The origin of the naked grains of maize

Nature 436, 714-719 DOI: 10.1038/nature03863

Citation Report

#	Article	IF	CITATIONS
2	Amazing grass: developmental genetics of maize domestication. Biochemical Society Transactions, 2005, 33, 1502-1506.	1.6	23
3	Amazing grass: developmental genetics of maize domestication. Biochemical Society Transactions, 2005, 33, 1502.	1.6	29
4	A regulator of nutritional copper signaling in Chlamydomonas is an SBP domain protein that recognizes the GTAC core of copper response element. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 18730-18735.	3.3	292
5	Contributions of Domesticated Plant Studies to our Understanding of Plant Evolution. Annals of Botany, 2005, 96, 953-963.	1.4	102
6	A Large-Scale Screen for Artificial Selection in Maize Identifies Candidate Agronomic Loci for Domestication and Crop Improvement. Plant Cell, 2005, 17, 2859-2872.	3.1	234
7	Rice Domestication by Reducing Shattering. Science, 2006, 311, 1936-1939.	6.0	789
8	Unfallen Grains: How Ancient Farmers Turned Weeds into Crops. Science, 2006, 312, 1318-1319.	6.0	124
9	The Molecular Genetics of Crop Domestication. Cell, 2006, 127, 1309-1321.	13.5	1,701
10	Evidence for a Selective Sweep on Chromosome 1 of Cultivated Sorghum. Crop Science, 2006, 46, S-27.	0.8	11
11	The rice heterochronic gene SUPERNUMERARY BRACT regulates the transition from spikelet meristem to floral meristem. Plant Journal, 2006, 49, 64-78.	2.8	154
12	An adaptive path through jungle DNA. Nature Genetics, 2006, 38, 506-507.	9.4	3
13	mtDNA clock runs out for dopaminergic neurons. Nature Genetics, 2006, 38, 507-508.	9.4	15
14	A distant upstream enhancer at the maize domestication gene tb1 has pleiotropic effects on plant and inflorescent architecture. Nature Genetics, 2006, 38, 594-597.	9.4	389
15	A naturally occurring epigenetic mutation in a gene encoding an SBP-box transcription factor inhibits tomato fruit ripening. Nature Genetics, 2006, 38, 948-952.	9.4	1,076
16	Comparative genome sequencing of Escherichia coli allows observation of bacterial evolution on a laboratory timescale. Nature Genetics, 2006, 38, 1406-1412.	9.4	354
17	Leafing through the genomes of our major crop plants: strategies for capturing unique information. Nature Reviews Genetics, 2006, 7, 174-184.	7.7	82
18	The proper place of hopeful monsters in evolutionary biology. Theory in Biosciences, 2006, 124, 349-369.	0.6	96
19	The comparative analysis based on maize integrated QTL map and meta-analysis of plant height QTLs.	1.7	47 _

#	Article	IF	CITATIONS
20	Documenting domestication: the intersection of genetics and archaeology. Trends in Genetics, 2006, 22, 139-155.	2.9	366
21	Genomic insights into positive selection. Trends in Genetics, 2006, 22, 437-446.	2.9	395
22	Advances in maize genomics: the emergence of positional cloning. Current Opinion in Plant Biology, 2006, 9, 164-171.	3.5	68
23	Molecular and functional diversity of maize. Current Opinion in Plant Biology, 2006, 9, 172-176.	3.5	201
24	Genetics of Grass Flower Development. Advances in Botanical Research, 2006, 44, 385-424.	0.5	29
25	How reliable are empirical genomic scans for selective sweeps?. Genome Research, 2006, 16, 702-712.	2.4	352
26	Natural History of Transposition in the Green Alga Chlamydomonas reinhardtii: Use of the AMT4 Locus as an Experimental System. Genetics, 2006, 173, 2005-2019.	1.2	26
27	The molecular genetic basis of plant adaptation. American Journal of Botany, 2006, 93, 953-962.	0.8	48
28	An SNP Caused Loss of Seed Shattering During Rice Domestication. Science, 2006, 312, 1392-1396.	6.0	833
29	Branching Out: The ramosa Pathway and the Evolution of Grass Inflorescence Morphology. Plant Cell, 2006, 18, 518-522.	3.1	55
30	The Shoot Stem Cell Niche in Angiosperms: Expression Patterns of WUS Orthologues in Rice and Maize Imply Major Modifications in the Course of Mono- and Dicot Evolution. Molecular Biology and Evolution, 2006, 23, 2492-2504.	3.5	175
31	Temporal regulation of shoot development in Arabidopsis thalianaby miR156 and its target SPL3. Development (Cambridge), 2006, 133, 3539-3547.	1.2	1,002
32	Microfossil evidence for pre-Columbian maize dispersals in the neotropics from San Andres, Tabasco, Mexico. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 6870-6875.	3.3	101
33	Linkage Mapping of Domestication Loci in a Large Maize–Teosinte Backcross Resource. Genetics, 2007, 177, 1915-1928.	1.2	97
34	Patterns of Selection and Tissue-Specific Expression among Maize Domestication and Crop Improvement Loci. Plant Physiology, 2007, 144, 1642-1653.	2.3	17
35	Grass Spikelet Genetics and Duplicate Gene Comparisons. International Journal of Plant Sciences, 2007, 168, 93-110.	0.6	33
36	Genomic Screening for Artificial Selection during Domestication and Improvement in Maize. Annals of Botany, 2007, 100, 967-973.	1.4	70
37	Genetic control of pungency in C. chinense via the Pun1 locus. Journal of Experimental Botany, 2007, 58, 979-991.	2.4	168

#	Article	IF	CITATIONS
38	How some people became farmers. , 2007, , 36-52.		0
39	Agricultural improvement in modern times. , 2007, , 261-278.		1
40	Crop evolution: from genetics to genomics. Current Opinion in Genetics and Development, 2007, 17, 525-532.	1.5	74
41	Comparative analysis of the SBP-box gene families in P. patens and seed plants. Gene, 2007, 401, 28-37.	1.0	137
42	Applications of Linkage Disequilibrium and Association Mapping in Crop Plants. , 2007, , 97-119.		95
43	Cloning Qtls in Plants. , 2007, , 207-225.		33
44	From Rice to Other Cereals: Comparative Genomics. , 2007, , 429-479.		3
46	Plant domestication, a unique opportunity to identify the genetic basis of adaptation. Proceedings of the United States of America, 2007, 104, 8641-8648.	3.3	385
47	Architectural Evolution and its Implications for Domestication in Grasses. Annals of Botany, 2007, 100, 941-950.	1.4	115
48	Domestication of Plants in the Americas: Insights from Mendelian and Molecular Genetics. Annals of Botany, 2007, 100, 925-940.	1.4	332
49	Extending the Phytolith Evidence for Early Maize (Zea mays ssp. mays) and Squash (Cucurbita sp.) in Central New York. American Antiquity, 2007, 72, 563-583.	0.6	71
50	The Molecularization of Public Sector Crop Breeding: Progress, Problems, and Prospects. Advances in Agronomy, 2007, , 163-318.	2.4	121
51	Distribution of Genes, Recombination, and Repetitive Elements in the Maize Genome. Crop Science, 2007, 47, S-83.	0.8	8
53	The heterochronic maize mutant Corngrass1 results from overexpression of a tandem microRNA. Nature Genetics, 2007, 39, 544-549.	9.4	583
54	Mechanistic approaches to the study of evolution: the functional synthesis. Nature Reviews Genetics, 2007, 8, 675-688.	7.7	336
55	Morphological evolution through multiple cis-regulatory mutations at a single gene. Nature, 2007, 448, 587-590.	13.7	306
56	The miRNA156/157 recognition element in the 3′ UTR of the Arabidopsis SBP box gene SPL3 prevents early flowering by translational inhibition in seedlings. Plant Journal, 2007, 49, 683-693.	2.8	545
57	The identification of a gene (<i>Cwp1</i>), silenced during <i>Solanum</i> evolution, which causes cuticle microfissuring and dehydration when expressed in tomato fruit. Plant Journal, 2007, 52, 627-639	2.8	66

	CITATION	LEPURI	
#	Article	IF	CITATIONS
58	The Puzzle of Rice Domestication. Journal of Integrative Plant Biology, 2007, 49, 760-768.	4.1	161
59	Compositional assessment of event DAS-59122-7 maize using substantial equivalence. Regulatory Toxicology and Pharmacology, 2007, 47, 37-47.	1.3	43
60	A survey of H2 gene sequences, including new wild-derived genes. International Journal of Immunogenetics, 2007, 34, 3-12.	0.8	2
61	Floral displays: genetic control of grass inflorescences. Current Opinion in Plant Biology, 2007, 10, 26-31.	3.5	93
62	Wine grape (Vitis vinifera L.) color associates with allelic variation in the domestication gene VvmybA1. Theoretical and Applied Genetics, 2007, 114, 723-730.	1.8	201
63	Origin of seed shattering in rice (Oryza sativa L.). Planta, 2007, 226, 11-20.	1.6	215
64	SBP-domain transcription factors as possible effectors of cryptochrome-mediated blue light signalling in the moss Physcomitrella patens. Planta, 2008, 227, 505-515.	1.6	38
65	The integration of mutant loci affecting maize endosperm development in a dense genetic map using an AFLP-based procedure. Molecular Breeding, 2008, 22, 527-541.	1.0	7
66	Ancient plant DNA in archaeobotany. Vegetation History and Archaeobotany, 2008, 17, 233-244.	1.0	94
67	Comparative QTL mapping of resistance to sugarcane mosaic virus in maize based on bioinformatics. Frontiers of Agriculture in China, 2008, 2, 365-371.	0.2	4
68	Feminized tassels of maize mop1 and ts1 mutants exhibit altered levels of miR156 and specific SBP-box genes. Planta, 2008, 229, 99-113.	1.6	85
69	Deletion in a gene associated with grain size increased yields during rice domestication. Nature Genetics, 2008, 40, 1023-1028.	9.4	794
70	Control of rice grain-filling and yield by a gene with a potential signature of domestication. Nature Genetics, 2008, 40, 1370-1374.	9.4	706
71	Genetic control of rice plant architecture under domestication. Nature Genetics, 2008, 40, 1365-1369.	9.4	384
72	Rice, rising. Nature Genetics, 2008, 40, 1273-1275.	9.4	50
73	Photoreceptors in evolution and disease. Nature Genetics, 2008, 40, 1275-1276.	9.4	7
74	Evaluating the role of natural selection in the evolution of gene regulation. Heredity, 2008, 100, 191-199.	1.2	150
75	Global analysis of gene expression in cotton fibers from wild and domesticated <i>Gossypium barbadense</i> . Evolution & Development, 2008, 10, 567-582.	1.1	77

	СПАНОМ	KEPORT	
#	Article	IF	CITATIONS
76	Microarray analysis of vegetative phase change in maize. Plant Journal, 2008, 56, 1045-1057.	2.8	37
77	Genetics and epigenetics of fruit development and ripening. Current Opinion in Plant Biology, 2008, 11, 58-63.	3.5	136
78	Kernel amino acid composition and protein content of introgression lines from Zea mays ssp. mexicana into cultivated maize. Journal of Cereal Science, 2008, 48, 387-393.	1.8	36
79	Epigenetics and Plant Breeding. , 2008, , 49-177.		27
80	Genomics of Tropical Crop Plants. , 2008, , .		13
81	Quantitative trait loci underlying domestication- and yield-related traits in an <i>Oryza sativa</i> Â× <i>Oryza rufipogon</i> advanced backcross population. Genome, 2008, 51, 692-704.	0.9	38
82	Safety assessment considerations for food and feed derived from plants with genetic modifications that modulate endogenous gene expression and pathways. Food and Chemical Toxicology, 2008, 46, 2591-2605.	1.8	23
83	The art of microRNA: Various strategies leading to gene silencing via an ancient pathway. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2008, 1779, 655-662.	0.9	40
84	Comparative study of SBP-box gene family in Arabidopsis and rice. Gene, 2008, 407, 1-11.	1.0	184
85	Genome-wide identification and evolutionary analysis of the plant specific SBP-box transcription factor family. Gene, 2008, 418, 1-8.	1.0	227
86	Identification of a Consensus DNA-Binding Site for the Arabidopsis thaliana SBP Domain Transcription Factor, AtSPL14, and Binding Kinetics by Surface Plasmon Resonance. Biochemistry, 2008, 47, 3645-3653.	1.2	66
87	The Evolution of Spinnable Cotton Fiber Entailed Prolonged Development and a Novel Metabolism. PLoS Genetics, 2008, 4, e25.	1.5	93
88	The Role of Regulatory Genes During Maize Domestication: Evidence From Nucleotide Polymorphism and Gene Expression. Genetics, 2008, 178, 2133-2143.	1.2	16
89	Inference of the japonica Rice Domestication Process from the Distribution of Six Functional Nucleotide Polymorphisms of Domestication-Related Genes in Various Landraces and Modern Cultivars. Plant and Cell Physiology, 2008, 49, 1283-1293.	1.5	42
90	<i>Barren inflorescence1</i> Functions in Organogenesis During Vegetative and Inflorescence Development in Maize. Genetics, 2008, 179, 389-401.	1.2	50
91	Barley grain with adhering hulls is controlled by an ERF family transcription factor gene regulating a lipid biosynthesis pathway. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 4062-4067.	3.3	296
92	A Genomic Scan for Selection Reveals Candidates for Genes Involved in the Evolution of Cultivated Sunflower (<i>Helianthus annuus</i>). Plant Cell, 2008, 20, 2931-2945.	3.1	269
93	Independent Losses of Function in a Polyphenol Oxidase in Rice: Differentiation in Grain Discoloration between Subspecies and the Role of Positive Selection under Domestication. Plant Cell, 2008, 20, 2946-2959.	3.1	80

	CITATION R	CITATION REPORT	
#	Article	IF	CITATIONS
94	The Genetics of Domestication of the Azuki Bean (<i>Vigna angularis</i>). Genetics, 2008, 178, 1013-1036.	1.2	119
95	Bioinformatics Tools for Plant Genomics. International Journal of Plant Genomics, 2008, 2008, 1-2.	2.2	4
96	Genetic Dissection of Seed Production Traits and Identification of a Majorâ€Effect Seed Retention QTL in Hybrid <i>Leymus</i> (Triticeae) Wildryes. Crop Science, 2009, 49, 29-40.	0.8	26
97	Using Association Mapping in Teosinte to Investigate the Function of Maize Selection-Candidate Genes. PLoS ONE, 2009, 4, e8227.	1.1	13
98	Tracking footprints of maize domestication and evidence for a massive selective sweep on chromosome 10. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 9979-9986.	3.3	133
99	Starch grain and phytolith evidence for early ninth millennium B.P. maize from the Central Balsas River Valley, Mexico. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5019-5024.	3.3	540
100	Genes and Mutations Underlying Domestication Transitions in Grasses. Plant Physiology, 2009, 149, 63-70.	2.3	78
101	Function Annotation of an SBP-box Gene in Arabidopsis Based on Analysis of Co-expression Networks and Promoters. International Journal of Molecular Sciences, 2009, 10, 116-132.	1.8	55
102	Advances in Maize Genomics and Their Value for Enhancing Genetic Gains from Breeding. International Journal of Plant Genomics, 2009, 2009, 1-30.	2.2	37
103	Mutagenesis – the Key to Genetic Analysis. , 2009, , 63-84.		8
104	A cellular study of teosinteZea mayssubsp.parviglumis(Poaceae) caryopsis development showing several processes conserved in maize. American Journal of Botany, 2009, 96, 1798-1807.	0.8	19
105	Artificial Selection and Domestication: Modern Lessons from Darwin's Enduring Analogy. Evolution: Education and Outreach, 2009, 2, 5-27.	0.3	55
106	Saltational evolution: hopeful monsters are here to stay. Theory in Biosciences, 2009, 128, 43-51.	0.6	99
107	The major threshability genes soft glume (sog) and tenacious glume (Tg), of diploid and polyploid wheat, trace their origin to independent mutations at non-orthologous loci. Theoretical and Applied Genetics, 2009, 119, 341-351.	1.8	79
108	A putative lipase gene <i>EXTRA GLUME1</i> regulates both emptyâ€glume fate and spikelet development in rice. Plant Journal, 2009, 57, 593-605.	2.8	81
109	The nature of selection during plant domestication. Nature, 2009, 457, 843-848.	13.7	818
110	GENETIC ARCHITECTURE FOR THE ADAPTIVE ORIGIN OF ANNUAL WILD RICE, <i>ORYZA NIVARA</i> . Evolution; International Journal of Organic Evolution, 2009, 63, 870-883.	1.1	59
111	Domestication of plants revisited - Darwin to the present day. Botanical Journal of the Linnean Society, 2009, 161, 203-212.	0.8	20

#	Article	IF	CITATIONS
112	SNP deserts of Asian cultivated rice: genomic regions under domestication. Journal of Evolutionary Biology, 2009, 22, 751-761.	0.8	43
113	A comparative view of the evolution of grasses under domestication. New Phytologist, 2009, 183, 273-290.	3.5	193
114	The molecular bases of cereal domestication and the history of rice. Comptes Rendus - Biologies, 2009, 332, 267-272.	0.1	15
115	miR156-Regulated SPL Transcription Factors Define an Endogenous Flowering Pathway in Arabidopsis thaliana. Cell, 2009, 138, 738-749.	13.5	1,255
116	Small RNAs and developmental timing in plants. Current Opinion in Genetics and Development, 2009, 19, 374-378.	1.5	185
117	Inherited Variation in Gene Expression. Annual Review of Genomics and Human Genetics, 2009, 10, 313-332.	2.5	71
119	Applications of Linkage Disequilibrium and Association Mapping in Maize. Biotechnology in Agriculture and Forestry, 2009, , 173-195.	0.2	41
121	What Has Natural Variation Taught Us about Plant Development, Physiology, and Adaptation?. Plant Cell, 2009, 21, 1877-1896.	3.1	401
122	Genome-wide identification, phylogeny, and expression analysis of the SBP-box gene family in grapevine. Russian Journal of Plant Physiology, 2010, 57, 273-282.	0.5	11
123	Nucleotide diversity and molecular evolution of the PSY1 gene in Zea mays compared to some other grass species. Theoretical and Applied Genetics, 2010, 120, 709-720.	1.8	36
124	Cloning and characterization of a putative GS3 ortholog involved in maize kernel development. Theoretical and Applied Genetics, 2010, 120, 753-763.	1.8	126
125	Identification of differentially expressed genes at two key endosperm development stages using two maize inbreds with large and small grain and integration with detected QTL for grain weight. Theoretical and Applied Genetics, 2010, 121, 433-447.	1.8	8
126	Expression QTLs: applications for crop improvement. Molecular Breeding, 2010, 26, 381-391.	1.0	26
127	Origin of agriculture and plant domestication in West Mesoamerica. Genetic Resources and Crop Evolution, 2010, 57, 813-825.	0.8	89
128	Association genetics in crop improvement. Current Opinion in Plant Biology, 2010, 13, 174-180.	3.5	410
129	Relationship, evolutionary fate and function of two maize co-orthologs of rice GW2 associated with kernel size and weight. BMC Plant Biology, 2010, 10, 143.	1.6	179
130	Functional evolutionary developmental biology (evo-devo) of morphological novelties in plants. Journal of Systematics and Evolution, 2010, 48, 94-101.	1.6	9
131	Gene expression in developing fibres of Upland cotton (Gossypium hirsutum L.) was massively altered by domestication. BMC Biology, 2010, 8, 139.	1.7	87

#	Article	IF	CITATIONS
132	<i>SQUAMOSA</i> Promoterâ€Binding Proteinâ€Like Transcription Factors: Star Players for Plant Growth and Development. Journal of Integrative Plant Biology, 2010, 52, 946-951.	4.1	244
133	Evidence of selection at the <i>ramosa1</i> locus during maize domestication. Molecular Ecology, 2010, 19, 1296-1311.	2.0	62
134	Tinkering with the C-Function: A Molecular Frame for the Selection of Double Flowers in Cultivated Roses. PLoS ONE, 2010, 5, e9288.	1.1	94
135	Adaptive Evolution of <i>Escherichia coli</i> K-12 MG1655 during Growth on a Nonnative Carbon Source, <scp>I</scp> -1,2-Propanediol. Applied and Environmental Microbiology, 2010, 76, 4158-4168.	1.4	140
136	The microRNA156 and microRNA172 gene regulation cascades at post-germinative stages in <i>Arabidopsis</i> . Seed Science Research, 2010, 20, 79-87.	0.8	55
137	The Past, Present, and Future of Vegetative Phase Change. Plant Physiology, 2010, 154, 541-544.	2.3	124
138	MicroRNA Gene Regulation Cascades During Early Stages of Plant Development. Plant and Cell Physiology, 2010, 51, 1840-1846.	1.5	64
139	Re-evaluating the history of the wheat domestication gene NAM-B1 using historical plant material. Journal of Archaeological Science, 2010, 37, 2303-2307.	1.2	32
140	Pre-pottery farmers on the Pacific coast of southern Mexico. Journal of Archaeological Science, 2010, 37, 3401-3411.	1.2	49
141	Application of food and feed safety assessment principles to evaluate transgenic approaches to gene modulation in crops. Food and Chemical Toxicology, 2010, 48, 1773-1790.	1.8	89
142	Genetic perspectives on crop domestication. Trends in Plant Science, 2010, 15, 529-537.	4.3	321
143	Fine mapping a domestication-related QTL for spike-related traits in a synthetic wheat. Genome, 2010, 53, 798-804.	0.9	10
144	The control of developmental phase transitions in plants. Development (Cambridge), 2011, 138, 4117-4129.	1.2	540
145	Backward Bottlenecks. Current Anthropology, 2011, 52, 77-104.	0.8	16
146	Zea. , 2011, , 457-488.		1
147	Artificial selection for a green revolution gene during <i>japonica</i> rice domestication. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11034-11039.	3.3	179
148	Contributions of Flowering Time Genes to Sunflower Domestication and Improvement. Genetics, 2011, 187, 271-287.	1.2	82
149	A European perspective on maize history. Comptes Rendus - Biologies, 2011, 334, 221-228.	0.1	111

#	ARTICLE	IF.	CITATIONS
150	450-457.	0.1	68
151	Developmental Genetics and New Sequencing Technologies: The Rise of Nonmodel Organisms. Developmental Cell, 2011, 21, 65-76.	3.1	24
152	Promoting the promoter. Plant Science, 2011, 180, 182-189.	1.7	15
153	Conservation and Diversity of Seed Associated Endophytes in Zea across Boundaries of Evolution, Ethnography and Ecology. PLoS ONE, 2011, 6, e20396.	1.1	480
154	Teosinte Inflorescence Phytolith Assemblages Mirror Zea Taxonomy. PLoS ONE, 2011, 6, e18349.	1.1	6
155	An 11-bp Insertion in Zea mays fatb Reduces the Palmitic Acid Content of Fatty Acids in Maize Grain. PLoS ONE, 2011, 6, e24699.	1.1	42
156	MADS-box genes of maize: frequent targets of selection during domestication. Genetical Research, 2011, 93, 65-75.	0.3	47
157	QTL mapping of coleorhiza length in maize (<i>Zea mays L.</i>) under two germination environmental conditions. Plant Breeding, 2011, 130, 625-632.	1.0	4
158	Genetic basis of pearl millet adaptation along an environmental gradient investigated by a combination of genome scan and association mapping. Molecular Ecology, 2011, 20, 80-91.	2.0	48
159	Sequencing crop genomes: approaches and applications. New Phytologist, 2011, 191, 915-925.	3.5	101
160	Contrasted patterns of selection since maize domestication on duplicated genes encoding a starch pathway enzyme. Theoretical and Applied Genetics, 2011, 122, 705-722.	1.8	16
161	High-resolution genetic mapping and candidate gene identification of the SLP1 locus that controls glume development in rice. Theoretical and Applied Genetics, 2011, 122, 1489-1496.	1.8	14
162	Genome-wide expression quantitative trait loci (eQTL) analysis in maize. BMC Genomics, 2011, 12, 336.	1.2	74
163	miR156-Targeted and Nontargeted SBP-Box Transcription Factors Act in Concert to Secure Male Fertility in <i>Arabidopsis</i> À Â. Plant Cell, 2011, 22, 3935-3950.	3.1	310
164	New players unveiled in early anther development. Plant Signaling and Behavior, 2011, 6, 934-938.	1.2	17
165	Sunflower domestication alleles support single domestication center in eastern North America. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 14360-14365.	3.3	97
166	Wild Crop Relatives: Genomic and Breeding Resources. , 2011, , .		70
167	Distinct Genetic Architectures for Male and Female Inflorescence Traits of Maize. PLoS Genetics, 2011, 7, e1002383.	1.5	231

#	Article	IF	CITATIONS
168	Expression and functional analysis of the barley Nud gene using transgenic rice. Breeding Science, 2011, 61, 35-42.	0.9	11
169	QTL Controlling Masculinization of Ear Tips in a Maize (<i>Zea mays</i> L.) Intraspecific Cross. G3: Genes, Genomes, Genetics, 2011, 1, 337-341.	0.8	6
170	Tracing soybean domestication history: From nucleotide to genome. Breeding Science, 2012, 61, 445-452.	0.9	79
171	A Stable <i>dw3</i> Allele in Sorghum and a Molecular Marker to Facilitate Selection. Crop Science, 2012, 52, 2063-2069.	0.8	9
172	Control of Tiller Growth of Rice by OsSPL14 and Strigolactones, Which Work in Two Independent Pathways. Plant and Cell Physiology, 2012, 53, 1793-1801.	1.5	94
173	Reshaping of the maize transcriptome by domestication. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11878-11883.	3.3	154
174	Bimodal expression level polymorphisms in <i>Arabidopsis thaliana</i> . Plant Signaling and Behavior, 2012, 7, 864-873.	1.2	0
175	Evolutionary History of Pearl Millet (Pennisetum glaucum [L.] R. Br.) and Selection on Flowering Genes since Its Domestication. Molecular Biology and Evolution, 2012, 29, 1199-1212.	3.5	48
176	Widespread Recurrent Evolution of Genomic Features. Genome Biology and Evolution, 2012, 4, 486-500.	1.1	34
177	De Novo Sequencing and Characterization of the Floral Transcriptome of Dendrocalamus latiflorus (Poaceae: Bambusoideae). PLoS ONE, 2012, 7, e42082.	1.1	111
178	Maize. , 2012, , 405-432.		3
179	Exome Sequencing and Advances in Crop Improvement. Advances in Genetics, 2012, 79, 87-121.	0.8	11
180	Teosinte as a model system for population and ecological genomics. Trends in Genetics, 2012, 28, 606-615.	2.9	65
181	Allelic variation for a candidate gene for GS7, responsible for grain shape in rice. Theoretical and Applied Genetics, 2012, 125, 1303-1312.	1.8	49
182	Divergences of MPF2-like MADS-domain proteins have an association with the evolution of the inflated calyx syndrome within Solanaceae. Planta, 2012, 236, 1247-1260.	1.6	16
183	Small RNA-Regulated Networks and the Evolution of Novel Structures in Plants. Cold Spring Harbor Symposia on Quantitative Biology, 2012, 77, 221-233.	2.0	11
184	Fruit development and ripening. , 2012, , 405-424.		12
185	Advances in identifying and exploiting natural genetic variation. , 2012, , 195-205.		0

	CITATION	Report	
# 186	ARTICLE Crop Traits crop/cropping trait : Gene Isolation crop/cropping trait gene isolation. , 2012, , 2689-2720.	IF	CITATIONS
187	Genetics and genomics of crop domestication. , 2012, , 3-18.		14
188	Molecular genetic basis of pod corn (<i>Tunicate</i> maize). Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7115-7120.	3.3	48
189	Comparative population genomics of maize domestication and improvement. Nature Genetics, 2012, 44, 808-811.	9.4	816
190	Control of grain size, shape and quality by OsSPL16 in rice. Nature Genetics, 2012, 44, 950-954.	9.4	1,004
191	Roles of miR156 and miR172 in Reproductive Development. Signaling and Communication in Plants, 2012, , 69-81.	0.5	3
192	Genomic organization, phylogenetic comparison and differential expression of the SBP-box family of transcription factors in tomato. Planta, 2012, 235, 1171-1184.	1.6	161
193	The role of <i>teosinte glume architecture</i> (<i>tga1</i>) in coordinated regulation and evolution of grass glumes and inflorescence axes. New Phytologist, 2012, 193, 204-215.	3.5	34
194	A Sequential Quantitative Trait Locus Fineâ€Mapping Strategy Using Recombinantâ€Derived Progeny ^F . Journal of Integrative Plant Biology, 2012, 54, 228-237.	4.1	55
195	Mapping QTL controlling maize deep-seeding tolerance-related traits and confirmation of a major QTL for mesocotyl length. Theoretical and Applied Genetics, 2012, 124, 223-232.	1.8	36
196	Fine-mapping of qRfg2, a QTL for resistance to Gibberella stalk rot in maize. Theoretical and Applied Genetics, 2012, 124, 585-596.	1.8	42
197	Fine mapping of a major quantitative trait locus that regulates pod shattering in soybean. Molecular Breeding, 2013, 32, 485-491.	1.0	21
198	Diagnostics in Plant Breeding. , 2013, , .		2
199	Crop crop/cropping Responses to Available Soil Water crop/cropping Responses to available soil water. , 2013, , 615-637.		0
200	Vegetative Phase Change and Shoot Maturation in Plants. Current Topics in Developmental Biology, 2013, 105, 125-152.	1.0	234
201	Plant science and agricultural productivity: Why are we hitting the yield ceiling?. Plant Science, 2013, 210, 159-176.	1.7	49
202	A genomic variation map provides insights into the genetic basis of cucumber domestication and diversity. Nature Genetics, 2013, 45, 1510-1515.	9.4	472
203	Evolution of crop species: genetics of domestication and diversification. Nature Reviews Genetics, 2013, 14, 840-852.	7.7	857

#	Article	IF	CITATIONS
205	Molecular footprints of domestication and improvement in soybean revealed by whole genome re-sequencing. BMC Genomics, 2013, 14, 579.	1.2	186
206	Designed transcriptional regulators for trait development. Plant Science, 2013, 201-202, 128-136.	1.7	28
207	Haplotype variation at Badh2, the gene determining fragrance in rice. Genomics, 2013, 101, 157-162.	1.3	54
208	Genome-wide identification and analysis of the SBP-box family genes in apple (MalusÂ×Âdomestica) Tj ETQq1 I	0,784314	4 rgβT /Overl £45
209	Zea mays (L.) P1 locus for cob glume color identified as a post-domestication selection target with an effect on temperate maize genomes. Crop Journal, 2013, 1, 15-24.	2.3	10
210	<i>ZmGA3ox2</i> , a candidate gene for a major <scp>QTL</scp> , <scp><i>qPH3.1</i></scp> , for plant height in maize. Plant Journal, 2013, 73, 405-416.	2.8	138
211	Carrying Capacity for Aquaculture, Modeling Frameworks for Determination of. , 2013, , 417-448.		13
213	Bridging the gap between genome analysis and precision breeding in potato. Trends in Genetics, 2013, 29, 248-256.	2.9	63
215	Crop Traits crop/cropping trait : Gene Isolation crop/cropping trait gene isolation. , 2013, , 667-698.		0
216	Evolutionary conservation of microRNA regulatory programs in plant flower development. Developmental Biology, 2013, 380, 133-144.	0.9	177
218	QTL Mapping: Methodology and Applications in Cereal Breeding. , 2013, , 275-318.		18
219	Molecular Genetic Basis of the Domestication Syndrome in Cereals. , 2013, , 319-340.		3
220	Genetics and Consequences of Crop Domestication. Journal of Agricultural and Food Chemistry, 2013, 61, 8267-8276.	2.4	123
221	Proteomic profiling of developing cotton fibers from wild and domesticated <i><scp>G</scp>ossypium barbadense</i> . New Phytologist, 2013, 200, 570-582.	3.5	72
222	The fruit, the whole fruit, and everything about the fruit. Journal of Experimental Botany, 2013, 65, 4491-4503.	2.4	19
223	Functional Evolution in the Plant SQUAMOSA-PROMOTER BINDING PROTEIN-LIKE (SPL) Gene Family. Frontiers in Plant Science, 2013, 4, 80.	1.7	225
224	From Many, One: Genetic Control of Prolificacy during Maize Domestication. PLoS Genetics, 2013, 9, e1003604.	1.5	111
225	Protein change in plant evolution: tracing one thread connecting molecular and phenotypic diversity. Frontiers in Plant Science, 2013, 4, 382.	1.7	15

#	Article	IF	CITATIONS
226	The Genomic Signature of Crop-Wild Introgression in Maize. PLoS Genetics, 2013, 9, e1003477.	1.5	291
227	Genetic control of inflorescence architecture during rice domestication. Nature Communications, 2013, 4, 2200.	5.8	134
228	Qualitative and Quantitative Trait Polymorphisms in Maize. , 2013, , 405-442.		1
229	A Change in <i>SHATTERPROOF</i> Protein Lies at the Origin of a Fruit Morphological Novelty and a New Strategy for Seed Dispersal in <i>Medicago</i> Genus Â. Plant Physiology, 2013, 162, 907-917.	2.3	54
232	Genomic Organization, Phylogenetic Comparison and Differential Expression of the SBP-Box Family Genes in Grape. PLoS ONE, 2013, 8, e59358.	1.1	102
233	Adaptation of Maize to Temperate Climates: Mid-Density Genome-Wide Association Genetics and Diversity Patterns Reveal Key Genomic Regions, with a Major Contribution of the Vgt2 (ZCN8) Locus. PLoS ONE, 2013, 8, e71377.	1.1	83
234	Sequence Evolution and Expression Regulation of Stress-Responsive Genes in Natural Populations of Wild Tomato. PLoS ONE, 2013, 8, e78182.	1.1	29
235	Detecting SNPs underlying domestication-related traits in soybean. BMC Plant Biology, 2014, 14, 251.	1.6	16
236	Decreased Nucleotide and Expression Diversity and Modified Coexpression Patterns Characterize Domestication in the Common Bean. Plant Cell, 2014, 26, 1901-1912.	3.1	103
237	The Role of cis Regulatory Evolution in Maize Domestication. PLoS Genetics, 2014, 10, e1004745.	1.5	144
238	Current perspectives on the hormonal control of seed development in Arabidopsis and maize: a focus on auxin. Frontiers in Plant Science, 2014, 5, 412.	1.7	143
239	Mining Natural Variation for Maize Improvement: Selection on Phenotypes and Genes. , 2014, , 615-649.		24
240	Differential SPL gene expression patterns reveal candidate genes underlying flowering time and architectural differences in Mimulus and Arabidopsis. Molecular Phylogenetics and Evolution, 2014, 73, 129-139.	1.2	18
241	Identification and suppression of the <i>pâ€</i> coumaroyl CoA:hydroxycinnamyl alcohol transferase in <i>Zea mays</i> L Plant Journal, 2014, 78, 850-864.	2.8	72
242	Molecular Characterization and Expression Analysis of <i>Triticum aestivum</i> Squamosaâ€Promoter Binding Proteinâ€Box Genes Involved in Ear Development. Journal of Integrative Plant Biology, 2014, 56, 571-581.	4.1	30
243	Evidence for Selection on Gene Expression in Cultivated Rice (Oryza sativa). Molecular Biology and Evolution, 2014, 31, 1514-1525.	3.5	29
244	Entering the second century of maize quantitative genetics. Heredity, 2014, 112, 30-38.	1.2	142
245	Functional characterization of the stunt lemma palea 1 mutant allele in rice. Plant Growth Regulation, 2014, 73, 257-265.	1.8	6

#	Article	IF	CITATIONS
246	Insect and pathogen attack and resistance in maize and its wild ancestors, the teosintes. New Phytologist, 2014, 204, 329-341.	3.5	118
247	Genetic Dissection of a Genomic Region with Pleiotropic Effects on Domestication Traits in Maize Reveals Multiple Linked QTL. Genetics, 2014, 198, 345-353.	1.2	34
248	Population Structure and Domestication Revealed by High-Depth Resequencing of Korean Cultivated and Wild Soybean Genomes. DNA Research, 2014, 21, 153-167.	1.5	92
249	The PH gene determines fruit acidity and contributes to the evolution of sweet melons. Nature Communications, 2014, 5, 4026.	5.8	100
250	Identification of large-effect QTL for kernel row number has potential for maize yield improvement. Molecular Breeding, 2014, 34, 1087-1096.	1.0	15
251	Genetic and Hormonal Regulation of Maize Inflorescence Development. Advances in Botanical Research, 2014, 72, 263-296.	0.5	8
252	Genomic basis of the differences between cider and dessert apple varieties. Evolutionary Applications, 2015, 8, 650-661.	1.5	33
253	The origin and evolution of maize in the Southwestern United States. Nature Plants, 2015, 1, 14003.	4.7	138
254	Transcriptome profiling of wheat glumes in wild emmer, hulled landraces and modern cultivars. BMC Genomics, 2015, 16, 777.	1.2	16
255	KRN4 Controls Quantitative Variation in Maize Kernel Row Number. PLoS Genetics, 2015, 11, e1005670.	1.5	147
256	Bacterial endophytes from wild maize suppress Fusarium graminearum in modern maize and inhibit mycotoxin accumulation. Frontiers in Plant Science, 2015, 6, 805.	1.7	90
259	Flowering Plants. Monocots. , 2015, , .		144
260	Comparative transcriptomics uncovers alternative splicing changes and signatures of selection from maize improvement. BMC Genomics, 2015, 16, 363.	1.2	33
261	Patterns of genomic changes with crop domestication and breeding. Current Opinion in Plant Biology, 2015, 24, 47-53.	3.5	83
262	Ancient DNA: Results and prospects (The 30th anniversary). Russian Journal of Genetics, 2015, 51, 529-544.	0.2	1
263	Using quantitative PCR with retrotransposon-based insertion polymorphisms as markers in sugarcane. Journal of Experimental Botany, 2015, 66, 4239-4250.	2.4	10
264	Evidence That the Origin of Naked Kernels During Maize Domestication Was Caused by a Single Amino Acid Substitution in <i>tga1</i> . Genetics, 2015, 200, 965-974.	1.2	86
265	Integrative detection and verification of QTL for plant traits in two connected RIL populations of high-oil maize. Euphytica, 2015, 206, 203-223.	0.6	14

#	Article	IF	CITATIONS
266	Parallel Domestication of the <i>Heading Date 1</i> Gene in Cereals. Molecular Biology and Evolution, 2015, 32, 2726-2737.	3.5	54
267	A rare SNP mutation in Brachytic2 moderately reduces plant height and increases yield potential in maize. Journal of Experimental Botany, 2015, 66, 3791-3802.	2.4	79
268	Genome-Wide Identification and Analysis of Drought-Responsive Genes and MicroRNAs in Tobacco. International Journal of Molecular Sciences, 2015, 16, 5714-5740.	1.8	32
269	The miR156/SPL Module, a Regulatory Hub and Versatile Toolbox, Gears up Crops for Enhanced Agronomic Traits. Molecular Plant, 2015, 8, 677-688.	3.9	273
270	Rapid selective sweep of pre-existing polymorphisms and slow fixation of new mutations in experimental evolution of <i>Desulfovibrio vulgaris</i> . ISME Journal, 2015, 9, 2360-2372.	4.4	24
271	A transposable element in a NAC gene is associated with drought tolerance in maize seedlings. Nature Communications, 2015, 6, 8326.	5.8	392
272	Characterization of Squamosa Promoter Binding Protein-LIKE genes in wheat. Journal of Plant Biology, 2015, 58, 220-229.	0.9	19
273	Positional cloning in maize (<i>Zea mays</i> subsp. <i>mays</i> , Poaceae). Applications in Plant Sciences, 2015, 3, 1400092.	0.8	21
274	Study of morphology and chemical composition of phytoliths on the surface of paddy straw. Paddy and Water Environment, 2015, 13, 521-527.	1.0	34
275	Teosinte before domestication: Experimental study of growth and phenotypic variability in Late Pleistocene and early Holocene environments. Quaternary International, 2015, 363, 65-77.	0.7	41
276	Genetic Diversity and Molecular Evolution of a Violaxanthin De-epoxidase Gene in Maize. Frontiers in Genetics, 2016, 7, 131.	1.1	6
277	Fine Mapping of a QTL Associated with Kernel Row Number on Chromosome 1 of Maize. PLoS ONE, 2016, 11, e0150276.	1.1	30
278	Using Ancient Traits to Convert Soil Health into Crop Yield: Impact of Selection on Maize Root and Rhizosphere Function. Frontiers in Plant Science, 2016, 7, 373.	1.7	86
279	Molecular Evolution and Association of Natural Variation in ZmARF31 with Low Phosphorus Tolerance in Maize. Frontiers in Plant Science, 2016, 7, 1076.	1.7	12
280	A comprehensive study of the genomic differentiation between temperate Dent and Flint maize. Genome Biology, 2016, 17, 137.	3.8	51
281	The earliest maize from San Marcos Tehuacán is a partial domesticate with genomic evidence of inbreeding. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14151-14156.	3.3	93
282	A Gene for Genetic Background in <i>Zea mays</i> : Fine-Mapping <i>enhancer of teosinte branched1.2</i> to a YABBY Class Transcription Factor. Genetics, 2016, 204, 1573-1585.	1.2	15
284	Genome-wide identification, phylogeny and expression analysis of the SBP-box gene family in maize (Zea) Tj ETQo	1 1 0.784 1.7	·314 rgBT /O

#	Article	IF	CITATIONS
285	Domestication of Plants in Mesoamerica: An Archaeological Review with Some Ethnobotanical Interpretations. Ethnobiology, 2016, , 207-231.	0.4	12
286	Ethnobotany of Mexico. Ethnobiology, 2016, , .	0.4	36
287	Regulatory modules controlling early shade avoidance response in maize seedlings. BMC Genomics, 2016, 17, 269.	1.2	42
288	Maize. , 2016, , 67-88.		12
289	Integrated mRNA and miRNA transcriptome reveal a cross-talk between developing response and hormone signaling for the seed kernels of Siberian apricot. Scientific Reports, 2016, 6, 35675.	1.6	23
290	Evo-Devo: Regulatory and Protein-Coding Evolution in Plant Diversification. , 2016, , 13-18.		0
291	Mapping Prolificacy QTL in Maize and Teosinte. Journal of Heredity, 2016, 107, 674-678.	1.0	2
292	Characterization of the teosinte transcriptome reveals adaptive sequence divergence during maize domestication. Molecular Ecology Resources, 2016, 16, 1465-1477.	2.2	7
293	Fine-mapping of qGW4.05, a major QTL for kernel weight and size in maize. BMC Plant Biology, 2016, 16, 81.	1.6	47
294	Transcriptome-wide identification and expression analysis of chrysanthemum SBP-like transcription factors. Plant Physiology and Biochemistry, 2016, 102, 10-16.	2.8	45
295	A comprehensive meta-analysis of plant morphology, yield, stay-green, and virus disease resistance QTL in maize (Zea mays L.). Planta, 2016, 243, 459-471.	1.6	74
296	The Multifaceted Roles of miR156-targeted SPL Transcription Factors in Plant Developmental Transitions. , 2016, , 281-293.		8
297	Genomic organization, phylogenetic comparison, and expression profiles of the SPL family genes and their regulation in soybean. Development Genes and Evolution, 2017, 227, 101-119.	0.4	60
298	Maize seedling morphology and defence hormone profiles, but not herbivory tolerance, were mediated by domestication and modern breeding. Annals of Applied Biology, 2017, 170, 315-332.	1.3	14
299	Accelerating the Domestication of New Crops: Feasibility and Approaches. Trends in Plant Science, 2017, 22, 373-384.	4.3	117
300	Functional Conservation and Divergence among Homoeologs of <i>TaSPL20</i> and <i>TaSPL21</i> , Two SBP-Box Genes Governing Yield-Related Traits in Hexaploid Wheat. Plant Physiology, 2017, 174, 1177-1191.	2.3	46
301	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.	1.8	60
302	Functional Mapping of Multiple Dynamic Traits. Journal of Agricultural, Biological, and Environmental Statistics, 2017, 22, 60-75.	0.7	2

#	Article	IF	CITATIONS
303	Genetic Differentiation and Crop Evolution of Foxtail Millet. Plant Genetics and Genomics: Crops and Models, 2017, , 115-131.	0.3	3
304	Genetics and Genomics of Setaria. Plant Genetics and Genomics: Crops and Models, 2017, , .	0.3	18
305	The Genetic Basis of Plant Architecture in 10 Maize Recombinant Inbred Line Populations. Plant Physiology, 2017, 175, 858-873.	2.3	97
306	Phytochrome-interacting factors directly suppress MIR156 expression to enhance shade-avoidance syndrome in Arabidopsis. Nature Communications, 2017, 8, 348.	5.8	144
307	Selection During Maize Domestication Targeted a Gene Network Controlling Plant and Inflorescence Architecture. Genetics, 2017, 207, 755-765.	1.2	75
308	Rhizotrophs: Plant Growth Promotion to Bioremediation. , 2017, , .		8
309	Corn and Its Interactions with Bacterial Communities. , 2017, , 145-163.		1
310	Cloning, molecular evolution and functional characterization of ZmbHLH16, the maize ortholog of OsTIP2 (OsbHLH142). Biology Open, 2017, 6, 1654-1663.	0.6	12
311	Genome-wide identification and characterization of the SPL gene family in Ziziphus jujuba. Gene, 2017, 627, 315-321.	1.0	43
312	Medical Subject Heading (MeSH) annotations illuminate maize genetics and evolution. Plant Methods, 2017, 13, 8.	1.9	7
313	Natural variations in stearoyl-acp desaturase genes affect the conversion of stearic to oleic acid in maize kernel. Theoretical and Applied Genetics, 2017, 130, 151-161.	1.8	23
314	Association mapping for phenology and plant architecture in maize shows higher power for developmental traits compared with growth influenced traits. Heredity, 2017, 118, 249-259.	1.2	45
315	Genome-Wide Organization and Expression Profiling of the SBP-Box Gene Family in Chinese Jujube (Ziziphus jujuba Mill.). International Journal of Molecular Sciences, 2017, 18, 1734.	1.8	25
316	The SBP-Box Gene VpSBP11 from Chinese Wild Vitis Is Involved in Floral Transition and Affects Leaf Development. International Journal of Molecular Sciences, 2017, 18, 1493.	1.8	13
317	Maize network analysis revealed gene modules involved in development, nutrients utilization, metabolism, and stress response. BMC Plant Biology, 2017, 17, 131.	1.6	24
318	Genetic diversity and evolution of reduced sulfur storage during domestication of maize. Plant Journal, 2018, 94, 943-955.	2.8	5
319	SPL6 represses signalling outputs of ER stress in control of panicle cell death in rice. Nature Plants, 2018, 4, 280-288.	4.7	60
320	Genetic and Molecular Mechanisms of Quantitative Trait Loci Controlling Maize Inflorescence Architecture. Plant and Cell Physiology, 2018, 59, 448-457.	1.5	37

#	Article	IF	CITATIONS
321	Genome-wide identification and characterization of the SBP-box gene family in Petunia. BMC Genomics, 2018, 19, 193.	1.2	64
322	Screening of major phenolics and antioxidant activities in teosinte populations and modern maize types. Journal of Cereal Science, 2018, 79, 276-285.	1.8	8
323	Selection Signatures Underlying Dramatic Male Inflorescence Transformation During Modern Hybrid Maize Breeding. Genetics, 2018, 210, 1125-1138.	1.2	45
324	Wonder and the Necessary Alliances of Science and Religion. , 2018, , 291-324.		1
325	The cotton HD-Zip transcription factor GhHB12 regulates flowering time and plant architecture via the GhmiR157-GhSPL pathway. Communications Biology, 2018, 1, 229.	2.0	14
326	On the Road to Breeding 4.0: Unraveling the Good, the Bad, and the Boring of Crop Quantitative Genomics. Annual Review of Genetics, 2018, 52, 421-444.	3.2	182
328	Population Genomics of Crop Domestication: Current State and Perspectives. Population Genomics, 2018, , 685-707.	0.2	1
329	QTL mapping in a maize F2 population using Genotyping-by-Sequencing and a modified fine-mapping strategy. Plant Science, 2018, 276, 171-180.	1.7	16
330	Differential transcriptome patterns associated with early seedling development in a wild and a domesticated common bean (Phaseolus vulgaris L.) accession. Plant Science, 2018, 274, 153-162.	1.7	9
331	Species-Associated Differences in the Below-Ground Microbiomes of Wild and Domesticated Setaria. Frontiers in Plant Science, 2018, 9, 1183.	1.7	31
332	Identification and Fine-Mapping of a Major Maize Leaf Width QTL in a Re-sequenced Large Recombinant Inbred Lines Population. Frontiers in Plant Science, 2018, 9, 101.	1.7	21
333	Maize domestication and gene interaction. New Phytologist, 2018, 220, 395-408.	3.5	90
334	Exploiting SPL genes to improve maize plant architecture tailored for high-density planting. Journal of Experimental Botany, 2018, 69, 4675-4688.	2.4	51
335	Constitutive Expression of Aechmea fasciata SPL14 (AfSPL14) Accelerates Flowering and Changes the Plant Architecture in Arabidopsis. International Journal of Molecular Sciences, 2018, 19, 2085.	1.8	7
336	Genetic Dissection of a Supergene Implicates <i>Tfap2a</i> in Craniofacial Evolution of Threespine Sticklebacks. Genetics, 2018, 209, 591-605.	1.2	25
337	Identification of minor effect QTLs for plant architecture related traits using super high density genotyping and large recombinant inbred population in maize (Zea mays). BMC Plant Biology, 2018, 18, 17.	1.6	33
338	Genome-wide analysis of the SPL/miR156 module and its interaction with the AP2/miR172 unit in barley. Scientific Reports, 2018, 8, 7085.	1.6	52
339	Barley Domestication, Adaptation and Population Genomics. Compendium of Plant Genomes, 2018, , 317-336.	0.3	12

#	Article	IF	CITATIONS
340	Biases induced by using geography and environment to guide ex situ conservation. Conservation Genetics, 2018, 19, 1281-1293.	0.8	6
341	Developmental Pleiotropy Shaped the Roots of the Domesticated Common Bean (<i>Phaseolus) Tj ETQq1 1 0.78</i>	4314 rgBT 2.3	/Qyerlock
342	Whole-Genome Sequencing Identifies a Rice Grain Shape Mutant, gs9–1. Rice, 2019, 12, 52.	1.7	5
343	Fine mapping and identification of ub4 as a candidate gene associated with tassel branch number in maize (Zea mays L.). Genetic Resources and Crop Evolution, 2019, 66, 1557-1571.	0.8	3
344	QTL mapping for leaf morphology traits in a large maize-teosinte population. Molecular Breeding, 2019, 39, 1.	1.0	17
345	Genome-wide identification and comparative analysis of drought-related microRNAs in two maize inbred lines with contrasting drought tolerance by deep sequencing. PLoS ONE, 2019, 14, e0219176.	1.1	40
346	Comparative genome analysis of the SPL gene family reveals novel evolutionary features in maize. Genetics and Molecular Biology, 2019, 42, 380-394.	0.6	13
347	MaizeSNPDB: A comprehensive database for efficient retrieve and analysis of SNPs among 1210 maize lines. Computational and Structural Biotechnology Journal, 2019, 17, 1377-1383.	1.9	12
348	Dissecting the genetic architecture of important traits that enhance wild germplasm resource usage in modern maize breeding. Molecular Breeding, 2019, 39, 1.	1.0	10
349	Natural Variation and Domestication Selection of ZmPGP1 Affects Plant Architecture and Yield-Related Traits in Maize. Genes, 2019, 10, 664.	1.0	21
350	The regulatory landscape of a core maize domestication module controlling bud dormancy and growth repression. Nature Communications, 2019, 10, 3810.	5.8	116
351	Molecular mapping and candidate gene analysis of the semi-dominant gene Vestigial glume1 in maize. Crop Journal, 2019, 7, 667-676.	2.3	1
352	How can developmental biology help feed a growing population?. Development (Cambridge), 2019, 146, .	1.2	18
353	Evolutionary Metabolomics Identifies Substantial Metabolic Divergence between Maize and Its Wild Ancestor, Teosinte. Plant Cell, 2019, 31, 1990-2009.	3.1	69
354	Perspectives on microRNAs and Phased Small Interfering RNAs in Maize (Zea mays L.): Functions and Big Impact on Agronomic Traits Enhancement. Plants, 2019, 8, 170.	1.6	18
355	Genome mapping of quantitative trait loci (QTL) controlling domestication traits of intermediate wheatgrass (Thinopyrum intermedium). Theoretical and Applied Genetics, 2019, 132, 2325-2351.	1.8	30
356	Experimenting with domestication: Understanding macro- and micro-phenotypes and developmental plasticity in teosinte in its ancestral pleistocene and early holocene environments. Journal of Archaeological Science, 2019, 108, 104970.	1.2	9
357	The dynamic mosaic phenotypes of flowering plants. New Phytologist, 2019, 224, 1021-1034.	3.5	24

ARTICLE IF CITATIONS # The Genomics of <i>Oryza</i> Species Provides Insights into Rice Domestication and Heterosis. Annual 358 80 8.6 Review of Plant Biology, 2019, 70, 639-665. De Novo Domestication: An Alternative Route toward New Crops for the Future. Molecular Plant, 2019, 12, 615-631. 360 Participatory Plant Breeding: Concept and Applications., 2019,,. 5 Cereals., 2019, , 129-173. Largeâ€scale metabolite quantitative trait locus analysis provides new insights for highâ€quality maize 362 2.8 37 improvement. Plant Journal, 2019, 99, 216-230. The genetic architecture of teosinte catalyzed and constrained maize domestication. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 5643-5652. 3.3 The complex geography of domestication of the African rice Oryza glaberrima. PLoS Genetics, 2019, 15, 364 1.5 30 e1007414. Identification and Functional Characterization of Squamosa Promoter Binding Protein-Like Gene 1.7 TaSPL16 in Wheat (Triticum aestivum L.). Frontiers in Plant Science, 2019, 10, 212. Maize <i>YABBY</i> genes <i>drooping leaf1</i> and <i>drooping leaf2</i> regulate floret development 366 1.2 28 and floral meristem determinacy. Development (Cambridge), 2019, 146, . CRISPR/Cas9-mediated targeted mutagenesis of GmSPL9 genes alters plant architecture in soybean. BMC 1.6 Plant Biology, 2019, 19, 131. Selection pressure causes differentiation of the SPL gene family in the Juglandaceae. Molecular 368 1.0 6 Genetics and Genomics, 2019, 294, 1037-1048. Wild Relatives of Maize., 2019, , 3-39. 369 Chromatin Evolution-Key Innovations Underpinning Morphological Complexity. Frontiers in Plant 370 1.7 10 Science, 2019, 10, 454. Genome-Wide Identification and Characterization of SQUAMOSAâ€"Promoter-Binding Protein (SBP) 371 1.8 Genes Involved in the Flowering Development of Citrus Clementina. Biomolecules, 2019, 9, 66. The analysis of functional genes in maize molecular breeding. Molecular Breeding, 2019, 39, 1. 372 1.0 3 RNA-Seq reveals new DELLA targets and regulation in transgenic GA-insensitive grapevines. BMC Plant Biology, 2019, 19, 80. Hybrid Decay: A Transgenerational Epigenetic Decline in Vigor and Viability Triggered in Backcross 374 1.2 7 Populations of Teosinte with Maize. Genetics, 2019, 213, 143-160. CRISPR/Cas9-mediated targeted mutagenesis of GmLHY genes alters plant height and internode length 98 1.6 in soybean. BMC Plant Biology, 2019, 19, 562.

		CITATION REPORT		
#	Article		IF	CITATIONS
376	Evolutionary and ecological functional genomics, from lab to the wild. Plant Journal, 20	19, 97, 40-55.	2.8	39
377	A domesticationâ€associated reduction in K ⁺ â€preferring HKT transporte maize shoot K ⁺ accumulation and salt tolerance. New Phytologist, 2019,	r activity underlies 222, 301-317.	3.5	65
378	The APETALA2-Like Transcription Factor SUPERNUMERARY BRACT Controls Rice Seed S Seed Size. Plant Cell, 2019, 31, 17-36.	hattering and	3.1	93
379	Understanding Grass Domestication through Maize Mutants. Trends in Genetics, 2019	, 35, 118-128.	2.9	27
380	Heterogeneous phosphate supply influences maize lateral root proliferation by regulati redistribution. Annals of Botany, 2020, 125, 119-130.	ng auxin	1.4	24
381	Quantitative trait loci for fruit size and flowering timeâ€related traits under domestica diversifying selection in cucumber (<i>Cucumis sativus</i>). Plant Breeding, 2020, 139	tion and , 176-191.	1.0	26
382	Genetic basis of kernel nutritional traits during maize domestication and improvement 2020, 101, 278-292.	. Plant Journal,	2.8	25
383	The Past, Present, and Future of Maize Improvement: Domestication, Genomics, and Fu Genomic Routes toward Crop Enhancement. Plant Communications, 2020, 1, 100010.	inctional	3.6	68
384	The Coix Genome Provides Insights into Panicoideae Evolution and Papery Hull Domest Molecular Plant, 2020, 13, 309-320.	cication.	3.9	28
385	Evolution and Domestication Footprints Uncovered from the Genomes of Coix. Molecu 13, 295-308.	lar Plant, 2020,	3.9	35
386	Archaeological Plant Remains. Interdisciplinary Contributions To Archaeology, 2020, , 2	267-291.	0.1	1
387	Evolutionary and functional genomics of DNA methylation in maize domestication and Nature Communications, 2020, 11, 5539.	improvement.	5.8	59
388	Teosinte (Zea mays ssp parviglumis) growth and transcriptomic response to weed stressimilarities and differences between varieties and with modern maize varieties. PLoS OI e0237715.	ss identifies NE, 2020, 15,	1.1	4
389	QTL mapping for resistance to ear rot caused by Fusarium graminearum using an IBM S population in maize. Molecular Breeding, 2020, 40, 1.	Syn10 DH	1.0	7
390	The Kernel Size-Related Quantitative Trait Locus <i>qKW9</i> Encodes a Pentatricoper Protein That Aaffects Photosynthesis and Grain Filling. Plant Physiology, 2020, 183, 16	otide Repeat 96-1709.	2.3	29
391	Genetic Dissection of Nitrogen Use Efficiency in Tropical Maize Through Genome-Wide Genomic Prediction. Frontiers in Plant Science, 2020, 11, 474.	Association and	1.7	33
392	Evolution of Plant Architecture in Oryza Driven by the PROG1 Locus. Frontiers in Plant 11, 876.	Science, 2020,	1.7	5
393	Prediction of the antioxidant capacity of maize (Zea mays) hybrids using mass fingerpr mining. Food Bioscience, 2020, 37, 100647.	inting and data	2.0	4

#	Article	IF	CITATIONS
394	Fine mapping and candidate gene analysis of qKW7b, a major QTL for kernel width in maize. Molecular Breeding, 2020, 40, 1.	1.0	4
395	Molecular and functional characterization of the SBP-box transcription factor SPL-CNR in tomato fruit ripening and cell death. Journal of Experimental Botany, 2020, 71, 2995-3011.	2.4	23
396	Phenotypic Plasticity Contributes to Maize Adaptation and Heterosis. Molecular Biology and Evolution, 2021, 38, 1262-1275.	3.5	32
397	Harnessing Knowledge from Maize and Rice Domestication for New Crop Breeding. Molecular Plant, 2021, 14, 9-26.	3.9	58
398	Using Interactome Big Data to Crack Genetic Mysteries and Enhance Future Crop Breeding. Molecular Plant, 2021, 14, 77-94.	3.9	34
399	Resequencing of global Tartary buckwheat accessions reveals multiple domestication events and key loci associated with agronomic traits. Genome Biology, 2021, 22, 23.	3.8	69
400	Neglected and Underutilized Crop Species: Are They Future Smart Crops in Fighting Poverty, Hunger and Malnutrition Under Changing Climate?. , 2021, , 1-50.		6
401	<i>Q^{Dtbn1}</i> , an Fâ€box gene affecting maize tassel branch number by a dominant model. Plant Biotechnology Journal, 2021, 19, 1183-1194.	4.1	14
402	Brief Insight into the Evolutionary History and Domestication of Wild Rice Relatives. , 2021, , 71-88.		0
403	Applications of CRISPR/Cas Beyond Simple Traits in Crops. , 2021, , 231-260.		0
404	Translating insights from the seed metabolome into improved prediction for lipid-composition traits in oat (<i>Avena sativa</i> L.). Genetics, 2021, 217, .	1.2	17
407	Structural variation at the maize WUSCHEL1 locus alters stem cell organization in inflorescences. Nature Communications, 2021, 12, 2378.	5.8	28
408	Systematic Identification, Evolution and Expression Analysis of the SPL Gene Family in Sugarcane (Saccharum spontaneum). Tropical Plant Biology, 2021, 14, 313.	1.0	7
409	DWARF53 interacts with transcription factors UB2/UB3/TSH4 to regulate maize tillering and tassel branching. Plant Physiology, 2021, 187, 947-962.	2.3	18
410	Integrating Omics and Gene Editing Tools for Rapid Improvement of Traditional Food Plants for Diversified and Sustainable Food Security. International Journal of Molecular Sciences, 2021, 22, 8093.	1.8	33
411	Identification and Expression Analysis of the SBP-box Gene Family Related to Abiotic Stress in Tea Plant (Camellia sinensis (L.) O. Kuntze). Plant Molecular Biology Reporter, 0, , 1.	1.0	3
412	Plasticity of root anatomy during domestication of a maize-teosinte derived population. Journal of Experimental Botany, 2022, 73, 139-153.	2.4	11
413	Wild Progenitor and Landraces Led Genetic Gain in the Modern-Day Maize (Zea mays L.). , 0, , .		3

#	Article	IF	CITATIONS
414	The Worldwide Gene Pool of G. hirsutum and its Improvement. , 2009, , 23-52.		27
415	Genomics of Tropical Maize, a Staple Food and Feed across the World. , 2008, , 333-370.		4
416	QTL for Agronomic Traits in Maize Production. , 2009, , 501-541.		28
417	Genomics of Long- and Short-Term Adaptation in Maize and Teosintes. Methods in Molecular Biology, 2020, 2090, 289-311.	0.4	9
418	Grass Flower Development. Methods in Molecular Biology, 2014, 1110, 57-84.	0.4	39
419	Fine mapping and gene cloning in the post-NGS era: advances and prospects. Theoretical and Applied Genetics, 2020, 133, 1791-1810.	1.8	94
420	Maize in the Americas. , 2006, , 9-20.		3
421	Origin of Polystichy in Maize. , 2006, , 21-53.		5
422	El Riego and Early Maize Agricultural Evolution. , 2006, , 73-82.		7
423	Early Maize on the Copacabana Peninsula. , 2006, , 415-428.		3
425	Imperial botany and the early scientific breeders. , 2007, , 247-260.		2
430	MaizeGDB: The Maize Model Organism Database for Basic, Translational, and Applied Research. International Journal of Plant Genomics, 2008, 2008, 1-10.	2.2	95
432	Transcription Factors, Gene Regulatory Networks and Agronomic Traits. Advances in Agroecology, 2011, , 65-94.	0.3	1
433	Investigations into Phytoliths as Diagnostic Markers for the Grasses (Poaceae) of Punjab. Universal Journal of Plant Science, 2014, 2, 107-122.	0.3	10
434	Independent introductions and admixtures have contributed to adaptation of European maize and its American counterparts. PLoS Genetics, 2017, 13, e1006666.	1.5	73
435	Deep Sequencing of Maize Small RNAs Reveals a Diverse Set of MicroRNA in Dry and Imbibed Seeds. PLoS ONE, 2013, 8, e55107.	1.1	73
436	Whole-Genome Analysis Revealed the Positively Selected Genes during the Differentiation of indica and Temperate japonica Rice. PLoS ONE, 2015, 10, e0119239.	1.1	15
437	The potential role of genetic assimilation during maize domestication. PLoS ONE, 2017, 12, e0184202.	1.1	17

#	Article	IF	CITATIONS
438	TeoNAM: A Nested Association Mapping Population for Domestication and Agronomic Trait Analysis in Maize. Genetics, 2019, 213, 1065-1078.	1.2	42
439	Growth response of maize plantlets inoculated with Enterobacter spp., as a model for alternative agriculture. Revista Argentina De Microbiologia, 2011, 43, 287-93.	0.4	17
441	Association Analysis and Its Application in Plant Genetic Research. Chinese Bulletin of Botany, 2011, 46, 108-118.	0.0	9
442	Genetic, evolutionary and plant breeding insights from the domestication of maize. ELife, 2015, 4, .	2.8	81
443	Revealing the genetic diversity of teosinte introgressed maize population by morphometric traits and microsatellite markers. Journal of Plant Biochemistry and Biotechnology, 2022, 31, 720-738.	0.9	1
444	Beyond the Cereal Box: Breeding Buckwheat as a Strategic Crop for Human Nutrition. Plant Foods for Human Nutrition, 2021, 76, 399-409.	1.4	6
445	Selective sorting of ancestral introgression in maize and teosinte along an elevational cline. PLoS Genetics, 2021, 17, e1009810.	1.5	50
446	Crop management in the classical and medieval periods. , 2007, , 221-233.		0
447	Fluid genomes, uncertain species, and the genetics of crop domestication. , 2007, , 65-77.		0
448	Agriculture: a mixed blessing. , 2007, , 124-136.		0
449	Evolution of agrourban cultures: III Africa, Europe, and the Americas. , 2007, , 189-218.		0
450	The domestication of cereal crops. , 2007, , 78-95.		1
451	Plant management and agriculture. , 2007, , 20-35.		0
452	People and the emergence of crops. , 2007, , 109-123.		0
453	The domestication of non-cereal crops. , 2007, , 96-106.		0
454	Evolution of agrourban cultures: II South and east Asia. , 2007, , 174-188.		0
455	Agricultural improvement and the rise of crop breeding. , 2007, , 234-246.		0
456	Plant genomes. , 2007, , 55-64.		0

#	Article	IF	CITATIONS
457	Evolution of agrourban cultures: I The Near East. , 2007, , 137-173.		0
458	The future of agriculture and humanity. , 2007, , 279-287.		0
459	Early human societies and their plants. , 2007, , 3-19.		0
460	Genetic mechanisms controlling branching pattern in rice. Plant Morphology, 2008, 19and20, 29-37.	0.1	0
462	An Overview of Advances in Plant Genomics in the New Millennium. , 2010, , 1-23.		0
463	Gene Expression and Selection of Major Genes. , 2016, , 133-159.		0
464	Toward the Rapid Domestication of Perennial Grains: Developing Genetic and Genomic Resources for Intermediate Wheatgrass. , 2016, , 227-241.		0
477	Gene network simulations provide testable predictions for the molecular domestication syndrome. Genetics, 2022, 220, .	1.2	8
478	Genetic dissection of maize plant architecture using a novel nested association mapping population. Plant Genome, 2022, 15, e20179.	1.6	5
479	Combining QTL-seq and linkage mapping to uncover the genetic basis of single vs. paired spikelets in the advanced populations of two-ranked maize×teosinte. BMC Plant Biology, 2021, 21, 572.	1.6	5
481	Genomic footprints of sorghum domestication and breeding selection for multiple end uses. Molecular Plant, 2022, 15, 537-551.	3.9	15
482	The Impact of Fasciation on Maize Inflorescence Architecture. Journal of Plant Biology, 2022, 65, 87-98.	0.9	6
484	Back to the wild: mining maize (Zea mays L.) disease resistance using advanced breeding tools. Molecular Biology Reports, 2022, 49, 5787-5803.	1.0	8
485	Identification of a major QTL and genome-wide epistatic interactions for single vs. paired spikelets in a maize-teosinte F2 population. Molecular Breeding, 2022, 42, 1.	1.0	1
486	Population genomics of Zea species identifies selection signatures during maize domestication and adaptation. BMC Plant Biology, 2022, 22, 72.	1.6	9
487	Expanding Gene-Editing Potential in Crop Improvement with Pangenomes. International Journal of Molecular Sciences, 2022, 23, 2276.	1.8	12
488	Natural variation in Glume Coverage 1 causes naked grains in sorghum. Nature Communications, 2022, 13, 1068.	5.8	15
489	Convergent selection of a WD40 protein that enhances grain yield in maize and rice. Science, 2022, 375, eabg7985	6.0	110

#	Article	IF	CITATIONS
490	The power of classic maize mutants: Driving forward our fundamental understanding of plants. Plant Cell, 2022, 34, 2505-2517.	3.1	10
491	Transposon Insertion Drove the Loss of Natural Seed Shattering during Foxtail Millet Domestication. Molecular Biology and Evolution, 2022, 39, .	3.5	8
510	Maize Breeding. , 2022, , 221-258.		4
511	A natural mutation of the <i>NST1</i> gene arrests secondary cell wall biosynthesis in the seed coat of a hull-less pumpkin accession. Horticulture Research, 2022, 9, .	2.9	10
512	Molecular Approaches in Conservation and Restoration of Agrobiodiversity. , 2022, , 169-216.		1
513	<scp>Rhizosphere</scp> <scp>bacterial communities differ among traditional maize landraces</scp> . Environmental DNA, 2022, 4, 1241-1249.	3.1	5
514	Molecular genetic variation of animals and plants under domestication. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	19
522	From Evolution to Revolution: Accelerating Crop Domestication through Genome Editing. Plant and Cell Physiology, 2022, 63, 1607-1623.	1.5	7
523	Fine mapping of candidate quantitative trait loci for plant and ear height in a maize nested-association mapping population. Frontiers in Plant Science, 0, 13, .	1.7	5
524	Genome-Wide Identification and Characterization of SPL Family Genes in Chenopodium quinoa. Genes, 2022, 13, 1455.	1.0	6
525	Management and Utilization of Plant Genetic Resources for a Sustainable Agriculture. Plants, 2022, 11, 2038.	1.6	31
526	The Use of CRISPR Technologies for Crop Improvement in Maize. , 2022, , 271-294.		2
527	2Gs and plant architecture: breaking grain yield ceiling through breeding approaches for next wave of revolution in rice (<i>Oryza sativa</i> L.). Critical Reviews in Biotechnology, 2024, 44, 139-162.	5.1	16
528	Natural variations of ZmSRO1d modulate the trade-off between drought resistance and yield by affecting ZmRBOHC-mediated stomatal ROS production in maize. Molecular Plant, 2022, 15, 1558-1574.	3.9	26
529	Identification and dynamic expression analysis of microRNAs associated with multi-tepal formation in Magnolia polytepala. Tree Genetics and Genomes, 2022, 18, .	0.6	0
530	Conflict over fertilization underlies the transient evolution of reinforcement. PLoS Biology, 2022, 20, e3001814.	2.6	5
531	<scp>CRISPR</scp> â€induced <scp>miRNA156</scp> â€recognition element mutations in <i>TaSPL13</i> improve multiple agronomic traits in wheat. Plant Biotechnology Journal, 2023, 21, 536-548.	4.1	25
532	Impacts of the Green Revolution on Rhizosphere Microbiology Related to Nutrient Acquisition. Applied Microbiology, 2022, 2, 992-1003.	0.7	4

#	Article	IF	CITATIONS
533	Interspecies transfer of <i>RAMOSA1</i> orthologs and promoter <i>cis</i> sequences impacts maize inflorescence architecture. Plant Physiology, 0, , .	2.3	0
534	Maize domestication phenotypes reveal strigolactone networks coordinating grain size evolution with kernel-bearing cupule architecture. Plant Cell, 2023, 35, 1013-1037.	3.1	8
535	Genetic basis of maize kernel protein content revealed by high-density bin mapping using recombinant inbred lines. Frontiers in Plant Science, 0, 13, .	1.7	2
536	Improved Evaluation of Cultivation Performance for Maize Based on Group Decision Method of Data Envelopment Analysis Model. Applied Sciences (Switzerland), 2023, 13, 521.	1.3	1
537	Identification of the egusi seed trait locus (eg) and its suppressor gene associated with the thin seed coat trait in watermelon. Frontiers in Plant Science, 0, 14, .	1.7	1
538	Genetic dissection of monosaccharides contents in rice whole grain using genomeâ€wide association study. Plant Genome, 2023, 16, .	1.6	2
539	Grasses. , 2012, , 140-322.		0
540	Accelerating crop domestication through genome editing for sustainable agriculture. Journal of Plant Biochemistry and Biotechnology, 2023, 32, 688-704.	0.9	3
541	Novel Deletion in Exon 7 of Betaine Aldehyde Dehydrogenase 2 (BADH2). Rice Science, 2023, 30, 104-112.	1.7	3
543	Novel insights into maize (Zea mays) development and organogenesis for agricultural optimization. Planta, 2023, 257, .	1.6	1
551	Population Genomics of Maize. Population Genomics, 2022, , .	0.2	1