A genomic variation map provides insights into the gen domestication and diversity

Nature Genetics 45, 1510-1515 DOI: 10.1038/ng.2801

Citation Report

#	Article	IF	CITATIONS
1	Genome-Wide Analysis of the bZIP Transcription Factors in Cucumber. PLoS ONE, 2014, 9, e96014.	2.5	191
2	Fastq_clean: An optimized pipeline to clean the Illumina sequencing data with quality control. , 2014, ,		51
3	What lies beyond the eye: the molecular mechanisms regulating tomato fruit weight and shape. Frontiers in Plant Science, 2014, 5, 227.	3.6	167
4	Genomeâ€wide variation within and between wild and domestic yak. Molecular Ecology Resources, 2014, 14, 794-801.	4.8	40
5	Biosynthesis, regulation, and domestication of bitterness in cucumber. Science, 2014, 346, 1084-1088.	12.6	388
6	An SNP-based saturated genetic map and QTL analysis of fruit-related traits in cucumber using specific-length amplified fragment (SLAF) sequencing. BMC Genomics, 2014, 15, 1158.	2.8	127
7	The contribution of genetic and genomic approaches to plant domestication studies. Current Opinion in Plant Biology, 2014, 18, 51-59.	7.1	93
8	Genomic analyses provide insights into the history of tomato breeding. Nature Genetics, 2014, 46, 1220-1226.	21.4	801
9	The complex domestication history of the common bean. Nature Genetics, 2014, 46, 663-664.	21.4	17
10	QTL-seq identifies an early flowering QTL located near Flowering Locus T in cucumber. Theoretical and Applied Genetics, 2014, 127, 1491-1499.	3.6	267
11	Investment in plant research and development bears fruit in China. Plant Cell Reports, 2014, 33, 541-550.	5.6	7
12	Transcriptome comparison reveals the patterns of selection in domesticated and wild ramie (Boehmeria nivea L. Gaud). Plant Molecular Biology, 2014, 86, 85-92.	3.9	43
13	A transposable element insertion in the susceptibility gene CsaMLO8 results in hypocotyl resistance to powdery mildew in cucumber. BMC Plant Biology, 2015, 15, 243.	3.6	104
15	QTL mapping of cucumber fruit flesh thickness by SLAF-seq. Scientific Reports, 2015, 5, 15829.	3.3	70
16	Bitter but tasty cucumber. National Science Review, 2015, 2, 129-130.	9.5	2
17	Transgenic cucumber lines expressing the chimeric <scp>pGT</scp> :: <i>Dhn24</i> gene do not show enhanced chilling tolerance in phytotron conditions. Plant Breeding, 2015, 134, 468-476.	1.9	3
18	Development of genomewide simple sequence repeat fingerprints and highly polymorphic markers in cucumbers based on nextâ€generation sequence data. Plant Breeding, 2015, 134, 605-611.	1.9	10
19	Genome-Wide Identification, Characterization and Evolutionary Analysis of Long Intergenic Noncoding RNAs in Cucumber. PLoS ONE, 2015, 10, e0121800.	2.5	98

ATION REDO

2

#	Article	IF	Citations
20	High-Throughput Sequencing Identifies Novel and Conserved Cucumber (Cucumis sativus L.) microRNAs in Response to Cucumber Green Mottle Mosaic Virus Infection. PLoS ONE, 2015, 10, e0129002.	2.5	26
21	Loss-of-Function Mutations in CsMLO1 Confer Durable Powdery Mildew Resistance in Cucumber (Cucumis sativus L.). Frontiers in Plant Science, 2015, 6, 1155.	3.6	65
22	Taxonomy and Genetic Differentiation among Wild and Cultivated Germplasm of <i>Solanum</i> sect. <i>Petota</i> . Plant Genome, 2015, 8, eplantgenome2014.06.0025.	2.8	52
23	Genome-Wide Mapping of Structural Variations Reveals a Copy Number Variant That Determines Reproductive Morphology in Cucumber. Plant Cell, 2015, 27, 1595-1604.	6.6	125
24	A Sequencing-Based Linkage Map of Cucumber. Molecular Plant, 2015, 8, 961-963.	8.3	28
25	Epidemiology and Population Biology of <i>Pseudoperonospora cubensis</i> : A Model System for Management of Downy Mildews. Annual Review of Phytopathology, 2015, 53, 223-246.	7.8	84
26	Evolution Is an Experiment: Assessing Parallelism in Crop Domestication and Experimental Evolution. Molecular Biology and Evolution, 2015, 32, 1661-1671.	8.9	41
27	Differential proteomic analysis of dwarf characteristics in cucumber (Cucumis sativus Linn.) stems. Acta Physiologiae Plantarum, 2015, 37, 1.	2.1	3
28	Patterns of genomic changes with crop domestication and breeding. Current Opinion in Plant Biology, 2015, 24, 47-53.	7.1	83
29	Molecular mapping and candidate gene analysis for yellow fruit flesh in cucumber. Molecular Breeding, 2015, 35, 1.	2.1	36
30	Resequencing 302 wild and cultivated accessions identifies genes related to domestication and improvement in soybean. Nature Biotechnology, 2015, 33, 408-414.	17.5	1,023
31	Identification and fine mapping of pm5.1: a recessive gene for powdery mildew resistance in cucumber (Cucumis sativus L.). Molecular Breeding, 2015, 35, 1.	2.1	46
32	QTL mapping in multiple populations and development stages reveals dynamic quantitative trait loci for fruit size in cucumbers of different market classes. Theoretical and Applied Genetics, 2015, 128, 1747-1763.	3.6	128
33	Transposon Insertions, Structural Variations, and SNPs Contribute to the Evolution of the Melon Genome. Molecular Biology and Evolution, 2015, 32, 2760-2774.	8.9	80
34	Resurgence of Cucurbit Downy Mildew in the United States: A Watershed Event for Research and Extension. Plant Disease, 2015, 99, 428-441.	1.4	117
35	Sequencing consolidates molecular markers with plant breeding practice. Theoretical and Applied Genetics, 2015, 128, 779-795.	3.6	96
36	An <i>ACCUMULATION AND REPLICATION OF CHLOROPLASTS 5</i> gene mutation confers light green peel in cucumber. Journal of Integrative Plant Biology, 2015, 57, 936-942.	8.5	53
37	Genetic diversity and evolutionary relationship analyses within and among Raphanus species using EST-SSR markers. Molecular Breeding, 2015, 35, 1.	2.1	26

#	Article	IF	CITATIONS
38	Transcriptomic analysis reveals the roles of microtubule-related genes and transcription factors in fruit length regulation in cucumber (Cucumis sativus L.). Scientific Reports, 2015, 5, 8031.	3.3	89
39	Genetic analysis and gene mapping of papaya ring spot virus resistance in cucumber. Molecular Breeding, 2015, 35, 1.	2.1	22
40	Fine genetic mapping of target leaf spot resistance gene cca-3 in cucumber, Cucumis sativus L. Theoretical and Applied Genetics, 2015, 128, 2495-2506.	3.6	38
41	A Rare SNP Identified a TCP Transcription Factor Essential for Tendril Development in Cucumber. Molecular Plant, 2015, 8, 1795-1808.	8.3	58
42	Combining niche modelling and landscape genetics to study local adaptation: A novel approach illustrated using alpine plants. Perspectives in Plant Ecology, Evolution and Systematics, 2015, 17, 491-499.	2.7	13
43	Genomics and the Contrasting Dynamics of Annual and Perennial Domestication. Trends in Genetics, 2015, 31, 709-719.	6.7	145
44	Phylogeography of Chinese cherry (<i>Prunus pseudocerasus</i> Lindl.) inferred from chloroplast and nuclear <scp>DNA</scp> : insights into evolutionary patterns and demographic history. Plant Biology, 2015, 17, 787-797.	3.8	17
45	Molecular mapping reveals structural rearrangements and quantitative trait loci underlying traits with local adaptation in semi-wild Xishuangbanna cucumber (Cucumis sativus L. var.) Tj ETQq1 1 0.784314 rgBT	/Overlock	1 Q. 0f 50 4.57
46	Genome-wide identification and evolutionary analysis of positively selected miRNA genes in domesticated rice. Molecular Genetics and Genomics, 2015, 290, 593-602.	2.1	13
47	Hierarchical Map of Orthologous Genomic Regions Reconstructed from Two Closely Related Genomes: Cucumber Case Study. Plant Genome, 2016, 9, plantgenome2015.10.0099.	2.8	1
48	The Jujube Genome Provides Insights into Genome Evolution and the Domestication of Sweetness/Acidity Taste in Fruit Trees. PLoS Genetics, 2016, 12, e1006433.	3.5	136
49	Genome-Wide Association Study Provides Insight into the Genetic Control of Plant Height in Rapeseed (Brassica napus L.). Frontiers in Plant Science, 2016, 7, 1102.	3.6	49
50	A Detailed Analysis of the BR1 Locus Suggests a New Mechanism for Bolting after Winter in Sugar Beet (Beta vulgaris L.). Frontiers in Plant Science, 2016, 7, 1662.	3.6	26
51	Coverage recommendation for genotyping analysis of highly heterologous species using next-generation sequencing technology. Scientific Reports, 2016, 6, 35736.	3.3	46
52	Identification and characterisation of Dof transcription factors in the cucumber genome. Scientific Reports, 2016, 6, 23072.	3.3	73
53	Landscape and Fruit Developmental Regulation of Alternative Splicing in Tomato by Genome-Wide Analysis. Horticultural Plant Journal, 2016, 2, 338-350.	5.0	11
54	The Cucumber Genome. Plant Genetics and Genomics: Crops and Models, 2016, , 183-197.	0.3	5
55	Databases and Bioinformatics for Cucurbit Species. Plant Genetics and Genomics: Crops and Models, 2016 253-267.	0.3	2

#	Article	IF	CITATIONS
56	Two genomic regions associated with fiber quality traits in Chinese upland cotton under apparent breeding selection. Scientific Reports, 2016, 6, 38496.	3.3	68
57	Germplasm resources of horticultural crops and sustainable development of horticultural industry in China. Acta Horticulturae, 2016, , 1-8.	0.2	1
58	Genetic Resources of Cucumber. Plant Genetics and Genomics: Crops and Models, 2016, , 61-86.	0.3	12
59	The Melon Genome. Plant Genetics and Genomics: Crops and Models, 2016, , 173-181.	0.3	3
60	Genomic Analysis of Cucurbit Fruit Growth. Plant Genetics and Genomics: Crops and Models, 2016, , 321-344.	0.3	7
61	Genetic diversity and genomic strategies for improving drought and waterlogging tolerance in soybeans. Journal of Experimental Botany, 2017, 68, erw433.	4.8	118
62	Integrative Analyses of Nontargeted Volatile Profiling and Transcriptome Data Provide Molecular Insight into VOC Diversity in Cucumber Plants (<i>Cucumis sativus</i>). Plant Physiology, 2016, 172, 603-618.	4.8	99
63	SHORT HYPOCOTYL 1 Encodes a SMARCA3-like Chromatin Remodeling Factor Regulating Elongation. Plant Physiology, 2016, 172, pp.00501.2016.	4.8	22
64	How the truffle got its mate: insights from genetic structure in spontaneous and planted Mediterranean populations of <i>Tuber melanosporum</i> . Molecular Ecology, 2016, 25, 5611-5627.	3.9	44
65	Genetic analysis and fine mapping of Watermelon mosaic virus resistance gene in cucumber. Molecular Breeding, 2016, 36, 1.	2.1	21
66	CsSNP: A Web-Based Tool for the Detecting of Comparative Segments SNPs. Journal of Computational Biology, 2016, 23, 597-602.	1.6	0
67	Rapid identification of fruit length loci in cucumber (Cucumis sativus L.) using next-generation sequencing (NGS)-based QTL analysis. Scientific Reports, 2016, 6, 27496.	3.3	63
68	Global investigation of the coâ€evolution of <i><scp>MIRNA</scp></i> genes and micro <scp>RNA</scp> targets during soybean domestication. Plant Journal, 2016, 85, 396-409.	5.7	36
69	Breeding for plant heat tolerance at vegetative and reproductive stages. Plant Reproduction, 2016, 29, 67-79.	2.2	175
70	Evaluation of genetic variation among Brazilian soybean cultivars through genome resequencing. BMC Genomics, 2016, 17, 110.	2.8	43
71	Genomics-based strategies for the use of natural variation in the improvement of crop metabolism. Plant Science, 2016, 242, 47-64.	3.6	60
72	A proposed regulatory framework for genome-edited crops. Nature Genetics, 2016, 48, 109-111.	21.4	184
73	Phloem transcriptome signatures underpin the physiological differentiation of the pedicel, stalk and fruit of cucumber (<i>Cucumis sativus</i> L.). Plant and Cell Physiology, 2016, 57, 19-34.	3.1	27

#	Article	IF	CITATIONS
74	A fragment substitution in the promoter of CsHDZIV11/CsGL3 is responsible for fruit spine density in cucumber (Cucumis sativus L.). Theoretical and Applied Genetics, 2016, 129, 1289-1301.	3.6	35
75	A Truncated F-Box Protein Confers the Dwarfism in Cucumber. Journal of Genetics and Genomics, 2016, 43, 223-226.	3.9	27
76	Integrated analysis in bi-parental and natural populations reveals CsCLAVATA3 (CsCLV3) underlying carpel number variations in cucumber. Theoretical and Applied Genetics, 2016, 129, 1007-1022.	3.6	43
77	Map-based cloning, identification and characterization of the w gene controlling white immature fruit color in cucumber (Cucumis sativus L.). Theoretical and Applied Genetics, 2016, 129, 1247-1256.	3.6	87
78	Databases for Solanaceae and Cucurbitaceae Research. Biotechnology in Agriculture and Forestry, 2016, , 31-42.	0.2	1
79	DNA Markers in Cucurbitaceae Breeding. Biotechnology in Agriculture and Forestry, 2016, , 59-74.	0.2	1
80	The complete chloroplast genome sequence of <i>Cucumis sativus</i> var. <i>Hardwickii</i> , the wild progenitor of cultivated cucumber. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 4627-4628.	0.7	8
81	The complete chloroplast genome sequence of wild cucumber (<i>Cucumis sativus</i> var.) Tj ETQq1 1 0.784314 4524-4525.	rgBT /Ove 0.7	rlock 10 Tf 3
82	Next generation sequencing and omics in cucumber (Cucumis sativus L.) breeding directed research. Plant Science, 2016, 242, 77-88.	3.6	35
83	Genomics of crop wild relatives: expanding the gene pool for crop improvement. Plant Biotechnology Journal, 2016, 14, 1070-1085.	8.3	303
84	Genomic analyses of primitive, wild and cultivated citrus provide insights into asexual reproduction. Nature Genetics, 2017, 49, 765-772.	21.4	316
85	Domestication rewired gene expression and nucleotide diversity patterns in tomato. Plant Journal, 2017, 91, 631-645.	5.7	34
86	The association of changes in DNA methylation with temperature-dependent sex determination in cucumber. Journal of Experimental Botany, 2017, 68, 2899-2912.	4.8	53
87	Variation in cucumber (Cucumis sativus L.) fruit size and shape results from multiple components acting pre-anthesis and post-pollination. Planta, 2017, 246, 641-658.	3.2	53
88	Transcriptomic analysis of short-fruit 1 (sf1) reveals new insights into the variation of fruit-related traits in Cucumis sativus. Scientific Reports, 2017, 7, 2950.	3.3	26
89	QTL mapping of domestication and diversifying selection related traits in round-fruited semi-wild Xishuangbanna cucumber (Cucumis sativus L. var. xishuangbannanesis). Theoretical and Applied Genetics, 2017, 130, 1531-1548.	3.6	60
90	Quantitative trait loci analysis of melon (Cucumis melo L.) domestication-related traits. Theoretical and Applied Genetics, 2017, 130, 1837-1856.	3.6	37
91	Genome-wide sequence variations between wild and cultivated tomato species revisited by whole genome sequence mapping. BMC Genomics, 2017, 18, 430.	2.8	24

#	Article	IF	CITATIONS
92	Transcriptomic and metabolomic analyses of cucumber fruit peels reveal a developmental increase in terpenoid glycosides associated with age-related resistance to Phytophthora capsici. Horticulture Research, 2017, 4, 17022.	6.3	54
93	Footprints of domestication revealed by RAD-tag resequencing in loquat: SNP data reveals a non-significant domestication bottleneck and a single domestication event. BMC Genomics, 2017, 18, 354.	2.8	13
94	Comparative Genomics of the Cucurbitaceae. Plant Genetics and Genomics: Crops and Models, 2017, , 229-240.	0.3	3
95	Genome diversity of tuber-bearing <i>Solanum</i> uncovers complex evolutionary history and targets of domestication in the cultivated potato. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E9999-E10008.	7.1	271
96	Genetics and Genomics of Cucurbitaceae. Plant Genetics and Genomics: Crops and Models, 2017, , .	0.3	22
97	A high-density linkage map and QTL mapping of fruit-related traits in pumpkin (Cucurbita moschata) Tj ETQq1 1 ().784314 ı 3.3	gßŢ /Overlo
98	The Genetics and Genomics of Plant Domestication. BioScience, 2017, 67, 971-982.	4.9	83
99	A genome-wide survey with different rapeseed ecotypes uncovers footprints of domestication and breeding. Journal of Experimental Botany, 2017, 68, 4791-4801.	4.8	52
100	Catastrophic Unbalanced Genome Rearrangements Cause Somatic Loss of Berry Color in Grapevine. Plant Physiology, 2017, 175, 786-801.	4.8	98
101	Variability among Cucurbitaceae species (melon, cucumber and watermelon) in a genomic region containing a cluster of NBS-LRR genes. BMC Genomics, 2017, 18, 138.	2.8	16
102	Genome-wide analysis of microRNA targeting impacted by SNPs in cucumber genome. BMC Genomics, 2017, 18, 275.	2.8	12
103	Functional characterization of cucumber (Cucumis sativus L.) Clade V MLO genes. BMC Plant Biology, 2017, 17, 80.	3.6	29
104	RNA sequencing provides insights into the evolution of lettuce and the regulation of flavonoid biosynthesis. Nature Communications, 2017, 8, 2264.	12.8	133
105	World Agriculture and Impact ofÂBiotechnology. , 2017, , 1-22.		1
107	Combined fine mapping, genetic diversity, and transcriptome profiling reveals that the auxin transporter gene ns plays an important role in cucumber fruit spine development. Theoretical and Applied Genetics, 2018, 131, 1239-1252.	3.6	33
108	Genome-wide association study identified genetic variations and candidate genes for plant architecture component traits in Chinese upland cotton. Theoretical and Applied Genetics, 2018, 131, 1299-1314.	3.6	62
109	Multiple R genes and phenolic compounds synthesis involved in the durable resistance to Phytophthora infestans in potato cv. Cooperation 88. Agri Gene, 2018, 8, 28-36.	1.9	6
110	Long distance <scp>RNA</scp> movement. New Phytologist, 2018, 218, 29-40.	7.3	137

#	Article	IF	CITATIONS
111	Genetic mapping reveals a candidate gene (CIFS1) for fruit shape in watermelon (Citrullus lanatus L.). Theoretical and Applied Genetics, 2018, 131, 947-958.	3.6	94
112	Development of Bi gene-based SNP markers for genotyping for bitter-free cucumber lines. Horticulture Environment and Biotechnology, 2018, 59, 231-238.	2.1	4
113	Development of cost-effective single nucleotide polymorphism marker assays for genetic diversity analysis in Brassica rapa. Molecular Breeding, 2018, 38, 1.	2.1	21
114	Exploiting natural variation for accelerating discoveries in plant specialized metabolism. Phytochemistry Reviews, 2018, 17, 17-36.	6.5	9
115	Transcriptome Comparison Reveals Distinct Selection Patterns in Domesticated and Wild Agave Species, the Important CAM Plants. International Journal of Genomics, 2018, 2018, 1-12.	1.6	29
116	Temperature and photoperiod changes affect cucumber sex expression by different epigenetic regulations. BMC Plant Biology, 2018, 18, 268.	3.6	35
117	Genome re-sequencing reveals the evolutionary history of peach fruit edibility. Nature Communications, 2018, 9, 5404.	12.8	84
118	Genetic mapping of psl locus and quantitative trait loci for angular leaf spot resistance in cucumber (Cucumis sativus L.). Molecular Breeding, 2018, 38, 111.	2.1	13
119	Genetic analysis and identification of a candidate gene associated with in vitro regeneration ability of cucumber. Theoretical and Applied Genetics, 2018, 131, 2663-2675.	3.6	11
120	Genetic mapping reveals a marker for yellow skin in watermelon (Citrullus lanatus L.). PLoS ONE, 2018, 13, e0200617.	2.5	47
121	Construction of A High-Density Genetic Map and Mapping of Fruit Traits in Watermelon (Citrullus) Tj ETQq0 0 0 1 19, 3268.	gBT /Over 4.1	lock 10 Tf 50 43
122	The USDA cucumber (Cucumis sativus L.) collection: genetic diversity, population structure, genome-wide association studies, and core collection development. Horticulture Research, 2018, 5, 64.	6.3	102
123	Carotenoid Accumulation and Its Contribution to Flower Coloration of Osmanthus fragrans. Frontiers in Plant Science, 2018, 9, 1499.	3.6	43
124	Unraveling the Roles of Regulatory Genes during Domestication of Cultivated Camellia: Evidence and Insights from Comparative and Evolutionary Genomics. Genes, 2018, 9, 488.	2.4	11
125	DNA methylation footprints during soybean domestication and improvement. Genome Biology, 2018, 19, 128.	8.8	61
126	Underutilised and Neglected Crops: Next Generation Sequencing Approaches for Crop Improvement and Better Food Security. , 2018, , 287-380.		3
127	The evolutionary road from wild moth to domestic silkworm. Nature Ecology and Evolution, 2018, 2, 1268-1279.	7.8	112
128	Signatures of Selection in the Genomes of Chinese Chestnut (Castanea mollissima Blume): The Roots of Nut Tree Domestication. Frontiers in Plant Science, 2018, 9, 810.	3.6	18

#	Article	IF	CITATIONS
129	Efficient identification of NLR by using a genome-wide protein domain and motif survey program, Ex-DOMAIN. Plant Biotechnology, 2018, 35, 177-180.	1.0	1
130	Genome-Wide Identification and Expression Analyses of the Fibrillin Family Genes Suggest Their Involvement in Photoprotection in Cucumber. Plants, 2018, 7, 50.	3.5	6
131	Genome of Wild Mandarin and Domestication History of Mandarin. Molecular Plant, 2018, 11, 1024-1037.	8.3	130
132	Genetic analysis and QTL mapping of fruit-related traits in wax gourd (Benincasa hispida). Euphytica, 2018, 214, 1.	1.2	13
133	Resequencing of 243 diploid cotton accessions based on an updated A genome identifies the genetic basis of key agronomic traits. Nature Genetics, 2018, 50, 796-802.	21.4	401
134	Genomics of Cucurbits. , 2018, , 413-432.		5
135	Using Genomic Data to Infer Historic Population Dynamics of Nonmodel Organisms. Annual Review of Ecology, Evolution, and Systematics, 2018, 49, 433-456.	8.3	143
136	<i>LITTLELEAF</i> (<i>LL</i>) encodes a WD40 repeat domainâ€containing protein associated with organ size variation in cucumber. Plant Journal, 2018, 95, 834-847.	5.7	58
137	The Evolutionary Consequences of Transposon-Related Pericentromer Expansion in Melon. Genome Biology and Evolution, 2018, 10, 1584-1595.	2.5	20
138	Identification of <scp>QTL</scp> s controlling lowâ€ŧemperature tolerance during the germination stage in cucumber (<i>Cucumis sativus</i> L.). Plant Breeding, 2018, 137, 629-637.	1.9	16
139	STAYGREEN, STAY HEALTHY: a lossâ€ofâ€susceptibility mutation in the <i>STAYGREEN</i> gene provides durable, broadâ€spectrum disease resistances for over 50Âyears of US cucumber production. New Phytologist, 2019, 221, 415-430.	7.3	72
140	CsBRC1 inhibits axillary bud outgrowth by directly repressing the auxin efflux carrier <i>CsPIN3</i> in cucumber. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17105-17114.	7.1	91
141	Genome-wide association analysis of nutrient traits in the oyster Crassostrea gigas: genetic effect and interaction network. BMC Genomics, 2019, 20, 625.	2.8	31
142	Genome Resequencing Reveals Congenital Causes of Embryo and Nestling Death in Crested Ibis (Nipponia nippon). Genome Biology and Evolution, 2019, 11, 2125-2135.	2.5	4
143	Combination of multi-locus genome-wide association study and QTL mapping reveals genetic basis of tassel architecture in maize. Molecular Genetics and Genomics, 2019, 294, 1421-1440.	2.1	12
144	Two types of mutations in the HEUKCHEEM gene functioning in cucumber spine color development can be used as signatures for cucumber domestication. Planta, 2019, 250, 1491-1504.	3.2	7
145	Genetic Diversity in Horticultural Plants. Sustainable Development and Biodiversity, 2019, , .	1.7	2
147	A comprehensive genome variation map of melon identifies multiple domestication events and loci influencing agronomic traits. Nature Genetics, 2019, 51, 1607-1615.	21.4	153

#	Article	IF	CITATIONS
148	The wax gourd genomes offer insights into the genetic diversity and ancestral cucurbit karyotype. Nature Communications, 2019, 10, 5158.	12.8	94
149	Natural Variation and Domestication Selection of ZmPGP1 Affects Plant Architecture and Yield-Related Traits in Maize. Genes, 2019, 10, 664.	2.4	21
150	Whole-Genome Resequencing of Seven Eggplant (Solanum melongena) and One Wild Relative (S.) Tj ETQq0 0 0 in Plant Science, 2019, 10, 1220.	rgBT /Ove 3.6	rlock 10 Tf 5 46
151	The bracteatus pineapple genome and domestication of clonally propagated crops. Nature Genetics, 2019, 51, 1549-1558.	21.4	60
152	A chromosome-scale genome assembly of cucumber (Cucumis sativus L.). GigaScience, 2019, 8, .	6.4	138
153	Re-evaluation of the role of Indian germplasm as center of melon diversification based on genotyping-by-sequencing analysis. BMC Genomics, 2019, 20, 448.	2.8	35
154	QTL mapping and genome-wide association study reveal two novel loci associated with green flesh color in cucumber. BMC Plant Biology, 2019, 19, 243.	3.6	35
155	The Eggplant Genome. Compendium of Plant Genomes, 2019, , .	0.5	8
156	Resequencing. Compendium of Plant Genomes, 2019, , 81-89.	0.5	1
157	Orange-fleshed cucumber (Cucumis sativus var. sativus L.) germplasm from North-East India: agro-morphological, biochemical and evolutionary studies. Genetic Resources and Crop Evolution, 2019, 66, 1217-1230.	1.6	7
158	Comparative Transcriptome Analysis in Eggplant Reveals Selection Trends during Eggplant Domestication. International Journal of Genomics, 2019, 2019, 1-12.	1.6	5
159	Target SSR-Seq: A Novel SSR Genotyping Technology Associate With Perfect SSRs in Genetic Analysis of Cucumber Varieties. Frontiers in Plant Science, 2019, 10, 531.	3.6	37
160	Microbial Profile and Genetic Polymorphism of Predominant Species in Some Traditional Fermented Seafoods of the Hainan Area in China. Frontiers in Microbiology, 2019, 10, 564.	3.5	14
161	Silencing of glycerol-3-phosphate acyltransferase 6 (CPAT6) gene using a newly established virus induced gene silencing (VIGS) system in cucumber alleviates autotoxicity mimicked by cinnamic acid (CA). Plant and Soil, 2019, 438, 329-346.	3.7	20
162	Tea Plant Information Archive: a comprehensive genomics and bioinformatics platform for tea plant. Plant Biotechnology Journal, 2019, 17, 1938-1953.	8.3	220
163	Genetic Regulation of Ethylene Dosage for Cucumber Fruit Elongation. Plant Cell, 2019, 31, 1063-1076.	6.6	85
164	A Functional Allele of <i>CsFUL1</i> Regulates Fruit Length through Repressing <i>CsSUP</i> and Inhibiting Auxin Transport in Cucumber. Plant Cell, 2019, 31, 1289-1307.	6.6	84
165	Comparative population genomics identified genomic regions and candidate genes associated with fruit domestication traits in peach. Plant Biotechnology Journal, 2019, 17, 1954-1970.	8.3	52

#	Article	IF	CITATIONS
166	Genomic analyses of an extensive collection of wild and cultivated accessions provide new insights into peach breeding history. Genome Biology, 2019, 20, 36.	8.8	120
167	Quantitative Trait Loci Mapping and Candidate Gene Analysis of Low Temperature Tolerance in Cucumber Seedlings. Frontiers in Plant Science, 2019, 10, 1620.	3.6	19
168	Linkage mapping of quantitative trait loci for fiber yield and its related traits in the population derived from cultivated ramie and wild B. nivea var. tenacissima. Scientific Reports, 2019, 9, 16855.	3.3	10
169	QTL and Transcriptomic Analyses Implicate Cuticle Transcription Factor SHINE as a Source of Natural Variation for Epidermal Traits in Cucumber Fruit. Frontiers in Plant Science, 2019, 10, 1536.	3.6	12
170	Selection footprints reflect genomic changes associated with breeding efforts in 56 cucumber inbred lines. Horticulture Research, 2019, 6, 127.	6.3	9
171	Resequencing of <i>cv</i> CRIâ€12 family reveals haplotype block inheritance and recombination of agronomically important genes in artificial selection. Plant Biotechnology Journal, 2019, 17, 945-955.	8.3	20
172	Translational genomics and multi-omics integrated approaches as a useful strategy for crop breeding. Genes and Genomics, 2019, 41, 133-146.	1.4	34
173	Transcriptomics profiling in response to cold stress in cultivated rice and weedy rice. Gene, 2019, 685, 96-105.	2.2	57
174	Cucurbit Genomics Database (CuGenDB): a central portal for comparative and functional genomics of cucurbit crops. Nucleic Acids Research, 2019, 47, D1128-D1136.	14.5	177
175	Novel loci fsd6.1 and Csgl3 regulate ultra-high fruit spine density in cucumber. Theoretical and Applied Genetics, 2019, 132, 27-40.	3.6	23
176	Molecular basis of cucumber fruit domestication. Current Opinion in Plant Biology, 2019, 47, 38-46.	7.1	96
177	<i>CsMYB60</i> is a key regulator of flavonols and proanthocyanidans that determine the colour of fruit spines in cucumber. Journal of Experimental Botany, 2019, 70, 69-84.	4.8	40
178	Origin and domestication of Cucurbitaceae crops: insights from phylogenies, genomics and archaeology. New Phytologist, 2020, 226, 1240-1255.	7.3	134
179	A high-quality cucumber genome assembly enhances computational comparative genomics. Molecular Genetics and Genomics, 2020, 295, 177-193.	2.1	30
180	Quantitative trait loci for fruit size and flowering timeâ€related traits under domestication and diversifying selection in cucumber (<i>Cucumis sativus</i>). Plant Breeding, 2020, 139, 176-191.	1.9	26
181	Genome-wide Target Mapping Shows Histone Deacetylase Complex1 Regulates Cell Proliferation in Cucumber Fruit. Plant Physiology, 2020, 182, 167-184.	4.8	47
182	Genome-based breeding approaches in major vegetable crops. Theoretical and Applied Genetics, 2020, 133, 1739-1752.	3.6	21
183	Molecular Mapping and Candidate Gene Analysis for GA3 Responsive Short Internode in Watermelon (Citrullus lanatus). International Journal of Molecular Sciences, 2020, 21, 290.	4.1	29

#	ARTICLE	IF	CITATIONS
184	The majorâ€effect quantitative trait locus Fnl7.1 encodes a late embryogenesis abundant protein associated with fruit neck length in cucumber. Plant Biotechnology Journal, 2020, 18, 1598-1609.	8.3	14
185	<i>FLOWERING LOCUS T</i> Improves Cucumber Adaptation to Higher Latitudes. Plant Physiology, 2020, 182, 908-918.	4.8	30
186	Super-Pangenome by Integrating the Wild Side of a Species for Accelerated Crop Improvement. Trends in Plant Science, 2020, 25, 148-158.	8.8	177
187	Favorable haplotypes and associated genes for flowering time and photoperiod sensitivity identified by comparative selective signature analysis and GWAS in temperate and tropical maize. Crop Journal, 2020, 8, 227-242.	5.2	6
188	Recent progress on the molecular breeding of Cucumis sativus L. in China. Theoretical and Applied Genetics, 2020, 133, 1777-1790.	3.6	25
189	Genetic architecture of fruit size and shape variation in cucurbits: a comparative perspective. Theoretical and Applied Genetics, 2020, 133, 1-21.	3.6	111
190	Molecularly tagged genes and quantitative trait loci in cucumber with recommendations for QTL nomenclature. Horticulture Research, 2020, 7, 3.	6.3	73
191	Insights on SNP types, detection methods and their utilization in Brassica species: Recent progress and future perspectives. Journal of Biotechnology, 2020, 324, 11-20.	3.8	8
192	Genomic, Transcriptomic and Epigenomic Tools to Study the Domestication of Plants and Animals: A Field Guide for Beginners. Frontiers in Genetics, 2020, 11, 742.	2.3	21
193	Genome-wide analysis revisits incipient sympatric and allopatric speciation in a beetle. Israel Journal of Ecology and Evolution, 2020, 67, 69-80.	0.6	3
194	Assessment of the Genetic Diversity of the Breeding Lines and a Genome Wide Association Study of Three Horticultural Traits Using Worldwide Cucumber (Cucumis spp.) Germplasm Collection. Agronomy, 2020, 10, 1736.	3.0	14
195	Analysis of QTL DM4.1 for Downy Mildew Resistance in Cucumber Reveals Multiple subQTL: A Novel RLK as Candidate Gene for the Most Important subQTL. Frontiers in Plant Science, 2020, 11, 569876.	3.6	14
196	The genome and transcriptome analysis of snake gourd provide insights into its evolution and fruit development and ripening. Horticulture Research, 2020, 7, 199.	6.3	22
197	Advances in Genomic, Transcriptomic, and Metabolomic Analyses of Fruit Quality in Fruit Crops. Horticultural Plant Journal, 2020, 6, 361-371.	5.0	33
198	High concentrations of CPPU promotes cucurbitacin B accumulation in melon (Cucumis melo var.) Tj ETQq0 0 0 0 2020, 154, 770-781.	rgBT /Ove 5.8	rlock 10 Tf 50 20
199	Development of alien addition lines from Cucumis hystrix in Cucumis sativus: cytological and molecular marker analyses. Genome, 2020, 63, 629-641.	2.0	1
200	Dynamic Changes of Fruit Shape Traits and Its Correlation to the Morphology of Other Organs in Cucumber. Agronomy, 2020, 10, 1111.	3.0	2
201	Comparative genomics of muskmelon reveals a potential role for retrotransposons in the modification of gene expression. Communications Biology, 2020, 3, 432.	4.4	29

#	Article	IF	CITATIONS
202	Heat tolerance in vegetables in the current genomic era: an overview. Plant Growth Regulation, 2020, 92, 497-516.	3.4	16
203	Identification of Novel Loci and Candidate Genes for Cucumber Downy Mildew Resistance Using GWAS. Plants, 2020, 9, 1659.	3.5	16
204	Evaluation of morpho-agronomic characterization Apple cucumber: a new variety of melon from Indonesia. IOP Conference Series: Earth and Environmental Science, 2020, 457, 012061.	0.3	2
205	QTL Mapping for Cucumber Fruit Size and Shape with Populations from Long and Round Fruited Inbred Lines. Horticultural Plant Journal, 2020, 6, 132-144.	5.0	20
206	Plant Genome Editing and the Relevance of Off-Target Changes. Plant Physiology, 2020, 183, 1453-1471.	4.8	68
207	Whole-genome sequencing provides insights into the genetic diversity and domestication of bitter gourd (Momordica spp.). Horticulture Research, 2020, 7, 85.	6.3	41
208	Identification of SCAR markers linked to the Foc gene governing resistance to Fusarium oxysporum f. sp. cucumerinum in cucumber cv. SMR-18. European Journal of Plant Pathology, 2020, 157, 845-855.	1.7	4
209	Resequencing of 297 melon accessions reveals the genomic history of improvement and loci related to fruit traits in melon. Plant Biotechnology Journal, 2020, 18, 2545-2558.	8.3	51
210	Genomic Insight into Differentiation and Selection Sweeps in the Improvement of Upland Cotton. Plants, 2020, 9, 711.	3.5	18
211	Recommendations for Choosing the Genotyping Method and Best Practices for Quality Control in Crop Genome-Wide Association Studies. Frontiers in Genetics, 2020, 11, 447.	2.3	48
212	Gynoecy instability in cucumber (Cucumis sativus L.) is due to unequal crossover at the copy number variation-dependent Femaleness (F) locus. Horticulture Research, 2020, 7, 32.	6.3	25
213	Comprehensive Characterization of Fruit Volatiles and Nutritional Quality of Three Cucumber (Cucumis sativus L.) Genotypes from Different Geographic Groups after Bagging Treatment. Foods, 2020, 9, 294.	4.3	14
214	Construction of a High-Density Genetic Map and Analysis of Seed-Related Traits Using Specific Length Amplified Fragment Sequencing for Cucurbita maxima. Frontiers in Plant Science, 2019, 10, 1782.	3.6	22
215	CsIVP functions in vasculature development and downy mildew resistance in cucumber. PLoS Biology, 2020, 18, e3000671.	5.6	30
216	Cucumber Fruit Size and Shape Variations Explored from the Aspects of Morphology, Histology, and Endogenous Hormones. Plants, 2020, 9, 772.	3.5	30
217	Genetic architecture, demographic history, and genomic differentiation of <i>Populus davidiana</i> revealed by wholeâ€genome resequencing. Evolutionary Applications, 2020, 13, 2582-2596.	3.1	10
218	Localization of quantitative trait loci for cucumber fruit shape by a population of chromosome segment substitution lines. Scientific Reports, 2020, 10, 11030.	3.3	11
219	Genetic mapping and localization of major QTL for bitterness in melon (Cucumis melo L.). Scientia Horticulturae, 2020, 266, 109286.	3.6	10

#	Article	IF	CITATIONS
220	Comparative population genomics reveals genetic divergence and selection in lotus, Nelumbo nucifera. BMC Genomics, 2020, 21, 146.	2.8	13
221	A mutation in CsHD encoding a histidine and aspartic acid domain-containing protein leads to yellow young leaf-1 (yyl-1) in cucumber (Cucumis sativus L.). Plant Science, 2020, 293, 110407.	3.6	14
223	VECA: visual comparison of phylogenetic trees for evolutionary genome analysis (ChinaVis 2019). Journal of Visualization, 2020, 23, 523-537.	1.8	1
224	A new SNP genotyping technology Target SNP-seq and its application in genetic analysis of cucumber varieties. Scientific Reports, 2020, 10, 5623.	3.3	64
225	Transcriptional and metabolite analysis reveal a shift in direct and indirect defences in response to spider-mite infestation in cucumber (Cucumis sativus). Plant Molecular Biology, 2020, 103, 489-505.	3.9	26
226	Comparative Transcriptomic Analysis of Two Bottle Gourd Accessions Differing in Fruit Size. Genes, 2020, 11, 359.	2.4	16
227	Genomic analyses reveal the genetic basis of early maturity and identification of loci and candidate genes in upland cotton (<i>Gossypium hirsutum</i> L.). Plant Biotechnology Journal, 2021, 19, 109-123.	8.3	42
228	Quantitative trait loci for horticulturally important traits defining the Sikkim cucumber, Cucumis sativus var. sikkimensis. Theoretical and Applied Genetics, 2021, 134, 229-247.	3.6	19
229	QTL-seq analysis of powdery mildew resistance in a Korean cucumber inbred line. Theoretical and Applied Genetics, 2021, 134, 435-451.	3.6	31
231	Genome- and transcriptome-wide association studies provide insights into the genetic basis of natural variation of seed oil content in Brassica napus. Molecular Plant, 2021, 14, 470-487.	8.3	107
232	Genomic analyses of diverse wild and cultivated accessions provide insights into the evolutionary history of jujube. Plant Biotechnology Journal, 2021, 19, 517-531.	8.3	41
233	Genotypic Selection in Vegetables for Adaptation to Climate Change. Advances in Olericulture, 2021, , 61-89.	0.4	2
234	Wholeâ€Genome Sequence of Synthesized Allopolyploids in <i>Cucumis</i> Reveals Insights into the Genome Evolution of Allopolyploidization. Advanced Science, 2021, 8, 2004222.	11.2	24
235	QTL Mapping of Heat Tolerance in Cucumber (Cucumis sativus L.) at Adult Stage. Plants, 2021, 10, 324.	3.5	15
237	Genetic Diversity Assessment and Cultivar Identification of Cucumber (Cucumis sativus L.) Using the Fluidigm Single Nucleotide Polymorphism Assay. Plants, 2021, 10, 395.	3.5	9
238	A high-quality genome assembly highlights rye genomic characteristics and agronomically important genes. Nature Genetics, 2021, 53, 574-584.	21.4	164
239	Development and validation of genome-wide InDel markers with high levels of polymorphism in bitter gourd (Momordica charantia). BMC Genomics, 2021, 22, 190.	2.8	8
240	Loquat (Eriobotrya japonica (Thunb.) Lindl) population genomics suggests a twoâ€staged domestication and identifies genes showing convergence/parallel selective sweeps with apple or peach. Plant Journal, 2021, 106, 942-952.	5.7	2

#	Article	IF	CITATIONS
241	A positive feedback loop mediated by <i>CsERF31</i> initiates female cucumber flower development. Plant Physiology, 2021, 186, 1088-1100.	4.8	11
242	Chromosome-scale genome assembly of <i>Cucumis hystrix</i> —a wild species interspecifically cross-compatible with cultivated cucumber. Horticulture Research, 2021, 8, 40.	6.3	18
243	Identification of Novel Loci and Candidate Genes for Resistance to Powdery Mildew in a Resequenced Cucumber Germplasm. Genes, 2021, 12, 584.	2.4	15
244	Genomic insights into the origin, domestication and genetic basis of agronomic traits of castor bean. Genome Biology, 2021, 22, 113.	8.8	32
245	Whole-genome resequencing of 445 Lactuca accessions reveals the domestication history of cultivated lettuce. Nature Genetics, 2021, 53, 752-760.	21.4	64
246	Highâ€quality chromosomeâ€level genomes of <i>Cucumis metuliferus</i> and <i>Cucumis melo</i> provide insight into <i>Cucumis</i> genome evolution. Plant Journal, 2021, 107, 136-148.	5.7	20
247	Introductory Chapter: Studies on Cucumber. , 0, , .		1
248	The amino acid permease (<i>AAP</i>) genes <i>CsAAP2A</i> and <i>SIAAP5A</i> /i>/ <i>B</i> are required for oomycete susceptibility in cucumber and tomato. Molecular Plant Pathology, 2021, 22, 658-672.	4.2	10
249	A chromosome-level genome of a Kordofan melon illuminates the origin of domesticated watermelons. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	37
250	Genetic divergence in transcriptional regulators of defense metabolism: insight into plant domestication and improvement. Plant Molecular Biology, 2022, 109, 401-411.	3.9	7
251	Genomic insight into the divergence and adaptive potential of a forgotten landrace G.Âhirsutum L. purpurascens. Journal of Genetics and Genomics, 2021, 48, 473-484.	3.9	19
252	A domestication-associated gene, CsLH, encodes a phytochrome B protein that regulates hypocotyl elongation in cucumber. Molecular Horticulture, 2021, 1, .	5.8	6
253	A mutation in CsHY2 encoding a phytochromobilin (PΦB) synthase leads to an elongated hypocotyl 1(elh1) phenotype in cucumber (Cucumis sativus L.). Theoretical and Applied Genetics, 2021, 134, 2639-2652.	3.6	8
254	Analysis of genome variants in dwarf soybean lines obtained in F6 derived from cross of normal parents (cultivated and wild soybean). Genomics and Informatics, 2021, 19, e19.	0.8	2
255	Molecular research progress and improvement approach of fruit quality traits in cucumber. Theoretical and Applied Genetics, 2021, 134, 3535-3552.	3.6	18
256	Development of genome-wide single nucleotide polymorphism markers for variety identificationÂof F1 hybrids in cucumber (Cucumis sativus L.). Scientia Horticulturae, 2021, 285, 110173.	3.6	4
257	Genetic regulation of shoot architecture in cucumber. Horticulture Research, 2021, 8, 143.	6.3	20
258	Using Cucumis sativus, Acalymma vittatum, Celatoria setosa, and generalist pollinators as a case study for plant–insect interactions. Arthropod-Plant Interactions, 2021, 15, 637-644.	1.1	0

	Сіт	CITATION REPORT		
#	Article		IF	CITATIONS
259	Genomic variation within the maize stiffâ€stalk heterotic germplasm pool. Plant Genome, 2021, 14, e2	20114.	2.8	14
260	Genomics and Marker-Assisted Improvement of Vegetable Crops. Critical Reviews in Plant Sciences, 2021, 40, 303-365.		5.7	33
261	An integrated transcriptome and metabolome approach reveals the accumulation of taste-related metabolites and gene regulatory networks during watermelon fruit development. Planta, 2021, 254, 3	5.	3.2	17
262	Recent advances in cucumber (<i>Cucumis sativus</i> L.). Journal of Horticultural Science and Biotechnology, 2022, 97, 3-23.		1.9	6
263	Progress on Genetic Improvement and Analysis of Bottle Gourd [Lagenaria siceraria (Molina) Standl.] for Agronomic Traits, Nutrient Compositions, and Stress Tolerance: A Review. Frontiers in Sustainable Food Systems, 2021, 5, .		3.9	9
264	Genetic Resources and Vulnerabilities of Major Cucurbit Crops. Genes, 2021, 12, 1222.		2.4	36
265	Genomic Prediction and the Practical Breeding of 12 Quantitative-Inherited Traits in Cucumber (Cucumis sativus L.). Frontiers in Plant Science, 2021, 12, 729328.		3.6	2
267	Genome-level diversification of eight ancient tea populations in the Guizhou and Yunnan regions identifies candidate genes for core agronomic traits. Horticulture Research, 2021, 8, 190.		6.3	24
268	The branchless gene Clbl in watermelon encoding a TERMINAL FLOWER 1 protein regulates the numbe of lateral branches. Theoretical and Applied Genetics, 2022, 135, 65-79.	r	3.6	11
269	Genetic relationships among Cucurbita pepo ornamental gourds based on EST-SSR markers. Czech Journal of Genetics and Plant Breeding, 2021, 57, 125-139.		0.8	1
270	The Formation of Fruit Quality in Cucumis sativus L Frontiers in Plant Science, 2021, 12, 729448.		3.6	10
271	Translational Genomics of Cucurbit Oil Seeds. , 2021, , 89-111.			0
272	Resurgence of Cucurbit Downy Mildew in the United States: A Watershed Event for Research and Extension. Plant Disease, 2015, 4015, 1-14.		1.4	1
275	A review of the safety and clinical utility of contrast echocardiography. Singapore Medical Journal, 2020, 61, 181-183.		0.6	5
276	Whole-genome resequencing: Current status and future prospects in genomics-assisted crop improvement. , 2016, , 187-211.			2
277	Ultrahigh-Density Linkage Map for Cultivated Cucumber (Cucumis sativus L.) Using a Single-Nucleotide Polymorphism Genotyping Array. PLoS ONE, 2015, 10, e0124101.	2	2.5	29
278	The CucCAP project: leveraging applied genomics to improve disease resistance in cucurbit crops. Acta Horticulturae, 2020, , 91-104.		0.2	5
279	Stability determination of candidate reference genes in cucumber plants subjected to stresses from Phytophthora melonis. Journal of Plant Science and Phytopathology, 2019, 3, 028-035.		0.6	3

ARTICLE IF CITATIONS Notulae to the Italian alien vascular flora: 9. Italian Botanist, 0, 9, 71-86. 280 0.0 11 A valid name for the Xishuangbanna gourd, a cucumber with carotene-rich fruits. PhytoKeys, 2017, 85, 1.0 9 87-94. Molecular characterization of the cucumber (Cucumis sativus L.) accessions held at the COMAV's 282 0.6 3 genebank. Spanish Journal of Agricultural Research, 2018, 16, e0701. Genome-Wide Identification and Classification of the AP2/EREBP Gene Family in the Cucurbitaceae 0.9 Species. Plant Breeding and Biotechnology, 2017, 5, 123-133. Genome-Wide Identification of the Dehydrin Genes in the Cucurbitaceae Species. Plant Breeding and 284 0.9 10 Biotechnology, 2017, 5, 282-292. Large-scale detection and application of expressed sequence tag single nucleotide polymorphisms in Nicotiana. Genetics and Molecular Research, 2015, 14, 7793-7800. 0.2 Phenotypic Diversity of Photosynthetic Characteristics in 16 Cucumber Accessions Selected from the 286 0 Core Collection. , 2016, , . Genetic analysis of molecular markers for propamocarb residue in Cucumis sativus using quantitative 0.2 trait locus mapping. Genetics and Molecular Research, 2016, 15, . Sexual Recombination and Selection During Domestication of Clonally Propagated Pineapple. SSRN 288 0.4 1 Electronic Journal, O, , . Genetic Diversity in Vegetable and FruitÂCrops. Sustainable Development and Biodiversity, 2019, , 87-125. 1.7 Accelerated Breeding in Cucumber Using Genomic Approaches., 2020, , 271-299. 291 2 Fine-mapping reveals that the bHLH gene Cla011508 regulates the bitterness of watermelon fruit. 3.6 Scientia Horticulturae, 2022, 292, 110626. Heterosis prediction system based on non-additive genomic prediction models in cucumber (Cucumis) Tj ETQq0 0 Q rgBT /Ovgrlock 10 T 293 Genetic and Genomic Resources and Their Exploitation for Unlocking Genetic Potential from the Wild 294 Relatives., 2020, , 193-210. Genetic resources from north eastern region of India and their role in improvement of vegetable 295 0.2 0 crops. International Journal of Innovative Horticulture, 2020, 9, 26. Plant-ImputeDB: an integrated multiple plant reference panel database for genotype imputation. Nucleic Acids Research, 2021, 49, D1480-D1488. 14.5 299 Population genetic studies in the genomic sequencing era. Zoological Research, 2015, 36, 223-32. 0.6 6 Screening and identification of candidate Fusarium wilt-resistance genes from pumpkin. Horticultural Plant Journal, 2022, 8, 583-592.

	CITATION REF	ORI	
# 301	ARTICLE Deletion of a cyclin-dependent protein kinase inhibitor, CsSMR1, leads to dwarf and determinate growth in cucumber (Cucumis sativus L.). Theoretical and Applied Genetics, 2022, 135, 915-927.	IF 3.6	CITATIONS
302	Genome-Wide Identification of TIFY Genes and Their Response to Various Pathogen Infections in Cucumber (Cucumis sativus L.). Scientia Horticulturae, 2022, 295, 110814.	3.6	10
303	Genome sequencing and population resequencing provide insights into the genetic basis of domestication and diversity of vegetable soybean. Horticulture Research, 2022, 9, .	6.3	10
304	Molecular Research Progress on Xishuangbanna Cucumber (Cucumis sativus L. var. Xishuangbannesis) Tj ETQq1 1	0.78431 3.0	4 rgBT /Over
305	Cucurbitaceae genome evolution, gene function, and molecular breeding. Horticulture Research, 2022, 9, .	6.3	34
306	Graph-based pan-genome reveals structural and sequence variations related to agronomic traits and domestication in cucumber. Nature Communications, 2022, 13, 682.	12.8	59
307	The genomes of 204 Vitis vinifera accessions reveal the origin of European wine grapes. Nature Communications, 2021, 12, 7240.	12.8	39
308	Light and Carbohydrate Signaling Genes Co-Regulate Carotenoid Accumulation in the Endocarp of Cucumber Fruit Under Photoperiodic Treatment as Revealed by Transcriptomic Analysis. SSRN Electronic Journal, 0, , .	0.4	0
309	Investigation of genome-wide InDel distribution and segregation in Populus with restriction-site associated DNA sequencing data. Tropical Plant Biology, 2022, 15, 171-180.	1.9	5
310	<i>NS</i> encodes an auxin transporter that regulates the â€~numerous spines' trait in cucumber (<i>Cucumis sativus</i>) fruit. Plant Journal, 2022, 110, 325-336.	5.7	10
311	<i>Alkaline α-galactosidase 2</i> (<i>CsAGA2</i>) plays a pivotal role in mediating source–sink communication in cucumber. Plant Physiology, 2022, 189, 1501-1518.	4.8	18
312	SPATULA and ALCATRAZ confer female sterility and fruit cavity via mediating pistil development in cucumber. Plant Physiology, 2022, 189, 1553-1569.	4.8	9
313	The vegetable SNP database: An integrated resource for plant breeders and scientists. Genomics, 2022, 114, 110348.	2.9	3
314	Rapid and visual monitoring of alien sequences using crop wild relatives specific oligo-painting: The case of cucumber chromosome engineering. Plant Science, 2022, 319, 111199.	3.6	1
315	Chitinase Chi 2 Positively Regulates Cucumber Resistance against Fusarium oxysporum f. sp. cucumerinum. Genes, 2022, 13, 62.	2.4	6
316	Identification of an Allelic Variant of the CsOr Gene Controlling Fruit Endocarp Color in Cucumber (Cucumis sativus L.) Using Genotyping-By-Sequencing (GBS) and Whole-Genome Sequencing. Frontiers in Plant Science, 2021, 12, 802864.	3.6	7
318	Mapping of fruit apex shape related QTLs across multi-genetic backgrounds in cucumber (Cucumis) Tj ETQq0 0 0	rgBT /Ove 5.0	rlock 10 Tf 5

319	Importance, Distribution, Bot	any and Genetics. Compendium of Plant Genomes, 2022, , 1-13.	
-----	-------------------------------	--	--

0.5 1

	Сітаті	CITATION REPORT	
#	Article	IF	CITATIONS
396	Next generation genomics: toward decoding domestication history of crops. , 2022, , 209-220.		0
397	Quite the pickle: an auxin influx carrier controls spine formation in cucumber. Plant Journal, 2022, 110, 323-324.	5.7	0
398	Population-specific, recent positive selection signatures in cultivated <i>Cucumis sativus</i> L. (cucumber). G3: Genes, Genomes, Genetics, 2022, , .	1.8	1
399	Screening and identifying cucurbitacins and cucurbitacin glycosides in <scp><i>Cucumis sativus</i></scp> using highâ€performance liquid chromatography/quadrupoleâ€timeâ€ofâ€flight mass spectrometry combined with inâ€source fragmentation and alkali adduct ions. Rapid Communications in Mass Spectrometry. 2022. 36. e9323.	1.5	3
400	Recent status of Genotyping by Sequencing (GBS) Technology in cucumber (Cucumis sativus L.): a review. Molecular Biology Reports, 2022, 49, 5547-5554.	2.3	5
401	Morphological Characterization and Integrated Transcriptome and Proteome Analysis of Organ Development Defective 1 (odd1) Mutant in Cucumis sativus L International Journal of Molecular Sciences, 2022, 23, 5843.	4.1	1
402	Genome-wide identification and development of InDel markers in tobacco (Nicotiana tabacum L.) using RAD-seq. Physiology and Molecular Biology of Plants, 2022, 28, 1077-1089.	3.1	4
403	Genome-Wide Association Studies Reveal Candidate Genes Related to Stem Diameter in Cucumber (Cucumis sativus L.). Genes, 2022, 13, 1095.	2.4	4
404	Modified photoperiod response of CsFT promotes day neutrality and early flowering in cultivated cucumber. Theoretical and Applied Genetics, 2022, 135, 2735-2746.	3.6	5
405	Genome-wide association study reveals candidate genes for gummy stem blight resistance in cucumber. Horticultural Plant Journal, 2023, 9, 261-272.	5.0	2
406	Genomic regions and candidate genes selected during the breeding of rice in Vietnam. Evolutionary Applications, 2022, 15, 1141-1161.	3.1	3
407	De Novo Domestication in the Multi-Omics Era. Plant and Cell Physiology, 0, , .	3.1	4
408	Identification and Characterization Roles of Phytoene Synthase (PSY) Genes in Watermelon Development. Genes, 2022, 13, 1189.	2.4	4
409	COMPILE: a GWAS computational pipeline for gene discovery in complex genomes. BMC Plant Biology, 2022, 22, .	3.6	2
410	Unravelling cucumber resistance to several viruses via genome-wide association studies highlighted resistance hotspots and new QTLs. Horticulture Research, 2022, 9, .	6.3	2
411	Genomic, metabonomic and transcriptomic analyses of sweet osmanthus varieties provide insights into floral aroma formation. Scientia Horticulturae, 2022, 306, 111442.	3.6	7
412	Multi-omics study revealed the genetic basis of beer flavor quality in yeast. LWT - Food Science and Technology, 2022, 168, 113932.	5.2	6
413	Genomic Designing for Abiotic Stress Tolerance in Cucurbits. , 2022, , 187-252.		0

#	Article	IF	CITATIONS
414	Omics studies for vegetable improvement. , 2022, , 215-238.		0
415	The CsHEC1-CsOVATE module contributes to fruit neck length variation via modulating auxin biosynthesis in cucumber. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	10
416	Fine mapping a quantitative trait locus underlying seedling resistance to gummy stem blight using a residual heterozygous lines-derived strategy in cucumber. Frontiers in Plant Science, 0, 13, .	3.6	1
417	Combination of Genomics, Transcriptomics Identifies Candidate Loci Related to Cold Tolerance in Dongxiang Wild Rice. Plants, 2022, 11, 2329.	3.5	3
418	Genomic analyses of rice bean landraces reveal adaptation and yield related loci to accelerate breeding. Nature Communications, 2022, 13, .	12.8	13
419	Genomic insights into the evolutionary history and diversification of bulb traits in garlic. Genome Biology, 2022, 23, .	8.8	6
420	Transcriptomic and Physiological Analyses Reveal Potential Genes Involved in Photoperiod-Regulated β-Carotene Accumulation Mechanisms in the Endocarp of Cucumber (Cucumis sativus L.) Fruit. International Journal of Molecular Sciences, 2022, 23, 12650.	4.1	0
421	CuGenDBv2: an updated database for cucurbit genomics. Nucleic Acids Research, 2023, 51, D1457-D1464.	14.5	33
422	Cucumber <i>glossy fruit 1</i> (<i>CsGLF1</i>) encodes the zinc finger protein 6 that regulates fruit glossiness by enhancing cuticular wax biosynthesis. Horticulture Research, 2023, 10, .	6.3	2
423	Identification of superior haplotypes and candidate genes for yield-related traits in tobacco (Nicotiana tabacum L.) using association mapping. Industrial Crops and Products, 2022, 189, 115886.	5.2	2
424	Machine learning assisted dynamic phenotypes and genomic variants help understand the ecotype divergence in rapeseed. Frontiers in Plant Science, 0, 13, .	3.6	0
425	Genome-scale investigation and identification of variations associated with early flowering based on whole genome resequencing and transcriptome integrated analysis in tree peony. Scientia Horticulturae, 2023, 310, 111695.	3.6	2
426	Natural variation in CRABS CLAW contributes to fruit length divergence in cucumber. Plant Cell, 2023, 35, 738-755.	6.6	11
427	Morphological and Genetic Diversity of Cucumber (Cucumis sativus L.) Fruit Development. Plants, 2023, 12, 23.	3.5	3
428	Vegetable biology and breeding in the genomics era. Science China Life Sciences, 2023, 66, 226-250.	4.9	10
429	Architecture design of cucurbit crops for enhanced productivity by a natural allele. Nature Plants, 2022, 8, 1394-1407.	9.3	12
430	Ash Gourd Genomics: Achievements, Challenges and Future Perspectives. , 2023, , 53-68.		0
431	Pollen tube emergence is mediated by ovary-expressed ALCATRAZ in cucumber. Nature Communications, 2023, 14, .	12.8	8

#	ARTICLE	IF	CITATIONS
432	Mutation in the GA3ox gene governs short-internode characteristic in a korean cucumber inbred line. Horticulture Environment and Biotechnology, 2023, 64, 485-495.	2.1	1
433	<i>FLOWERING LOCUS T</i> (<i>FT</i>) gene regulates short-day flowering in low latitude Xishuangbanna cucumber (<i>Cucumis sativus</i> var.) Tj ETQq1 1 0.784314 rgBT /Overlock	10017506	971Td (<18
434	Identification of clade-wide putative <i>cis</i> -regulatory elements from conserved non-coding sequences in Cucurbitaceae genomes. Horticulture Research, 2023, 10, .	6.3	1
435	A Genome-Wide Association Study to Identify Novel Candidate Genes Related to Low-Nitrogen Tolerance in Cucumber (Cucumis sativus L.). Genes, 2023, 14, 662.	2.4	0
436	Identification of Causal Gene-Specific SNP Markers for the Development of Gynoecious Hybrids in Cucumber (Cucumis sativa L.) Using the PathoLogic Algorithm. Horticulturae, 2023, 9, 389.	2.8	0
437	GWAS Characterization of the Genetic Regions Associated with Nine Important Agronomic Traits in Tomato (Solanum lycopersicum L.). Agronomy, 2023, 13, 1191.	3.0	1
438	Developments on Core Collections of Plant Genetic Resources: Do We Know Enough?. Forests, 2023, 14, 926.	2.1	5
439	Genetics and marker-assisted breeding for sex expression in cucumber. Frontiers in Genetics, 0, 14, .	2.3	0
440	Silencing the novel gene CsARR-9 increases photosynthetic efficiency and alleviates autotoxicity in cucumber. Scientia Horticulturae, 2023, 320, 112160.	3.6	2
441	Chloroplast Pan-Genomes and Comparative Transcriptomics Reveal Genetic Variation and Temperature Adaptation in the Cucumber. International Journal of Molecular Sciences, 2023, 24, 8943.	4.1	2
444	Genetics, resistance mechanism, and breeding of powdery mildew resistance in cucumbers (Cucumis) Tj ETQq0 () 0 ₅ .gBT /C)verlock 107
445	Cucumber abscisic acid 8′-hydroxylase Csyf2 regulates yellow flesh by modulating carotenoid biosynthesis. Plant Physiology, 2023, 193, 1001-1015.	4.8	2
446	The <scp>COPII</scp> subunit <i>CsSEC23</i> mediates fruit glossiness in cucumber. Plant Journal, 2023, 116, 524-540.	5.7	1
447	Functional Diversity of Endophytic Microbiota in Crop Management of Cucumis sativus L. , 2023, , 269-284.		0
448	The NLR Family of Disease Resistance Genes in Cultivated Watermelon and Other Cucurbits: Opportunities and Challenges. Compendium of Plant Genomes, 2023, , 37-67.	0.5	0
449	Recent Advances in Genomics, Genetic Resources of Watermelon. Compendium of Plant Genomes, 2023, , 131-142.	0.5	0
450	Comprehensive dissection of meiotic DNA double-strand breaks and crossovers in cucumber. Plant Physiology, 2023, 193, 1913-1932.	4.8	1
451	QTL mapping and transcriptomic analysis of fruit length in cucumber. Frontiers in Plant Science, 0, 14,	3.6	0

#	Article	IF	CITATIONS
452	Fine-Scale analysis of both wild and cultivated horned galls provides insight into their quality differentiation. BMC Plant Biology, 2023, 23, .	3.6	0
453	Identification and evolution of nsLTPs in the root nodule nitrogen fixation clade and molecular response of Frankia to AgLTP24. Scientific Reports, 2023, 13, .	3.3	0
454	Identification of a gene causing yellow endocarp in Cucumis sativus through high-throughput sequencing. Scientia Horticulturae, 2024, 323, 112515.	3.6	0
455	A Genome-wide association study identifies candidate genes for heat tolerance in adult cucumber (Cucumis sativus L.) plants. Horticultural Plant Journal, 2023, , .	5.0	0
456	Haplotype variation and KASP markers for SiPSY1 – A key gene controlling yellow kernel pigmentation in foxtail millet. Crop Journal, 2023, 11, 1902-1911.	5.2	0
457	Identification of QTL associated with resistance to Phytophthora fruit rot in cucumber (Cucumis) Tj ETQq1 1 0.78	34314 rgB	T /Overlock
458	Lipid-Related Domestication Accounts for the Extreme Cold Sensitivity of Semiwild and Tropic Xishuangbanna Cucumber (Cucumis sativus L. var. xishuangbannanesis). International Journal of Molecular Sciences, 2024, 25, 79.	4.1	1
459	From Sequencing to Genome Editing in Cucurbitaceae: Application of Modern Genomic Techniques to Enhance Plant Traits. Agriculture (Switzerland), 2024, 14, 90.	3.1	0
460	Effect of Activation of Cucumber Seeds with Different Concentrations of Zinc under Different Soaking Periods on Growth and Yield Characteristics (Cucumis sativus L.). IOP Conference Series: Earth and Environmental Science, 2023, 1214, 012048.	0.3	0
461	N-myristoyltransferase1 regulates biomass accumulation in cucumber (Cucumis sativus L.)1. Journal of Integrative Agriculture, 2024, , .	3.5	0
462	CsHLS1 sSCL28 module regulates compact plant architecture in cucumber. Plant Biotechnology Journal, 0, , .	8.3	0
463	Cucumber (Cucumis sativus L.) with heterologous poly-Î ³ -glutamic acid has skin moisturizing, whitening and anti-wrinkle effects. International Journal of Biological Macromolecules, 2024, 262, 130026.	7.5	0
464	Association Analysis Provides Insights into Plant Mitonuclear Interactions. Molecular Biology and Evolution, 2024, 41, .	8.9	0
465	Multiplex gene editing reveals cucumber MILDEW RESISTANCE LOCUS O family roles in powdery mildew resistance. Plant Physiology, 0, , .	4.8	0
466	Large-scale gene expression alterations introduced by structural variation drive morphotype diversification in Brassica oleracea. Nature Genetics, 2024, 56, 517-529.	21.4	1
467	Status, Gaps and Perspectives of Powdery Mildew Resistance Research and Breeding in Cucurbits. Critical Reviews in Plant Sciences, 0, , 1-80.	5.7	0
468	Genome-wide association study reveals the candidate genes for petiole length and diameter in cucumber. Scientia Horticulturae, 2024, 330, 113038.	3.6	0
469	Determining the genetic basis of ginsenosides variation during ginseng domestication by evolutionary transcriptomics. Industrial Crops and Products, 2024, 212, 118369.	5.2	0

#	Article	IF	CITATIONS
470	A nanopore-based cucumber genome assembly reveals structural variations at two QTLs controlling hypocotyl elongation. Plant Physiology, 0, , .	4.8	0
471	A second update to the checklist of the vascular flora alien to Italy. Plant Biosystems, 2024, 158, 297-340.	1.6	0
472	Genomic and pangenomic analyses provide insights into the population history and genomic diversification of bottle gourd. New Phytologist, 2024, 242, 2285-2300.	7.3	0