

QTL mapping in multiple populations and development
trait loci for fruit size in cucumbers of different market

Theoretical and Applied Genetics

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Citation Report

#	ARTICLE	IF	CITATIONS
1	A High-Density Genetic Linkage Map for Cucumber (<i>Cucumis sativus</i> L.): Based on Specific Length Amplified Fragment (SLAF) Sequencing and QTL Analysis of Fruit Traits in Cucumber. <i>Frontiers in Plant Science</i> , 2016, 7, 437.	1.7	120
2	Genetic Mapping of Complex Traits in Cucurbits. <i>Plant Genetics and Genomics: Crops and Models</i> , 2016, , 269-290.	0.3	3
3	Genomic Analysis of Cucurbit Fruit Growth. <i>Plant Genetics and Genomics: Crops and Models</i> , 2016, , 321-344.	0.3	7
4	SHORT HYPOCOTYL 1 Encodes a SMARCA3-like Chromatin Remodeling Factor Regulating Elongation. <i>Plant Physiology</i> , 2016, 172, pp.00501.2016.	2.3	22
5	QTL mapping of parthenocarpic fruit set in North American processing cucumber. <i>Theoretical and Applied Genetics</i> , 2016, 129, 2387-2401.	1.8	42
6	Rapid identification of fruit length loci in cucumber (<i>Cucumis sativus</i> L.) using next-generation sequencing (NGS)-based QTL analysis. <i>Scientific Reports</i> , 2016, 6, 27496.	1.6	63
7	Integrated analysis in bi-parental and natural populations reveals CsCLAVATA3 (CsCLV3) underlying carpel number variations in cucumber. <i>Theoretical and Applied Genetics</i> , 2016, 129, 1007-1022.	1.8	43
8	Variation in cucumber (<i>Cucumis sativus</i> L.) fruit size and shape results from multiple components acting pre-anthesis and post-pollination. <i>Planta</i> , 2017, 246, 641-658.	1.6	53
9	Transcriptomic analysis of short-fruit 1 (sf1) reveals new insights into the variation of fruit-related traits in <i>Cucumis sativus</i> . <i>Scientific Reports</i> , 2017, 7, 2950.	1.6	26
10	QTL mapping of domestication and diversifying selection related traits in round-fruited semi-wild Xishuangbanna cucumber (<i>Cucumis sativus</i> L. var. <i>xishuangbannanesis</i>). <i>Theoretical and Applied Genetics</i> , 2017, 130, 1531-1548.	1.8	60
11	Quantitative trait locus analysis of cucumber fruit morphological traits based on image analysis. <i>Euphytica</i> , 2017, 213, 1.	0.6	15
12	Round fruit shape in WI7239 cucumber is controlled by two interacting quantitative trait loci with one putatively encoding a tomato SUN homolog. <i>Theoretical and Applied Genetics</i> , 2017, 130, 573-586.	1.8	80
13	Genetics and Genomics of Cucurbitaceae. <i>Plant Genetics and Genomics: Crops and Models</i> , 2017, , .	0.3	22
14	A high-density linkage map and QTL mapping of fruit-related traits in pumpkin (<i>Cucurbita moschata</i>) Tj ETQq1 1 0.784314 rgBT /Over	1.6	55
15	STAYGREEN (CsSGR) is a candidate for the anthracnose (<i>Colletotrichum orbiculare</i>) resistance locus cla in Gy14 cucumber. <i>Theoretical and Applied Genetics</i> , 2018, 131, 1577-1587.	1.8	21
16	Genetic mapping reveals a candidate gene (CIFS1) for fruit shape in watermelon (<i>Citrullus lanatus</i> L.). <i>Theoretical and Applied Genetics</i> , 2018, 131, 947-958.	1.8	94
17	Dynamic and epistatic QTL mapping reveals the complex genetic architecture of waterlogging tolerance in chrysanthemum. <i>Planta</i> , 2018, 247, 899-924.	1.6	21
18	QTL Analysis for Downy Mildew Resistance in Cucumber Inbred Line PI 197088. <i>Plant Disease</i> , 2018, 102, 1240-1245.	0.7	33

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19	Genetic variation of dynamic fiber elongation and developmental quantitative trait locus mapping of fiber length in upland cotton (<i>Gossypium hirsutum</i> L.). <i>BMC Genomics</i> , 2018, 19, 882.	1.2	33
20	Identification of Conserved and Diverse Metabolic Shift of the Styler, Intermediate and Peduncular Segments of Cucumber Fruit during Development. <i>International Journal of Molecular Sciences</i> , 2018, 19, 135.	1.8	14
21	<i>LITTLELEAF</i> (<i>LL</i>) encodes a WD40 repeat domain-containing protein associated with organ size variation in cucumber. <i>Plant Journal</i> , 2018, 95, 834-847.	2.8	58
22	Identification of <i>QTL</i> s controlling low temperature tolerance during the germination stage in cucumber (<i>Cucumis sativus</i> L.). <i>Plant Breeding</i> , 2018, 137, 629-637.	1.0	16
23	STAYGREEN, STAY HEALTHY: a loss of susceptibility mutation in the <i>STAYGREEN</i> gene provides durable, broad spectrum disease resistances for over 50 years of US cucumber production. <i>New Phytologist</i> , 2019, 221, 415-430.	3.5	72
24	Quantitative trait loci analysis of hormone levels in <i>Arabidopsis</i> roots. <i>PLoS ONE</i> , 2019, 14, e0219008.	1.1	3
25	Mapping quantitative trait loci for yield-related traits and predicting candidate genes for grain weight in maize. <i>Scientific Reports</i> , 2019, 9, 16112.	1.6	15
26	QTL mapping and genome-wide association study reveal two novel loci associated with green flesh color in cucumber. <i>BMC Plant Biology</i> , 2019, 19, 243.	1.6	35
27	Target SSR-Seq: A Novel SSR Genotyping Technology Associate With Perfect SSRs in Genetic Analysis of Cucumber Varieties. <i>Frontiers in Plant Science</i> , 2019, 10, 531.	1.7	37
28	Genetic Regulation of Ethylene Dosage for Cucumber Fruit Elongation. <i>Plant Cell</i> , 2019, 31, 1063-1076.	3.1	85
29	A Functional Allele of <i>CsFUL1</i> Regulates Fruit Length through Repressing <i>CsSUP</i> and Inhibiting Auxin Transport in Cucumber. <i>Plant Cell</i> , 2019, 31, 1289-1307.	3.1	84
30	QTL mapping of low temperature germination ability in cucumber. <i>Euphytica</i> , 2019, 215, 1.	0.6	17
31	Genetic analysis and QTL mapping of fruit length and diameter in a cucumber (<i>Cucumis sativus</i> L.) recombinant inbred line (RIL) population. <i>Scientia Horticulturae</i> , 2019, 250, 214-222.	1.7	13
32	QTL mapping for 11 agronomic traits based on a genome-wide Bin-map in a large F2 population of foxtail millet (<i>Setaria italica</i> (L.) P. Beauv). <i>Molecular Breeding</i> , 2019, 39, 1.	1.0	24
33	Quantitative Trait Loci Mapping and Candidate Gene Analysis of Low Temperature Tolerance in Cucumber Seedlings. <i>Frontiers in Plant Science</i> , 2019, 10, 1620.	1.7	19
34	QTL and Transcriptomic Analyses Implicate Cuticle Transcription Factor SHINE as a Source of Natural Variation for Epidermal Traits in Cucumber Fruit. <i>Frontiers in Plant Science</i> , 2019, 10, 1536.	1.7	12
35	Novel loci <i>fsd6.1</i> and <i>Csgl3</i> regulate ultra-high fruit spine density in cucumber. <i>Theoretical and Applied Genetics</i> , 2019, 132, 27-40.	1.8	23
36	Molecular basis of cucumber fruit domestication. <i>Current Opinion in Plant Biology</i> , 2019, 47, 38-46.	3.5	96

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37	Origin and domestication of Cucurbitaceae crops: insights from phylogenies, genomics and archaeology. <i>New Phytologist</i> , 2020, 226, 1240-1255.	3.5	134
38	Quantitative trait loci for fruit size and flowering time-related traits under domestication and diversifying selection in cucumber (<i>Cucumis sativus</i>). <i>Plant Breeding</i> , 2020, 139, 176-191.	1.0	26
39	Genome-wide Target Mapping Shows Histone Deacetylase Complex1 Regulates Cell Proliferation in Cucumber Fruit. <i>Plant Physiology</i> , 2020, 182, 167-184.	2.3	47
40	Map-based cloning of qBWT-c12 discovered brassinosteroid-mediated control of organ size in cotton. <i>Plant Science</i> , 2020, 291, 110315.	1.7	4
41	The major-effect quantitative trait locus Fnl7.1 encodes a late embryogenesis abundant protein associated with fruit neck length in cucumber. <i>Plant Biotechnology Journal</i> , 2020, 18, 1598-1609.	4.1	14
42	Genetic architecture of fruit size and shape variation in cucurbits: a comparative perspective. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1-21.	1.8	111
43	Identification of fruit size associated quantitative trait loci featuring SLAF based high-density linkage map of goji berry (<i>Lycium spp.</i>). <i>BMC Plant Biology</i> , 2020, 20, 474.	1.6	18
44	A durum wheat adult plant stripe rust resistance QTL and its relationship with the bread wheat Yr80 locus. <i>Theoretical and Applied Genetics</i> , 2020, 133, 3049-3066.	1.8	10
45	Dynamic Changes of Fruit Shape Traits and Its Correlation to the Morphology of Other Organs in Cucumber. <i>Agronomy</i> , 2020, 10, 1111.	1.3	2
46	Identification of QTLs for grain yield and other traits in tropical maize under <i>Striga</i> infestation. <i>PLoS ONE</i> , 2020, 15, e0239205.	1.1	14
47	QTL Mapping for Cucumber Fruit Size and Shape with Populations from Long and Round Fruited Inbred Lines. <i>Horticultural Plant Journal</i> , 2020, 6, 132-144.	2.3	20
48	Detection of putative QTL regions associated with ovary traits in melon using SNP-CAPS markers. <i>Scientia Horticulturae</i> , 2020, 270, 109445.	1.7	14
50	Gene regulatory network of carpel number variation in cucumber. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	16
51	The MADS-Box Gene CsSHP Participates in Fruit Maturation and Floral Organ Development in Cucumber. <i>Frontiers in Plant Science</i> , 2019, 10, 1781.	1.7	11
52	Cucumber Fruit Size and Shape Variations Explored from the Aspects of Morphology, Histology, and Endogenous Hormones. <i>Plants</i> , 2020, 9, 772.	1.6	30
53	Localization of quantitative trait loci for cucumber fruit shape by a population of chromosome segment substitution lines. <i>Scientific Reports</i> , 2020, 10, 11030.	1.6	11
54	Markers for selection of three alleles of CISUN25-26-27a (Cla011257) associated with fruit shape in watermelon. <i>Molecular Breeding</i> , 2020, 40, 1.	1.0	12
55	QTL for horticulturally important traits associated with pleiotropic andromonoecy and carpel number loci, and a paracentric inversion in cucumber. <i>Theoretical and Applied Genetics</i> , 2020, 133, 2271-2290.	1.8	8

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56	Quantitative trait loci for horticulturally important traits defining the Sikkim cucumber, <i>Cucumis sativus</i> var. <i>sikkimensis</i> . <i>Theoretical and Applied Genetics</i> , 2021, 134, 229-247.	1.8	19
58	Genetic linkage mapping and QTLs identification for morphology and fruit quality related traits of melon by SNP based CAPS markers. <i>Scientia Horticulturae</i> , 2021, 278, 109849.	1.7	18
59	Identification of quantitative trait loci for powdery mildew resistance in highly resistant cucumber (<i>Cucumis sativus</i> L.) using ddRAD-seq analysis. <i>Breeding Science</i> , 2021, 71, 326-333.	0.9	2
60	Quantitative trait locus analysis of cucumber fruit texture using double digest restriction associated DNA sequencing. <i>Euphytica</i> , 2021, 217, 1.	0.6	2
61	CsKTN1 for a katanin p60 subunit is associated with the regulation of fruit elongation in cucumber (<i>Cucumis sativus</i> L.). <i>Theoretical and Applied Genetics</i> , 2021, 134, 2429-2441.	1.8	15
62	Molecular research progress and improvement approach of fruit quality traits in cucumber. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3535-3552.	1.8	18
63	Recent advances in cucumber (<i>Cucumis sativus</i> L.). <i>Journal of Horticultural Science and Biotechnology</i> , 2022, 97, 3-23.	0.9	6
64	Long-read genome assembly and genetic architecture of fruit shape in the bottle gourd. <i>Plant Journal</i> , 2021, 107, 956-968.	2.8	23
65	Genomic Prediction and the Practical Breeding of 12 Quantitative-Inherited Traits in Cucumber (<i>Cucumis sativus</i> L.). <i>Frontiers in Plant Science</i> , 2021, 12, 729328.	1.7	2
66	Fine mapping and identification of the candidate gene BFS for fruit shape in wax gourd (<i>Benincasa</i>) Tj ETQq1 1 0.784314 rgBT / Overlock 16	1.8	16
67	A Genotyping-by-sequencing Single Nucleotide Polymorphism-based Map and Genetic Analysis of Root Traits in an Interspecific Tomato Population. <i>Journal of the American Society for Horticultural Science</i> , 2019, 144, 394-404.	0.5	4
68	Classical Genetics and Traditional Breeding in Cucumber (<i>Cucumis sativus</i> L.). , 0, , .		1
69	Genome-wide analysis of expansins and their role in fruit spine development in cucumber (<i>Cucumis</i>) Tj ETQq0 0 0 rgBT / Overlock 10 Tf 5	2.3	8
70	<i>CmFSI8</i> / <i>CmOFP13</i> encoding an OVATE family protein controls fruit shape in melon. <i>Journal of Experimental Botany</i> , 2022, 73, 1370-1384.	2.4	17
71	Promoter variation in a homeobox gene, <i>CpDII</i> , is associated with deeply lobed leaf in <i>Cucurbita pepo</i> L. <i>Theoretical and Applied Genetics</i> , 2022, 135, 1223-1234.	1.8	5
72	Genetic and Molecular Regulation Mechanisms in the Formation and Development of Vegetable Fruit Shape. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 1514.	1.3	4
73	Mapping of genetic loci controlling fruit linked morphological traits of melon using developed CAPS markers. <i>Molecular Biology Reports</i> , 2022, 49, 5459-5472.	1.0	9
74	Genome-wide analysis of OVATE family proteins in cucumber (<i>Cucumis sativus</i> L.). <i>Journal of Integrative Agriculture</i> , 2022, 21, 1321-1331.	1.7	5

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76	Mapping of fruit apex shape related QTLs across multi-genetic backgrounds in cucumber (<i>Cucumis</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.3	10
100	Functional copy number variation of CsSHINE1 is associated with fruit skin netting intensity in cucumber, <i>Cucumis sativus</i> . <i>Theoretical and Applied Genetics</i> , 2022, 135, 2101-2119.	1.8	5
101	Identification of QTLs linked with watermelon fruit and seed traits using GBS-based high-resolution genetic mapping. <i>Scientia Horticulturae</i> , 2022, 303, 111237.	1.7	8
102	Serial-Omics and Molecular Function Study Provide Novel Insight into Cucumber Variety Improvement. <i>Plants</i> , 2022, 11, 1609.	1.6	2
103	QTL mapping for pumpkin fruit traits using a GBS-based high-density genetic map. <i>Euphytica</i> , 2022, 218, .	0.6	2
104	Quantitative trait locus mapping of fruit aroma compounds in cucumber (<i>Cucumis sativus</i>L.) based on a recombinant inbred line population. <i>Horticulture Research</i> , 2022, 9, .	2.9	2
105	Mapping and Validation of a New Quantitative Trait Loci (Qtl) for Fruit Size in Watermelon (<i>Citrullus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.4	0
106	Research Progress on the Leaf Morphology, Fruit Development and Plant Architecture of the Cucumber. <i>Plants</i> , 2022, 11, 2128.	1.6	3
107	Identification of QTLs controlling cold tolerance in cucumber (<i>Cucumis sativus</i> L.) seedlings. <i>Scientia Horticulturae</i> , 2022, 305, 111383.	1.7	2
108	QTL analysis of early flowering of female flowers in zucchini (<i>Cucurbita pepo</i> L.). <i>Journal of Integrative Agriculture</i> , 2023, 22, 3321-3330.	1.7	3
109	Genomic Designing for Abiotic Stress Tolerance in Cucurbits. , 2022, , 187-252.		0
110	Sigma factor binding protein 1 (CsSIB1) is a putative candidate of the major-effect QTL dm5.3 for downy mildew resistance in cucumber (<i>Cucumis sativus</i>). <i>Theoretical and Applied Genetics</i> , 2022, 135, 4197-4215.	1.8	4
111	The CsHEC1-CsOVATE module contributes to fruit neck length variation via modulating auxin biosynthesis in cucumber. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	10
112	Ectopic Expression of CsSUN in Tomato Results in Elongated Fruit Shape via Regulation of Longitudinal Cell Division. <i>International Journal of Molecular Sciences</i> , 2022, 23, 9973.	1.8	1
113	Phenotypic Characterization and Fine Mapping of a Major-Effect Fruit Shape QTL FS5.2 in Cucumber, <i>Cucumis sativus</i> L., with Near-Isogenic Line-Derived Segregating Populations. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13384.	1.8	2
114	Relationship between Key Environmental Factors and the Architecture of Fruit Shape and Size in Near-Isogenic Lines of Cucumber (<i>Cucumis sativus</i> L.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 14033.	1.8	7
115	Natural variation in CRABS CLAW contributes to fruit length divergence in cucumber. <i>Plant Cell</i> , 2023, 35, 738-755.	3.1	11
116	Morphological and Genetic Diversity of Cucumber (<i>Cucumis sativus</i> L.) Fruit Development. <i>Plants</i> , 2023, 12, 23.	1.6	3

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117	Primary mapping of quantitative trait loci regulating multivariate horticultural phenotypes of watermelon (<i>Citrullus lanatus</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
118	<i>CsTRM5</i> regulates fruit shape via mediating cell division direction and cell expansion in cucumber. <i>Horticulture Research</i> , 2023, 10, .	2.9	9
119	Genetic Mapping and QTL Analysis of Fruit Traits in Melon (<i>Cucumis melo</i> L.). <i>Current Issues in Molecular Biology</i> , 2023, 45, 3419-3433.	1.0	3