

A Functional Allele of *CsFUL1* Regulates Fruit Length, *CsSUC2* and Inhibiting Auxin Transport in Cucumbers

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Citation Report

#	ARTICLE	IF	CITATIONS
1	CsBRC1 inhibits axillary bud outgrowth by directly repressing the auxin efflux carrier <i>CsPIN3</i> in cucumber. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17105-17114.	3.3	91
2	A Growing Reputation for <i>FRUITFULL</i> Genes. <i>Plant Cell</i> , 2019, 31, 1220-1221.	3.1	0
3	Recent progress on the molecular breeding of <i>Cucumis sativus</i> L. in China. <i>Theoretical and Applied Genetics</i> , 2020, 133, 1777-1790.	1.8	25
4	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
5	Molecularly tagged genes and quantitative trait loci in cucumber with recommendations for QTL nomenclature. <i>Horticulture Research</i> , 2020, 7, 3.	2.9	73
6	Characterization of an <i>APETALA1</i> and a <i>FRUITFUL</i> -like homolog in chrysanthemum. <i>Scientia Horticulturae</i> , 2020, 272, 109518.	1.7	6
7	The <i>VvSUPERMAN</i> -like Gene Is Differentially Expressed between Bicarpellate and Tricarpellate Florets of <i>Vitis vinifera</i> L. Cv. 'Xiangfei' and Its Heterologous Expression Reduces Carpel Number in Tomato. <i>Plant and Cell Physiology</i> , 2020, 61, 1760-1774.	1.5	4
8	<i>Arabidopsis Col/Ler</i> and <i>Ws/Ler</i> hybrids and Hybrid Mimics produce seed yield heterosis through increased height, inflorescence branch and silique number. <i>Planta</i> , 2020, 252, 40.	1.6	5
9	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
10	Localization shift of a sugar transporter contributes to phloem unloading in sweet watermelons. <i>New Phytologist</i> , 2020, 227, 1858-1871.	3.5	32
12	Comparative population genomics dissects the genetic basis of seven domestication traits in jujube. <i>Horticulture Research</i> , 2020, 7, 89.	2.9	20
13	Gene regulatory network of carpel number variation in cucumber. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	16
14	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
15	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
16	A fast, simple, high efficient and one-step generation of composite cucumber plants with transgenic roots by <i>Agrobacterium rhizogenes</i> -mediated transformation. <i>Plant Cell, Tissue and Organ Culture</i> , 2020, 141, 207-216.	1.2	19
17	Glutamine application promotes nitrogen and biomass accumulation in the shoot of seedlings of the maize hybrid ZD958. <i>Planta</i> , 2020, 251, 66.	1.6	27
18	A <i>MADS</i> -box transcription factor from grapevine, <i>VvMADS45</i> , influences seed development. <i>Plant Cell, Tissue and Organ Culture</i> , 2020, 141, 105-118.	1.2	11
19	Genome-wide analysis of <i>CsWOX</i> transcription factor gene family in cucumber (<i>Cucumis sativus</i> L.). <i>Scientific Reports</i> , 2020, 10, 6216.	1.6	16

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20	Roles of CsBRC1-like in leaf and lateral branch development in cucumber. <i>Plant Science</i> , 2021, 302, 110681.	1.7	7
21	Transcriptional control of local auxin distribution by the CsDFB1-CsPHB module regulates floral organogenesis in cucumber. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2023942118.	3.3	12
22	A fruit ripening-associated transcription factor CsMADS5 positively regulates carotenoid biosynthesis in citrus. <i>Journal of Experimental Botany</i> , 2021, 72, 3028-3043.	2.4	47
23	A positive feedback loop mediated by <i>CsERF31</i> initiates female cucumber flower development. <i>Plant Physiology</i> , 2021, 186, 1088-1100.	2.3	11
24	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
25	GmFULa improves soybean yield by enhancing carbon assimilation without altering flowering time or maturity. <i>Plant Cell Reports</i> , 2021, 40, 1875-1888.	2.8	9
26	Recent advances in cucumber (<i>Cucumis sativus</i> L.). <i>Journal of Horticultural Science and Biotechnology</i> , 2022, 97, 3-23.	0.9	6
27	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
28	EjBZR1 represses fruit enlargement by binding to the <i>EjCYP90</i> promoter in loquat. <i>Horticulture Research</i> , 2021, 8, 152.	2.9	18
29	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 10	1.8	16
30	GmFULc Is Induced by Short Days in Soybean and May Accelerate Flowering in Transgenic <i>Arabidopsis thaliana</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 10333.	1.8	7
31	The Formation of Fruit Quality in <i>Cucumis sativus</i> L.. <i>Frontiers in Plant Science</i> , 2021, 12, 729448.	1.7	10
32	The Putative Role of the NAC Transcription Factor EjNACL47 in Cell Enlargement of Loquat (<i>Eriobotrya</i>) Tj ETQq0 0 0 rgBT /Overlock 10	1.2	4
34	<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
35	PrupeFUL4 regulates ripening and softening of peach fruits through ethylene biosynthesis. <i>Acta Physiologiae Plantarum</i> , 2022, 44, 1.	1.0	4
36	OsMADS14 and NF-YB1 cooperate in the direct activation of <i>OsAGPL2</i> and <i>Waxy</i> during starch synthesis in rice endosperm. <i>New Phytologist</i> , 2022, 234, 77-92.	3.5	18
37	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
38	Pepper Fruit Elongation Is Controlled by <i>Capsicum annuum</i> Ovate Family Protein 20. <i>Frontiers in Plant Science</i> , 2021, 12, 815589.	1.7	12

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39	Cucurbitaceae genome evolution, gene function, and molecular breeding. <i>Horticulture Research</i> , 2022, 9, .	2.9	34
40	Gentian FLOWERING LOCUS T orthologs regulate phase transitions: floral induction and endodormancy release. <i>Plant Physiology</i> , 2022, , .	2.3	15
41	<i>NS</i> encodes an auxin transporter that regulates the "numerous spines"™ trait in cucumber (<i>Cucumis sativus</i>) fruit. <i>Plant Journal</i> , 2022, 110, 325-336.	2.8	10
42	Advances in Understanding and Harnessing the Molecular Regulatory Mechanisms of Vegetable Quality. <i>Frontiers in Plant Science</i> , 2022, 13, 836515.	1.7	4
43	Genome-wide analysis of OVATE family proteins in cucumber (<i>Cucumissativus L.</i>). <i>Journal of Integrative Agriculture</i> , 2022, 21, 1321-1331.	1.7	5
46	Mapping of fruit apex shape related QTLs across multi-genetic backgrounds in cucumber (<i>Cucumis</i>). <i>Tj ETQq1 1 0.784314 rgBT/Overl</i>	2.3	10
47	FRUITFULL-like genes regulate flowering time and inflorescence architecture in tomato. <i>Plant Cell</i> , 2022, 34, 1002-1019.	3.1	24
48	Ethylene plays a dual role in sex determination and fruit shape in cucurbits. <i>Current Biology</i> , 2022, 32, 2390-2401.e4.	1.8	7
49	Recent Progress in the Regeneration and Genetic Transformation System of Cucumber. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 7180.	1.3	8
50	Transcriptome Analysis of Sponge Gourd (<i>Luffa cylindrica</i>) Reveals Candidate Genes Associated with Fruit Size. <i>Agronomy</i> , 2022, 12, 1810.	1.3	1
51	Integrated multi-omics analysis uncovers roles of <i>miR164</i> in MdORE1<i> in strigolactone-mediated inhibition of adventitious root formation in apple. <i>Plant, Cell and Environment</i> , 2022, 45, 3582-3603.	2.8	7
52	Research Progress on the Leaf Morphology, Fruit Development and Plant Architecture of the Cucumber. <i>Plants</i> , 2022, 11, 2128.	1.6	3
53	Involvement of auxin in growth and stress response of cucumber. <i>Vegetable Research</i> , 2022, 2, 1-9.	0.2	15
54	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
55	Roles of Auxin in the Growth, Development, and Stress Tolerance of Horticultural Plants. <i>Cells</i> , 2022, 11, 2761.	1.8	18
56	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
57	CsIPT1b and CsUGT85A2 delay female corolla opening in cucumber by regulating the content of cytokinins. <i>Horticultural Plant Journal</i> , 2023, 9, 754-762.	2.3	1
58	Phenotypic Characterization and Fine Mapping of a Major-Effect Fruit Shape QTL FS5.2 in Cucumber, <i>Cucumis sativus L.</i>, with Near-Isogenic Line-Derived Segregating Populations. <i>International Journal of Molecular Sciences</i> , 2022, 23, 13384.	1.8	2

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59	Transcriptome and hormones analysis provide insights into elongated fruit somaclonal mutant in 'Akihime'™ strawberry. <i>Scientia Horticulturae</i> , 2023, 309, 111608.	1.7	3
60	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
61	QTL mapping reveals candidate genes for main agronomic traits in Luffa based on a high-resolution genetic map. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	0
62	Natural variation in CRABS CLAW contributes to fruit length divergence in cucumber. <i>Plant Cell</i> , 2023, 35, 738-755.	3.1	11
63	Morphological and Genetic Diversity of Cucumber (<i>Cucumis sativus</i> L.) Fruit Development. <i>Plants</i> , 2023, 12, 23.	1.6	3
64	Genome-wide association study provides genetic insights into natural variation in watermelon rind thickness and single fruit weight. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	1
65	Reference genes identification for qRT-PCR normalization of gene expression analysis in <i>Cucumis sativus</i> under <i>Meloidogyne incognita</i> infection and <i>Pseudomonas</i> treatment. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
66	Vegetable biology and breeding in the genomics era. <i>Science China Life Sciences</i> , 2023, 66, 226-250.	2.3	10
67	Pollen tube emergence is mediated by ovary-expressed ALCATRAZ in cucumber. <i>Nature Communications</i> , 2023, 14, .	5.8	8
68	Identification of Bottle Gourd (<i>Lagenaria siceraria</i>) OVATE Family Genes and Functional Characterization of LsOVATE1. <i>Biomolecules</i> , 2023, 13, 85.	1.8	1
69	<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
70	Variations in the 'CRABS CLAW' modulate fruit elongation in cucumber. <i>Vegetable Research</i> , 2023, 3, 0-0.	0.2	0
71	Gene network associates with CsCRC regulating fruit elongation in cucumber. <i>Vegetable Research</i> , 2023, 3, 1-4.	0.2	1
72	Improving <i>Agrobacterium tumefaciens</i> -Mediated Genetic Transformation for Gene Function Studies and Mutagenesis in Cucumber (<i>Cucumis sativus</i> L.). <i>Genes</i> , 2023, 14, 601.	1.0	4
73	Mapping and identification of CsSF4, a gene encoding a UDP-N-acetyl glucosamine-peptide N-acetylglucosaminyltransferase required for fruit elongation in cucumber (<i>Cucumis sativus</i> L.). <i>Theoretical and Applied Genetics</i> , 2023, 136, .	1.8	2