

Pan-Genome of Wild and Cultivated Soybeans

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Soybean DICER-LIKE2 Regulates Seed Coat Color via Production of Primary 22-Nucleotide Small Interfering RNAs from Long Inverted Repeats. <i>Plant Cell</i> , 2020, 32, 3662-3673.	3.1	35
2	A Collinearity-Incorporating Homology Inference Strategy for Connecting Emerging Assemblies in the Triticeae Tribe as a Pilot Practice in the Plant Pangenomic Era. <i>Molecular Plant</i> , 2020, 13, 1694-1708.	3.9	126
3	A Graph-Based Pan-Genome Guides Biological Discovery. <i>Molecular Plant</i> , 2020, 13, 1247-1249.	3.9	10
4	The lowest hanging fruit: Beneficial gene knockouts in past, present, and future crop evolution. <i>Current Plant Biology</i> , 2020, 24, 100185.	2.3	11
5	Review: Proteomic Techniques for the Development of Flood-Tolerant Soybean. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7497.	1.8	12
6	Advanced Strategic Research to Promote the Use of Rice Genetic Resources. <i>Agronomy</i> , 2020, 10, 1629.	1.3	7
7	The Modification of Circadian Clock Components in Soybean During Domestication and Improvement. <i>Frontiers in Genetics</i> , 2020, 11, 571188.	1.1	19
8	Breeding and biotechnological interventions for trait improvement: status and prospects. <i>Planta</i> , 2020, 252, 54.	1.6	48
9	Mutation Mechanism of Leaf Color in Plants: A Review. <i>Forests</i> , 2020, 11, 851.	0.9	60
10	From one linear genome to a graph-based pan-genome: a new era for genomics. <i>Science China Life Sciences</i> , 2020, 63, 1938-1941.	2.3	14
11	Chromosome-Scale Assembly of the Bread Wheat Genome Reveals Thousands of Additional Gene Copies. <i>Genetics</i> , 2020, 216, 599-608.	1.2	34
12	CRISPR-Cas9-mediated 75.5-Mb inversion in maize. <i>Nature Plants</i> , 2020, 6, 1427-1431.	4.7	67
13	Resolving the roles of structural variants. <i>Nature Reviews Genetics</i> , 2020, 21, 507-507.	7.7	4
14	Designing future crops: challenges and strategies for sustainable agriculture. <i>Plant Journal</i> , 2021, 105, 1165-1178.	2.8	110
15	A new decade and new data at SoyBase, the USDA-ARS soybean genetics and genomics database. <i>Nucleic Acids Research</i> , 2021, 49, D1496-D1501.	6.5	49
16	Recent advances in <i>Cannabis sativa</i> genomics research. <i>New Phytologist</i> , 2021, 230, 73-89.	3.5	66
17	Integrating multi-omics data for crop improvement. <i>Journal of Plant Physiology</i> , 2021, 257, 153352.	1.6	78
18	The changing face of genome assemblies: Guidance on achieving high-quality reference genomes. <i>Molecular Ecology Resources</i> , 2021, 21, 641-652.	2.2	44

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20	An expedient survey and characterization of the soybean JAGGED 1 (GmJAG1) transcription factor binding preference in the soybean genome by modified ChIPmentation on soybean protoplasts. <i>Genomics</i> , 2021, 113, 344-355.	1.3	5
21	Overview and Application of Soybean Genomics Study. , 2021, , 37-51.		0
22	Genome structure variation analyses of peach reveal population dynamics and a 1.67â€‰Mb causal inversion for fruit shape. <i>Genome Biology</i> , 2021, 22, 13.	3.8	50
23	How the pan-genome is changing crop genomics and improvement. <i>Genome Biology</i> , 2021, 22, 3.	3.8	142
24	Mapping quantitative trait loci related to nodule number in soybean (<i>Glycine max</i> (L.) Merr.) in response to the <i>Sinorhizobium</i> (Ensifer) <i>fredii</i> HH103 NopT type III effector. <i>Journal of Plant Interactions</i> , 2021, 16, 126-135.	1.0	10
25	Chromosome-level & de novo genome assemblies of over 100 plant species. <i>Breeding Science</i> , 2021, 71, 117-124.	0.9	19
26	The patterns of deleterious mutations during the domestication of soybean. <i>Nature Communications</i> , 2021, 12, 97.	5.8	49
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29	Genomic resources in plant breeding for sustainable agriculture. <i>Journal of Plant Physiology</i> , 2021, 257, 153351.	1.6	90
30	Plant NLR diversity: the known unknowns of pan-NLRomes. <i>Plant Cell</i> , 2021, 33, 814-831.	3.1	99
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42	Crop breeding for a changing climate: integrating phenomics and genomics with bioinformatics. <i>Theoretical and Applied Genetics</i> , 2021, 134, 1677-1690.	1.8	38
43	Cotranscriptional and Posttranscriptional Features of the Transcriptome in Soybean Shoot Apex and Leaf. <i>Frontiers in Plant Science</i> , 2021, 12, 649634.	1.7	6
44	Dissecting cis-regulatory control of quantitative trait variation in a plant stem cell circuit. <i>Nature Plants</i> , 2021, 7, 419-427.	4.7	72
45	The Synchronized Efforts to Decipher the Molecular Basis for Soybean Maturity Loci E1, E2, and E3 That Regulate Flowering and Maturity. <i>Frontiers in Plant Science</i> , 2021, 12, 632754.	1.7	9
46	Abiotic stress through time. <i>New Phytologist</i> , 2021, 231, 40-46.	3.5	34
47	Balancing selection maintains hyper-divergent haplotypes in <i>Caenorhabditis elegans</i> . <i>Nature Ecology and Evolution</i> , 2021, 5, 794-807.	3.4	89
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50	Genome sequencing sheds light on the contribution of structural variants to <i>Brassica oleracea</i> diversification. <i>BMC Biology</i> , 2021, 19, 93.	1.7	41
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55	Recent innovations of ultrasound green technology in herbal phytochemistry: A review. <i>Ultrasonics Sonochemistry</i> , 2021, 73, 105538.	3.8	62
56	Systems biology for crop improvement. <i>Plant Genome</i> , 2021, 14, e20098.	1.6	48
57	Towards population-scale long-read sequencing. <i>Nature Reviews Genetics</i> , 2021, 22, 572-587.	7.7	163
58	Plant Pan-Genomics Comes of Age. <i>Annual Review of Plant Biology</i> , 2021, 72, 411-435.	8.6	56

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60	Pan-genome analysis of 33 genetically diverse rice accessions reveals hidden genomic variations. <i>Cell</i> , 2021, 184, 3542-3558.e16.	13.5	237
61	Designing Future Crops: Genomics-Assisted Breeding Comes of Age. <i>Trends in Plant Science</i> , 2021, 26, 631-649.	4.3	244
62	Natural Variation in Crops: Realized Understanding, Continuing Promise. <i>Annual Review of Plant Biology</i> , 2021, 72, 357-385.	8.6	73
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66	<i>Oryza</i> pan-genomics: A new foundation for future rice research and improvement. <i>Crop Journal</i> , 2021, 9, 622-632.	2.3	7
67	Transposable Elements Contribute to Genome Dynamics and Gene Expression Variation in the Fungal Plant Pathogen <i>Verticillium dahliae</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	26
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69	The pan-genome of the cultivated soybean (PanSoy) reveals an extraordinarily conserved gene content. <i>Plant Biotechnology Journal</i> , 2021, 19, 1852-1862.	4.1	41
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72	Creation and judicious application of a wheat resistance gene atlas. <i>Molecular Plant</i> , 2021, 14, 1053-1070.	3.9	66
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79	Eight soybean reference genome resources from varying latitudes and agronomic traits. <i>Scientific Data</i> , 2021, 8, 164.	2.4	13
80	Restructuring plant types for developing tailor-made crops. <i>Plant Biotechnology Journal</i> , 2023, 21, 1106-1122.	4.1	10
82	<i>Amborella</i> gene presence/absence variation is associated with abiotic stress responses that may contribute to environmental adaptation. <i>New Phytologist</i> , 2022, 233, 1548-1555.	3.5	16
83	Genomic structural variants constrain and facilitate adaptation in natural populations of <i>Theobroma cacao</i> , the chocolate tree. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	50
84	Gradual evolution of allopolyploidy in <i>Arabidopsis suecica</i> . <i>Nature Ecology and Evolution</i> , 2021, 5, 1367-1381.	3.4	64
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88	Megabase-scale presence-absence variation with <i>Tripsacum</i> origin was under selection during maize domestication and adaptation. <i>Genome Biology</i> , 2021, 22, 237.	3.8	21
89	Modelling of gene loss propensity in the pangenomes of three <i>Brassica</i> species suggests different mechanisms between polyploids and diploids. <i>Plant Biotechnology Journal</i> , 2021, 19, 2488-2500.	4.1	44
90	Pan-genome of <i>Raphanus</i> highlights genetic variation and introgression among domesticated, wild, and weedy radishes. <i>Molecular Plant</i> , 2021, 14, 2032-2055.	3.9	56
91	How noncoding open chromatin regions shape soybean domestication. <i>Trends in Plant Science</i> , 2021, 26, 876-878.	4.3	1
93	Boosting the power of transcriptomics by developing an efficient gene expression profiling approach. <i>Plant Biotechnology Journal</i> , 2021, , .	4.1	2
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96	De-novo Domestication for Improving Salt Tolerance in Crops. <i>Frontiers in Plant Science</i> , 2021, 12, 681367.	1.7	19
97	Genome-wide identification of ascorbate-glutathione cycle gene families in soybean (<i>Glycine max</i>) reveals gene duplication events and specificity of gene members linked to development and stress conditions. <i>International Journal of Biological Macromolecules</i> , 2021, 187, 528-543.	3.6	12
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114	Genome-wide analysis of deletions in maize population reveals abundant genetic diversity and functional impact. <i>Theoretical and Applied Genetics</i> , 2021, 135, 273.	1.8	4
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123	Genome-wide Identification and Evolutionary Analysis of NBS-LRR Genes From <i>Secale cereale</i> . <i>Frontiers in Genetics</i> , 2021, 12, 771814.	1.1	6
124	A giant NLR gene confers broad-spectrum resistance to <i>Phytophthora sojae</i> in soybean. <i>Nature Communications</i> , 2021, 12, 6263.	5.8	35
128	A donor-DNA-free CRISPR/Cas-based approach to gene knock-up in rice. <i>Nature Plants</i> , 2021, 7, 1445-1452.	4.7	44
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134	The Asian lotus (<i>Nelumbo nucifera</i>) pan-plastome: diversity and divergence in a living fossil grown for seed, rhizome, and aesthetics. <i>Ornamental Plant Research</i> , 2022, 2, 1-10.	0.2	3
135	Omics-based interdisciplinarity is accelerating plant breeding. <i>Current Opinion in Plant Biology</i> , 2022, 66, 102167.	3.5	26
136	Genome sequencing and population resequencing provide insights into the genetic basis of domestication and diversity of vegetable soybean. <i>Horticulture Research</i> , 2022, 9, .	2.9	10
138	Applications of CRISPR/Cas System in Plants. , 2022, , 285-309.		1
139	Phased, chromosome-scale genome assemblies of tetraploid potato reveal a complex genome, transcriptome, and predicted proteome landscape underpinning genetic diversity. <i>Molecular Plant</i> , 2022, 15, 520-536.	3.9	72
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141	QTL mapping and genomic analyses of earliness and fruit ripening traits in a melon recombinant inbred lines population supported by <i>de novo</i> assembly of their parental genomes. <i>Horticulture Research</i> , 2022, 9, .	2.9	12
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145	Improvement of Soybean; A Way Forward Transition from Genetic Engineering to New Plant Breeding Technologies. <i>Molecular Biotechnology</i> , 2023, 65, 162-180.	1.3	24

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147	Putative variants, genetic diversity and population structure among Soybean cultivars bred at different ages in Huang-Huai-Hai region. <i>Scientific Reports</i> , 2022, 12, 2372.	1.6	1
148	Haplotype mapping uncovers unexplored variation in wild and domesticated soybean at the major protein locus <i>cqProt-003</i> . <i>Theoretical and Applied Genetics</i> , 2022, 135, 1443-1455.	1.8	13
149	Graph-based pan-genome reveals structural and sequence variations related to agronomic traits and domestication in cucumber. <i>Nature Communications</i> , 2022, 13, 682.	5.8	59
153	Understanding carotenoid biosynthetic pathway control points using metabolomic analysis and natural genetic variation. <i>Methods in Enzymology</i> , 2022, , .	0.4	0
154	Genomic research on soybean and its impact on molecular breeding. <i>Advances in Botanical Research</i> , 2022, , .	0.5	2
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158	Pangenomes as a Resource to Accelerate Breeding of Under-Utilised Crop Species. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2671.	1.8	14
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161	Combined use of Oxford Nanopore and Illumina sequencing yields insights into soybean structural variation biology. <i>BMC Biology</i> , 2022, 20, 53.	1.7	10
162	Transposable element insertion: a hidden major source of domesticated phenotypic variation in <i>Brassica rapa</i> . <i>Plant Biotechnology Journal</i> , 2022, 20, 1298-1310.	4.1	29
163	Development of a versatile resource for post-genomic research through consolidating and characterizing 1500 diverse wild and cultivated soybean genomes. <i>BMC Genomics</i> , 2022, 23, 250.	1.2	11
164	Using the Knowledge of Post-transcriptional Regulations to Guide Gene Selections for Molecular Breeding in Soybean. <i>Frontiers in Plant Science</i> , 2022, 13, 867731.	1.7	0
165	SoySNP618K array: A high-resolution single nucleotide polymorphism platform as a valuable genomic resource for soybean genetics and breeding. <i>Journal of Integrative Plant Biology</i> , 2022, 64, 632-648.	4.1	7
166	Identification of <i>ST1</i> reveals a selection involving hitchhiking of seed morphology and oil content during soybean domestication. <i>Plant Biotechnology Journal</i> , 2022, 20, 1110-1121.	4.1	33
167	Phylogenomics of the genus <i>Glycine</i> sheds light on polyploid evolution and life-strategy transition. <i>Nature Plants</i> , 2022, 8, 233-244.	4.7	26
169	Haplotype-resolved Chinese male genome assembly based on high-fidelity sequencing. <i>Fundamental Research</i> , 2022, 2, 946-953.	1.6	11

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171	Better together: Protein partnerships for lineage-specific oil accumulation. <i>Current Opinion in Plant Biology</i> , 2022, 66, 102191.	3.5	9
173	Hard vs. soft selective sweeps during domestication and improvement in soybean. <i>Molecular Ecology</i> , 2022, , .	2.0	4
174	Downregulation of a gibberellin 3 β -hydroxylase enhances photosynthesis and increases seed yield in soybean. <i>New Phytologist</i> , 2022, 235, 502-517.	3.5	26
175	Long-read sequencing of 111 rice genomes reveals significantly larger pan-genomes. <i>Genome Research</i> , 2022, , .	2.4	21
177	Mapping of partial resistance to <i>Phytophthora sojae</i> in soybean PIs using whole-genome sequencing reveals a major QTL. <i>Plant Genome</i> , 2022, 15, e20184.	1.6	11
178	Pangenomics in crop improvement—from coding structural variations to finding regulatory variants with pangenome graphs. <i>Plant Genome</i> , 2022, 15, e20177.	1.6	33
179	Daisychain: Search and Interactive Visualisation of Homologs in Genome Assemblies. <i>Agronomy</i> , 2021, 11, 2587.	1.3	0
180	USE OF SEQUENCING METHODS FOR SPECIES IDENTIFICATION EXEMPLIFIED BY PHYLOGENETIC RELATIONSHIPS WITHIN GENUS HEDYSARUM L.. <i>Farmatsiya I Farmakologiya</i> , 2021, 9, 506-518.	0.2	0
181	Identification of an ATP-Binding Cassette Transporter Implicated in Aluminum Tolerance in Wild Soybean (<i>Glycine soja</i>). <i>International Journal of Molecular Sciences</i> , 2021, 22, 13264.	1.8	7
182	Genome-Wide Identification and Characterization of Caffeic Acid O-Methyltransferase Gene Family in Soybean. <i>Plants</i> , 2021, 10, 2816.	1.6	13
183	Intraspecific <i>de novo</i> gene birth revealed by presence-absence variant genes in <i>Caenorhabditis elegans</i> . <i>NAR Genomics and Bioinformatics</i> , 2022, 4, lqac031.	1.5	7
184	Population-scale long-read sequencing uncovers transposable elements associated with gene expression variation and adaptive signatures in <i>Drosophila</i> . <i>Nature Communications</i> , 2022, 13, 1948.	5.8	53
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