

# Genomic insights into the origin, domestication and div

Nature Genetics

53, 1392-1402

DOI: [10.1038/s41588-021-00922-y](https://doi.org/10.1038/s41588-021-00922-y)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Oil plant genomes: current state of the science. <i>Journal of Experimental Botany</i> , 2022, 73, 2859-2874.	4.8	16
2	Brassica juncea Genome Assembliesâ€™ Characteristics and Utilization. <i>Compendium of Plant Genomes</i> , 2022, , 241-255.	0.5	0
5	Comparative Analysis of Seed Transcriptome and Coexpression Analysis Reveal Candidate Genes for Enhancing Seed Size/Weight in Brassica juncea. <i>Frontiers in Genetics</i> , 2022, 13, 814486.	2.3	6
6	Genetic origin and expression patterns of acetohydroxyacid synthase multigene family in <i>Brassica juncea</i> and <i>B. carinata</i> and their progenitors. <i>Physiologia Plantarum</i> , 2022, 174, e13669.	5.2	0
7	Assembly and marker analysis of mitochondrial genomes provide insights into origin, evolution and spread of Brassica juncea (L.) Czern. et Coss.. <i>Crop Journal</i> , 2021, , .	5.2	1
8	Genome-Wide Identification, Characterization, and Expression Profiling Analysis of SPL Gene Family during the Inflorescence Development in <i>Trifolium repens</i> . <i>Genes</i> , 2022, 13, 900.	2.4	4
9	Understanding R Gene Evolution in Brassica. <i>Agronomy</i> , 2022, 12, 1591.	3.0	0
11	Genetic diversity and population structure of the USDA collection of Brassica juncea L.. <i>Industrial Crops and Products</i> , 2022, 187, 115379.	5.2	6
12	Diversity of glucosinolates among common Brassicaceae vegetables in China. <i>Horticultural Plant Journal</i> , 2023, 9, 365-380.	5.0	7
13	The final piece of the Triangle of U: Evolution of the tetraploid <i>Brassica carinata</i> genome. <i>Plant Cell</i> , 2022, 34, 4143-4172.	6.6	18
14	Investigation of <i>Brassica</i> and its relative genomes in the post-genomics era. <i>Horticulture Research</i> , 2022, 9, .	6.3	7
15	Selective Modes Affect Gene Feature of Brassica Species between Diploids and Polyploids. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
16	Quantitative trait loci mapping reveals important genomic regions controlling root architecture and shoot biomass under nitrogen, phosphorus, and potassium stress in rapeseed ( <i>Brassica napus</i> L.). <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	5
17	Genomic insights into the evolutionary history and diversification of bulb traits in garlic. <i>Genome Biology</i> , 2022, 23, .	8.8	6
18	Genomic insight into genetic changes and shaping of major inbred rice cultivars in China. <i>New Phytologist</i> , 0, , .	7.3	1
20	Key Advances in the New Era of Genomics-Assisted Disease Resistance Improvement of <i>Brassica</i> Species. <i>Phytopathology</i> , 2023, 113, 771-785.	2.2	3
21	Conservation and Divergence of the Trihelix Genes in Brassica and Expression Profiles of BnaTH Genes in Brassica napus under Abiotic Stresses. <i>International Journal of Molecular Sciences</i> , 2022, 23, 15766.	4.1	7
22	Multi-omics revolution to promote plant breeding efficiency. <i>Frontiers in Plant Science</i> , 0, 13, .	3.6	10

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23	Genetic Diversity and Population Structure Analysis of Barley Landraces from Shanghai Region Using Genotyping-by-Sequencing. <i>Phyton</i> , 2023, 92, 1275-1287.	0.7	0
24	A chromosome-level genome assembly of radish ( <i>Raphanus sativus</i> L.) reveals insights into genome adaptation and differential bolting regulation. <i>Plant Biotechnology Journal</i> , 2023, 21, 990-1004.	8.3	14
25	Exchanges of economic plants along the land silk road. <i>BMC Plant Biology</i> , 2022, 22, .	3.6	4
26	HDF1, a novel flowering time regulator identified in a mutant suppressing sensitivity to red light reduced 1 early flowering. <i>Scientific Reports</i> , 2023, 13, .	3.3	0
27	Genome-wide identification and expression analysis of the anthocyanin-related genes during seed coat development in six Brassica species. <i>BMC Genomics</i> , 2023, 24, .	2.8	3
28	Selective modes affect gene feature and function differentiation of tetraploid Brassica species in their evolution and domestication. <i>Frontiers in Plant Science</i> , 0, 14, .	3.6	2
29	Whole-Genome Resequencing Reveals the Genetic Diversity and Selection Signatures of the Brassica juncea from the Yunnan-Guizhou Plateau. <i>Agronomy</i> , 2023, 13, 1053.	3.0	1
30	A near-complete genome assembly of <i>Brassica rapa</i> provides new insights into the evolution of centromeres. <i>Plant Biotechnology Journal</i> , 2023, 21, 1022-1032.	8.3	19
31	Genome-Wide Analysis of MYB Transcription Factor Gene Superfamily Reveals BjPHL2a Involved in Modulating the Expression of BjCHI1 in Brassica juncea. <i>Plants</i> , 2023, 12, 1011.	3.5	0
32	Developing multifunctional crops by engineering Brassicaceae glucosinolate pathways. <i>Plant Communications</i> , 2023, 4, 100565.	7.7	7
33	Phytoremediation: Low input-based ecological approach for sustainable environment. <i>Applied Water Science</i> , 2023, 13, .	5.6	9
34	Floral Pollen Bioactive Properties and Their Synergy in Honeybee Pollen. <i>Chemistry and Biodiversity</i> , 2023, 20, .	2.1	0
37	Genetic Diversity in Oilseed and Vegetable Mustard ( <i>Brassica juncea</i> L.) Accessions Revealed by Nuclear and Mitochondrial Molecular Markers. <i>Agronomy</i> , 2023, 13, 919.	3.0	2
38	Genetic mapping of some key plant architecture traits in Brassica juncea using a doubled haploid population derived from a cross between two distinct lines: vegetable type Tumida and oleiferous Varuna. <i>Theoretical and Applied Genetics</i> , 2023, 136, .	3.6	0
40	Xanthophyll esterases in association with fibrillins control the stable storage of carotenoids in yellow flowers of rapeseed ( <i>Brassica juncea</i> ). <i>New Phytologist</i> , 2023, 240, 285-301.	7.3	8
41	Differentiation and decreased genetic diversity in field contaminated oysters <i>Crassostrea hongkongensis</i> : Identification of selection signatures. <i>Environmental Pollution</i> , 2023, 333, 122101.	7.5	0
42	Molecular Mechanism of Exogenous Selenium Affecting the Nutritional Quality, Species and Content of Organic Selenium in Mustard. <i>Agronomy</i> , 2023, 13, 1425.	3.0	3
43	Phylogenetic and comparative genomics establishes origin of paralogy between homologs of AtMYB42 and AtMYB85 in last common ancestor of Brassicaceae via segmental duplication. <i>Plant Gene</i> , 2023, 35, 100424.	2.3	0

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44	Genomic Designing for Nutraceuticals in Brassica juncea: Advances and Future Prospects. , 2023, , 1-52.		0
45	Plant genome resequencing and population genomics: Current status and future prospects. Molecular Plant, 2023, 16, 1252-1268.	8.3	8
47	Expression in A. thaliana and cellular localization reveal involvement of BjNRAMP1 in cadmium uptake. Frontiers in Plant Science, 0, 14, .	3.6	1
48	A complex locus regulates highly lobed-leaf formation in Brassica juncea. Theoretical and Applied Genetics, 2023, 136, .	3.6	0
49	Pan-genome analysis of 13 Malus accessions reveals structural and sequence variations associated with fruit traits. Nature Communications, 2023, 14, .	12.8	2
50	MIR159 regulates multiple aspects of stamen and carpel development and requires dissection and delimitation of differential downstream regulatory network for manipulating fertility traits. Physiology and Molecular Biology of Plants, 2023, 29, 1437-1456.	3.1	0
51	Genomic Designing for Nutraceuticals in Brassica juncea: Advances and Future Prospects. , 2023, , 419-469.		0
52	Subgenome phasing for complex allopolyploidy: case-based benchmarking and recommendations. Briefings in Bioinformatics, 2023, 25, .	6.5	0
53	Molecular evolution analysis of MYB5 in Brassicaceae with specific focus on seed coat color of Brassica napus. BMC Plant Biology, 2024, 24, .	3.6	0
54	Fucoidanâ€™s Molecular Targets: A Comprehensive Review of Its Unique and Multiple Targets Accounting for Promising Bioactivities Supported by In Silico Studies. Marine Drugs, 2024, 22, 29.	4.6	0
55	High density linkage mapping and QTL analysis of salt tolerance-related traits using ddRAD sequencing in Indian mustard [Brassica juncea (L.) Czern & Coss]. Environmental and Experimental Botany, 2024, 219, 105655.	4.2	0
56	BL-Hi-C reveals the 3D genome structure of <i>Brassica</i> crops with high sensitivity. Horticulture Research, 2024, 11, .	6.3	0
57	Identification and Characterization of the BnFAR1/FHY3 Gene Family and Expression Analysis under Shading and Low-Temperature Responses in Brassica napus L.. Agronomy, 2024, 14, 202.	3.0	0
58	Origins and Diversity of <i>Brassica</i> and Its Relatives. , 2024, , 1-41.		0
59	How high-throughput sequencing empowers the research of polyploidy in vegetable crops. Vegetable Research, 2024, 4, 0-0.	0.7	0
61	Identification of Yellow Seed Color Genes Using Bulk Segregant RNA Sequencing in Brassica juncea L.. International Journal of Molecular Sciences, 2024, 25, 1573.	4.1	0
62	High throughput phenotyping of functional traits and key indices for selection of salt tolerant Mustard [<i>Brassica juncea</i> (L.) Czern & Coss] genotypes. Physiologia Plantarum, 2024, 176, .	5.2	0
63	A genomic variation map provides insights into peanut diversity in China and associations with 28 agronomic traits. Nature Genetics, 2024, 56, 530-540.	21.4	0

#	ARTICLE	IF	CITATIONS
64	Genomic insight into the origin, domestication, dispersal, diversification and human selection of Tartary buckwheat. <i>Genome Biology</i> , 2024, 25, .	8.8	0