tolerance in upland cotton. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 1731-1745.	3.1	11
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124	Identification of genomewide single-nucleotide polymorphisms associated with presummer, summer and autumn bolls in upland cotton. Journal of Genetics, 2019, 98, .	0.7	1
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130	Genetic Diversity, QTL Mapping, and Marker-Assisted Selection Technology in Cotton (<i>Gossypium</i> spp.). Frontiers in Plant Science, 2021, 12, 779386.	3.6	29
131	Quantitative Trait Loci and Transcriptome Analysis Reveal Genetic Basis of Fiber Quality Traits in CCR170 RIL Population of <i>Gossypium hirsutum</i> . Frontiers in Plant Science, 2021, 12, 753755.	3.6	5
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218	Development and validation of Kompetitive allele-specific PCR (KASP) markers for bacterial blight resistant locus <i>BbBL13</i> in Upland cotton (<i>Gossypium hirsutum</i> L.). <i>Crop Science</i> , 0, , .	1.8	0
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221	Genetic diversity and population structure analyses and genome-wide association studies of photoperiod sensitivity in cotton (<i>Gossypium hirsutum</i> L.). <i>Theoretical and Applied Genetics</i> , 2023, 136, .	3.6	0
222	Application of a High-Density Single Nucleotide Polymorphism Genetic Map in Mapping Quantitative Trait Loci of Early-Maturing Traits in Upland Cotton. <i>Agronomy</i> , 2023, 13, 2716.	3.0	0
223	Genetic linkage analysis of stable QTLs in <i>Gossypium hirsutum</i> RIL population revealed function of GhCesA4 in fiber development. <i>Journal of Advanced Research</i> , 2023, , .	9.5	0
224	Molecular-genetic and cytogenetic analyses of cotton chromosome introgression from <i>Gossypium barbadense</i> L. into the genome of <i>G. hirsutum</i> L. in BC ₂ F ₁ hybrids. <i>Vavilovskii Zhurnal Genetiki i Seleksii</i> , 2023, 27, 958-970.	1.1	1
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