

Stepwise cis-Regulatory Changes in ZCN8 Contribute to

Current Biology

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Plant Genetics: Two Steps on the Path to Maize Adaptation. <i>Current Biology</i> , 2018, 28, R1098-R1101.	1.8	1
2	A key variant in the cis-regulatory element of flowering gene <i>Ghd8</i> associated with cold tolerance in rice. <i>Scientific Reports</i> , 2019, 9, 9603.	1.6	16
3	Revolutions in agriculture chart a course for targeted breeding of old and new crops. <i>Science</i> , 2019, 366, .	6.0	197
4	Evolutionary Metabolomics Identifies Substantial Metabolic Divergence between Maize and Its Wild Ancestor, Teosinte. <i>Plant Cell</i> , 2019, 31, 1990-2009.	3.1	69
5	Large-scale metabolite quantitative trait locus analysis provides new insights for high-quality maize improvement. <i>Plant Journal</i> , 2019, 99, 216-230.	2.8	37
6	Over-expression of the photoperiod response regulator <i>ZmCCT10</i> modifies plant architecture, flowering time and inflorescence morphology in maize. <i>PLoS ONE</i> , 2019, 14, e0203728.	1.1	30
7	The Genomic Basis for Short-Term Evolution of Environmental Adaptation in Maize. <i>Genetics</i> , 2019, 213, 1479-1494.	1.2	23
8	<i>ZmMADS69</i> functions as a flowering activator through the <i>ZmRap2.7-ZCN8</i> regulatory module and contributes to maize flowering time adaptation. <i>New Phytologist</i> , 2019, 221, 2335-2347.	3.5	100
9	Evolutionary processes from the perspective of flowering time diversity. <i>New Phytologist</i> , 2020, 225, 1883-1898.	3.5	70
10	Genetic basis of kernel nutritional traits during maize domestication and improvement. <i>Plant Journal</i> , 2020, 101, 278-292.	2.8	25
11	Adaptive introgression from maize has facilitated the establishment of teosinte as a noxious weed in Europe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 25618-25627.	3.3	54
12	Interaction Between Induced and Natural Variation at <i>oil yellow1</i> Delays Reproductive Maturity in Maize. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 797-810.	0.8	3
13	Maize adaptation across temperate climates was obtained via expression of two florigen genes. <i>PLoS Genetics</i> , 2020, 16, e1008882.	1.5	23
14	Stepwise selection on homeologous PRR genes controlling flowering and maturity during soybean domestication. <i>Nature Genetics</i> , 2020, 52, 428-436.	9.4	229
15	Disentangling group specific QTL allele effects from genetic background epistasis using admixed individuals in GWAS: An application to maize flowering. <i>PLoS Genetics</i> , 2020, 16, e1008241.	1.5	44
16	Make it bloom! <i>CONSTANS</i> contributes to day neutrality in rose. <i>Journal of Experimental Botany</i> , 2020, 71, 3923-3926.	2.4	4
17	<i>dlf1</i> promotes floral transition by directly activating <i>ZmMADS4</i> and <i>ZmMADS67</i> in the maize shoot apex. <i>New Phytologist</i> , 2020, 228, 1386-1400.	3.5	26
18	Adaptation to novel environments during crop diversification. <i>Current Opinion in Plant Biology</i> , 2020, 56, 203-217.	3.5	22

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19	High-Throughput CRISPR/Cas9 Mutagenesis Streamlines Trait Gene Identification in Maize. <i>Plant Cell</i> , 2020, 32, 1397-1413.	3.1	148
20	Phenotypic Plasticity Contributes to Maize Adaptation and Heterosis. <i>Molecular Biology and Evolution</i> , 2021, 38, 1262-1275.	3.5	32
21	Harnessing Knowledge from Maize and Rice Domestication for New Crop Breeding. <i>Molecular Plant</i> , 2021, 14, 9-26.	3.9	58
22	Mapping QTL for flowering time-related traits under three plant densities in maize. <i>Crop Journal</i> , 2021, 9, 372-379.	2.3	6
25	Joint analysis of days to flowering reveals independent temperate adaptations in maize. <i>Heredity</i> , 2021, 126, 929-941.	1.2	4
26	Molecular Parallelism Underlies Convergent Highland Adaptation of Maize Landraces. <i>Molecular Biology and Evolution</i> , 2021, 38, 3567-3580.	3.5	35
28	Ancient relaxation of an obligate short-day requirement in common bean through loss of CONSTANS-like gene function. <i>Current Biology</i> , 2021, 31, 1643-1652.e2.	1.8	11
29	Phosphorylation-mediated signalling in flowering: prospects and retrospects of phosphoproteomics in crops. <i>Biological Reviews</i> , 2021, 96, 2164-2191.	4.7	6
30	Forecasting rice latitude adaptation through a daylength-sensing-based environment adaptation simulator. <i>Nature Food</i> , 2021, 2, 348-362.	6.2	16
31	The genetic mechanism of heterosis utilization in maize improvement. <i>Genome Biology</i> , 2021, 22, 148.	3.8	69
32	Natural Variation in Crops: Realized Understanding, Continuing Promise. <i>Annual Review of Plant Biology</i> , 2021, 72, 357-385.	8.6	73
33	Natural variation and artificial selection of photoperiodic flowering genes and their applications in crop adaptation. <i>ABIOTECH</i> , 2021, 2, 156-169.	1.8	23
34	An integrated framework reinstating the environmental dimension for GWAS and genomic selection in crops. <i>Molecular Plant</i> , 2021, 14, 874-887.	3.9	56
36	Combined QTL mapping and association study reveals candidate genes for leaf number and flowering time in maize. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3459-3472.	1.8	7
37	Reinventing the wheel? Reassessing the roles of gene flow, sorting and convergence in repeated evolution. <i>Molecular Ecology</i> , 2021, 30, 4162-4172.	2.0	26
38	A natural single-nucleotide polymorphism variant in <i>sulfite reductase</i> influences sulfur assimilation in maize. <i>New Phytologist</i> , 2021, 232, 692-704.	3.5	2
39	A gene regulatory network for tiller development mediated by <i>Tin8</i> in maize. <i>Journal of Experimental Botany</i> , 2022, 73, 110-122.	2.4	1
40	Identification of <i>ZmNF-YC2</i> and its regulatory network for maize flowering time. <i>Journal of Experimental Botany</i> , 2021, 72, 7792-7807.	2.4	17

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42	Genomic basis underlying the metabolome-mediated drought adaptation of maize. <i>Genome Biology</i> , 2021, 22, 260.	3.8	44
43	Genetic basis and adaptation trajectory of soybean from its temperate origin to tropics. <i>Nature Communications</i> , 2021, 12, 5445.	5.8	64
45	TeoNAM: A Nested Association Mapping Population for Domestication and Agronomic Trait Analysis in Maize. <i>Genetics</i> , 2019, 213, 1065-1078.	1.2	42
46	ZmCCT regulates photoperiod-dependent flowering and response to stresses in maize. <i>BMC Plant Biology</i> , 2021, 21, 453.	1.6	19
47	The arches and spandrels of maize domestication, adaptation, and improvement. <i>Current Opinion in Plant Biology</i> , 2021, 64, 102124.	3.5	2
54	A Daylength Recognition Model of Photoperiodic Flowering. <i>Frontiers in Plant Science</i> , 2021, 12, 778515.	1.7	12
55	Genome Assembly of Alfalfa Cultivar Zhongmu-4 and Identification of SNPs Associated with Agronomic Traits. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 14-28.	3.0	26
56	Modeling allelic diversity of multiparent mapping populations affects detection of quantitative trait loci. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	4
57	A B73–Palomero Toluque mapping population reveals local adaptation in Mexican highland maize. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	11
59	Photoperiod Control of Plant Growth: Flowering Time Genes Beyond Flowering. <i>Frontiers in Plant Science</i> , 2021, 12, 805635.	1.7	38
60	A Heterochromatic Knob Reducing the Flowering Time in Maize. <i>Frontiers in Genetics</i> , 2021, 12, 799681.	1.1	0
61	Population genomics of <i>Zea</i> species identifies selection signatures during maize domestication and adaptation. <i>BMC Plant Biology</i> , 2022, 22, 72.	1.6	9
63	Plant clock modifications for adapting flowering time to local environments. <i>Plant Physiology</i> , 2022, 190, 952-967.	2.3	17
64	A functionally divergent SOC1 homolog improves soybean yield and latitudinal adaptation. <i>Current Biology</i> , 2022, 32, 1728-1742.e6.	1.8	46
65	The genetic architecture of flowering time changes in pea from wild to crop. <i>Journal of Experimental Botany</i> , 2022, 73, 3978-3990.	2.4	7
66	The vegetable SNP database: An integrated resource for plant breeders and scientists. <i>Genomics</i> , 2022, 114, 110348.	1.3	3
67	Genetic mapping and prediction of flowering time and plant height in a maize Stiff Stalk MAGIC population. <i>Genetics</i> , 2022, 221, .	1.2	5
68	Putting the pea in photoPEAriod. <i>Journal of Experimental Botany</i> , 2022, 73, 3825-3827.	2.4	2

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69	Flowering time: Soybean adapts to the tropics. <i>Current Biology</i> , 2022, 32, R360-R362.	1.8	0
70	Photoperiod-Dependent Mechanisms of Flowering Initiation in <i>Arabidopsis thaliana</i> L. and <i>Zea mays</i> L. <i>Russian Journal of Plant Physiology</i> , 2022, 69, 1.	0.5	0
71	Genome-Wide Association Studies Provide Insights Into the Genetic Architecture of Seed Germination Traits in Maize. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
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73	De Novo Domestication in the Multi-Omics Era. <i>Plant and Cell Physiology</i> , 0, , .	1.5	4
74	Linkage mapping combined with GWAS revealed the genetic structural relationship and candidate genes of maize flowering time-related traits. <i>BMC Plant Biology</i> , 2022, 22, .	1.6	6
76	SDG102, a H3K36-Methyltransferase-Encoding Gene, Plays Pleiotropic Roles in Growth and Development of Maize (<i>Zea mays</i> L.). <i>International Journal of Molecular Sciences</i> , 2022, 23, 7458.	1.8	2
77	A single nucleotide polymorphism in <i>WRKY33</i> promoter is associated with the cold sensitivity in cultivated tomato. <i>New Phytologist</i> , 2022, 236, 989-1005.	3.5	18
78	<i>cis</i> regulatory variation affecting gene expression contributes to the improvement of maize kernel size. <i>Plant Journal</i> , 0, , .	2.8	2
79	Advances in research and utilization of maize wild relatives. <i>Chinese Science Bulletin</i> , 2022, 67, 4370-4387.	0.4	1
80	Linkage Mapping Reveals QTL for Flowering Time-Related Traits under Multiple Abiotic Stress Conditions in Maize. <i>International Journal of Molecular Sciences</i> , 2022, 23, 8410.	1.8	8
81	A Pleiotropic Flowering Time QTL Exhibits Gene-by-Environment Interaction for Fitness in a Perennial Grass. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	2
82	The evening complex promotes maize flowering and adaptation to temperate regions. <i>Plant Cell</i> , 2023, 35, 369-389.	3.1	16
83	Dissecting the Regulatory Network of Maize Phase Change in <i>ZmEPC1</i> Mutant by Transcriptome Analysis. <i>Genes</i> , 2022, 13, 1713.	1.0	0
84	The genome of <i>Aechmea fasciata</i> provides insights into the evolution of tank epiphytic habits and ethylene-induced flowering. <i>Communications Biology</i> , 2022, 5, .	2.0	4
85	Gradual daylength sensing coupled with optimum cropping modes enhances multi-latitude adaptation of rice and maize. <i>Plant Communications</i> , 2023, 4, 100433.	3.6	5
86	The role of transposon inverted repeats in balancing drought tolerance and yield-related traits in maize. <i>Nature Biotechnology</i> , 2023, 41, 120-127.	9.4	22
88	Temperature-mediated flower size plasticity in <i>Arabidopsis</i> . <i>IScience</i> , 2022, 25, 105411.	1.9	6

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89	Allele-specific expression reveals multiple paths to highland adaptation in maize. <i>Molecular Biology and Evolution</i> , 0, , .	3.5	2
90	On the role of transposons in balancing drought tolerance and yield. <i>Trends in Plant Science</i> , 2022, , .	4.3	0
91	Leaves and stolons transcriptomic analysis provide insight into the role of <i>phytochrome F</i> in potato flowering and tuberization. <i>Plant Journal</i> , 2023, 113, 402-415.	2.8	4
92	De novo genome assembly and analyses of 12 founder inbred lines provide insights into maize heterosis. <i>Nature Genetics</i> , 2023, 55, 312-323.	9.4	29
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95	A common resequencing-based genetic marker data set for global maize diversity. <i>Plant Journal</i> , 2023, 113, 1109-1121.	2.8	10
97	Photoperiod Genes Contribute to Daylength-Sensing and Breeding in Rice. <i>Plants</i> , 2023, 12, 899.	1.6	1
98	Natural variation of <i>FKF1</i> controls flowering and adaptation during soybean domestication and improvement. <i>New Phytologist</i> , 2023, 238, 1671-1684.	3.5	7
99	The Allele Catalog Tool: a web-based interactive tool for allele discovery and analysis. <i>BMC Genomics</i> , 2023, 24, .	1.2	3
100	Embracing diversity: a genetic marker dataset with increased marker density facilitates association studies in maize. <i>Plant Journal</i> , 2023, 113, 1107-1108.	2.8	0
101	Diurnal transcriptome dynamics reveal the photoperiod response of <i>Pyrus</i> . <i>Physiologia Plantarum</i> , 2023, 175, .	2.6	0
102	Integration of GWAS, linkage analysis and transcriptome analysis to reveal the genetic basis of flowering time-related traits in maize. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	2
103	Divergent selection of <i>KNR6</i> maximizes grain production by balancing the flowering-time adaptation and ear size in maize. <i>Plant Biotechnology Journal</i> , 0, , .	4.1	2