

Ancestral polyploidy in seed plants and angiosperms

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Evolution and Diversity of Woody and Seed Plants. , 2010, , 129-162.		1
2	A mystery unveiled. <i>Genome Biology</i> , 2011, 12, 113.	13.9	40
3	Phylogenetic Perspectives on the Origins of Nodulation. <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 1289-1295.	1.4	199
4	Discovering numerical laws of plant microRNA by evolution. <i>Biochemical and Biophysical Research Communications</i> , 2011, 415, 313-318.	1.0	7
5	Recently Formed Polyploid Plants Diversify at Lower Rates. <i>Science</i> , 2011, 333, 1257-1257.	6.0	424
6	The Genomes of All Angiosperms: A Call for a Coordinated Global Census. <i>Journal of Botany</i> , 2011, 2011, 1-10.	1.2	10
7	Protein?Protein and Protein?DNA Dosage Balance and Differential Paralog Transcription Factor Retention in Polyploids. <i>Frontiers in Plant Science</i> , 2011, 2, 64.	1.7	16
8	Analysis of two abundant, highly related satellites in the allotetraploid <i>Nicotiana amentsii</i> using double-strand conformation polymorphism analysis and sequencing. <i>New Phytologist</i> , 2011, 192, 747-759.	3.5	12
9	Chasing the hare - Evaluating the phylogenetic utility of a nuclear single copy gene region at and below species level within the species rich group <i>Peperomia</i> (Piperaceae). <i>BMC Evolutionary Biology</i> , 2011, 11, 357.	3.2	27
10	Complex patterns of autopolyploid evolution in alfalfa and allies (<i>Medicago sativa</i>); Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.8	32
11	Organ and Cell Type-Specific Complementary Expression Patterns and Regulatory Neofunctionalization between Duplicated Genes in <i>Arabidopsis thaliana</i> . <i>Genome Biology and Evolution</i> , 2011, 3, 1419-1436.	1.1	55
12	Extensive changes to alternative splicing patterns following allopolyploidy in natural and resynthesized polyploids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 16122-16127.	3.3	94
13	The complex evolutionary dynamics of ancient and recent polyploidy in <i>Leucaena</i> (Leguminosae); Tj ETQq0 0.0 rgBT /Overlock 10 Tf 23	0.8	23
14	<i>Stacks</i> : Building and Genotyping Loci <i>De Novo</i> From Short-Read Sequences. <i>G3: Genes, Genomes, Genetics</i> , 2011, 1, 171-182.	0.8	1,643
15	Genomically Biased Accumulation of Seed Storage Proteins in Allopolyploid Cotton. <i>Genetics</i> , 2011, 189, 1103-1115.	1.2	53
16	Selection for Higher Gene Copy Number after Different Types of Plant Gene Duplications. <i>Genome Biology and Evolution</i> , 2011, 3, 1369-1380.	1.1	27
17	Different Gene Families in <i>Arabidopsis thaliana</i> Transposed in Different Epochs and at Different Frequencies throughout the Rosids. <i>Plant Cell</i> , 2011, 23, 4241-4253.	3.1	41
18	Escape from Preferential Retention Following Repeated Whole Genome Duplications in Plants. <i>Frontiers in Plant Science</i> , 2012, 3, 94.	1.7	73

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19	Evolution of the Land Plant Exocyst Complexes. <i>Frontiers in Plant Science</i> , 2012, 3, 159.	1.7	127
20	Unleashing the Genome of <i>Brassica Rapa</i> . <i>Frontiers in Plant Science</i> , 2012, 3, 172.	1.7	44
21	Molecular Tools for Exploring Polyploid Genomes in Plants. <i>International Journal of Molecular Sciences</i> , 2012, 13, 10316-10335.	1.8	40
22	Phylogeny of Galactolipid Synthase Homologs Together with their Enzymatic Analyses Revealed a Possible Origin and Divergence Time for Photosynthetic Membrane Biogenesis. <i>DNA Research</i> , 2012, 19, 91-102.	1.5	37
23	Correlation networks visualization. <i>Frontiers in Plant Science</i> , 2012, 3, 240.	1.7	24
24	Development of Eighteen Microsatellite Markers in <i>Anemone amurensis</i> (Ranunculaceae) and Cross-Amplification in Congeneric Species. <i>International Journal of Molecular Sciences</i> , 2012, 13, 4889-4895.	1.8	1
25	The Cytonuclear Dimension of Allopolyploid Evolution: An Example from Cotton Using Rubisco. <i>Molecular Biology and Evolution</i> , 2012, 29, 3023-3036.	3.5	59
26	Anatomical, biochemical, and photosynthetic responses to recent allopolyploidy in <i>Glycine dolichocarpa</i> (Fabaceae). <i>American Journal of Botany</i> , 2012, 99, 55-67.	0.8	64
27	i-ADHoRe 3.0: fast and sensitive detection of genomic homology in extremely large data sets. <i>Nucleic Acids Research</i> , 2012, 40, e11-e11.	6.5	192
28	Analysis of <i>Arabidopsis</i> genome-wide variations before and after meiosis and meiotic recombination by resequencing Landsberg <i>erecta</i> and all four products of a single meiosis. <i>Genome Research</i> , 2012, 22, 508-518.	2.4	125
29	Systematics Agenda 2020: The Mission Evolves. <i>Systematic Biology</i> , 2012, 61, 549-552.	2.7	14
30	MCSanX: a toolkit for detection and evolutionary analysis of gene synteny and collinearity. <i>Nucleic Acids Research</i> , 2012, 40, e49-e49.	6.5	4,252
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33	Variable Changes in Genome Size Associated with Different Polyploid Events in <i>Plantago</i> (Plantaginaceae). <i>Journal of Heredity</i> , 2012, 103, 711-719.	1.0	23
34	A comparative transcriptomic study of an allotetraploid and its diploid progenitors illustrates the unique advantages and challenges of RNA-seq in plant species. <i>American Journal of Botany</i> , 2012, 99, 383-396.	0.8	80
35	Pericentromeric Effects Shape the Patterns of Divergence, Retention, and Expression of Duplicated Genes in the Paleopolyploid Soybean \checkmark . <i>Plant Cell</i> , 2012, 24, 21-32.	3.1	79
36	Targeted sequence capture as a powerful tool for evolutionary analysis. <i>American Journal of Botany</i> , 2012, 99, 312-319.	0.8	146

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37	The Plant Proteome Folding Project: Structure and Positive Selection in Plant Protein Families. <i>Genome Biology and Evolution</i> , 2012, 4, 360-371.	1.1	13
38	Polyploidy associated with altered and broader ecological niches in the <i>Claytonia perfoliata</i> (Portulacaceae) species complex. <i>American Journal of Botany</i> , 2012, 99, 655-662.	0.8	99
39	Reconstruction of Oomycete Genome Evolution Identifies Differences in Evolutionary Trajectories Leading to Present-Day Large Gene Families. <i>Genome Biology and Evolution</i> , 2012, 4, 199-211.	1.1	44
40	Dynamics and Adaptive Benefits of Protein Domain Emergence and Arrangements during Plant Genome Evolution. <i>Genome Biology and Evolution</i> , 2012, 4, 316-329.	1.1	66
41	Decoding Plant and Animal Genome Plasticity from Differential Paleo-Evolutionary Patterns and Processes. <i>Genome Biology and Evolution</i> , 2012, 4, 917-928.	1.1	69
42	Cytogeography and genome size variation in the <i>Claytonia perfoliata</i> (Portulacaceae) polyploid complex. <i>Annals of Botany</i> , 2012, 110, 1195-1203.	1.4	12
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44	Preferential Retention of Circadian Clock Genes during Diploidization following Whole Genome Triplication in <i>Brassica rapa</i> . <i>Plant Cell</i> , 2012, 24, 2415-2426.	3.1	114
45	Entangling Ancient Allotetraploidization in Asian <i>Mitella</i> : An Integrated Approach for Multilocus Combinations. <i>Molecular Biology and Evolution</i> , 2012, 29, 429-439.	3.5	24
46	<i>Tie-dyed2</i> Encodes a Callose Synthase That Functions in Vein Development and Affects Symplastic Trafficking within the Phloem of Maize Leaves. <i>Plant Physiology</i> , 2012, 160, 1540-1550.	2.3	67
47	Gamma Paleohexaploidy in the Stem Lineage of Core Eudicots: Significance for MADS-Box Gene and Species Diversification. <i>Molecular Biology and Evolution</i> , 2012, 29, 3793-3806.	3.5	127
48	Five Nuclear Loci Resolve the Polyploid History of Switchgrass (<i>Panicum virgatum</i> L.) and Relatives. <i>PLoS ONE</i> , 2012, 7, e38702.	1.1	61
49	Why size really matters when sequencing plant genomes. <i>Plant Ecology and Diversity</i> , 2012, 5, 415-425.	1.0	27
50	Tearing down barriers: understanding the molecular mechanisms of interploidy hybridizations. <i>Journal of Experimental Botany</i> , 2012, 63, 6059-6067.	2.4	44
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54	Gene duplication within the Green Lineage: the case of TEL genes. <i>Journal of Experimental Botany</i> , 2012, 63, 5061-5077.	2.4	35

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56	Integrated consensus genetic and physical maps of flax (<i>Linum usitatissimum</i> L.). <i>Theoretical and Applied Genetics</i> , 2012, 125, 1783-1795.	1.8	93
57	Celebrating Giant Steps toward a Synthetic History of Angiosperm Evolution. <i>International Journal of Plant Sciences</i> , 2012, 173, 559-560.	0.6	0
58	Contrasting patterns of evolution following whole genome versus tandem duplication events in <i>Populus</i> . <i>Genome Research</i> , 2012, 22, 95-105.	2.4	126
59	The <i>ARC1</i> E3 Ligase Gene Is Frequently Deleted in Self-Compatible Brassicaceae Species and Has a Conserved Role in <i>Arabidopsis lyrata</i> Self-Pollen Rejection. <i>Plant Cell</i> , 2012, 24, 4607-4620.	3.1	94
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64	Cytogeography of the Humifusa clade of <i>Opuntia</i> s.s. Mill. 1754 (Cactaceae, Opuntioideae, Opuntieae): correlations with pleistocene refugia and morphological traits in a polyploid complex. <i>Comparative Cytogenetics</i> , 2012, 6, 53-77.	0.3	52
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66	Escaping the lianoid habit: Evolution of shrub-like growth forms in <i>Aristolochia</i> subgenus <i>Isotrema</i> (Aristolochiaceae). <i>American Journal of Botany</i> , 2012, 99, 1609-1629.	0.8	44
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68	Complex evolutionary history and diverse domain organization of SET proteins suggest divergent regulatory interactions. <i>New Phytologist</i> , 2012, 195, 248-263.	3.5	65
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70	Evolution and Diversification of the CYC/TB1 Gene Family in Asteraceae--A Comparative Study in <i>Gerbera</i> (Mutisieae) and <i>Sunflower</i> (Heliantheae). <i>Molecular Biology and Evolution</i> , 2012, 29, 1155-1166.	3.5	127
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74	Whole genome comparisons of <i>Fragaria</i> , <i>Prunus</i> and <i>Malus</i> reveal different modes of evolution between Rosaceous subfamilies. <i>BMC Genomics</i> , 2012, 13, 129.	1.2	77
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76	High-throughput sequencing of black pepper root transcriptome. <i>BMC Plant Biology</i> , 2012, 12, 168.	1.6	55
77	A spruce gene map infers ancient plant genome reshuffling and subsequent slow evolution in the gymnosperm lineage leading to extant conifers. <i>BMC Biology</i> , 2012, 10, 84.	1.7	97
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79	Identifying the Phylogenetic Context of Whole-Genome Duplications in Plants. , 2012, , 77-92.		1
80	Using nuclear gene data for plant phylogenetics: Progress and prospects. <i>Molecular Phylogenetics and Evolution</i> , 2012, 65, 774-785.	1.2	101
81	Responses of Transposable Elements to Polyploidy. <i>Topics in Current Genetics</i> , 2012, , 147-168.	0.7	37
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85	Origins of Novel Phenotypic Variation in Polyploids. , 2012, , 57-76.		15
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87	Evolutionary Implications of Genome and Karyotype Restructuring in <i>Nicotiana tabacum</i> L. , 2012, , 209-224.		6
88	Allopolyploid Speciation in Action: The Origins and Evolution of <i>Senecio cambrensis</i> . , 2012, , 245-270.		22
89	The Early Stages of Polyploidy: Rapid and Repeated Evolution in <i>Tragopogon</i> . , 2012, , 271-292.		36
90	Polyploidy and Genome Evolution. , 2012, , .		93

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91	Plant Transposable Elements. Topics in Current Genetics, 2012, , .	0.7	8
92	Reproductive isolation between diploid and tetraploid cytotypes of <i>Libidibia ferrea</i> (= <i>Caesalpinia</i>) Tj ETQq1 1 0.784314 rgBT /Overloc 298, 1371-1381.	0.3	35
93	Auxin response factor gene family in <i>Brassica rapa</i> : genomic organization, divergence, expression, and evolution. Molecular Genetics and Genomics, 2012, 287, 765-784.	1.0	57
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101	Phylogeny of the Asparagales based on three plastid and two mitochondrial genes. American Journal of Botany, 2012, 99, 875-889.	0.8	84
102	The banana (<i>Musa acuminata</i>) genome and the evolution of monocotyledonous plants. Nature, 2012, 488, 213-217.	13.7	1,049
103	Evolution of the tetraploid <i>Anemone multifida</i> (2n = 32) and hexaploid <i>A. baldensis</i> (2n = 48) (Ranunculaceae) was accompanied by rDNA loci loss and intergenomic translocation: evidence for their common genome origin. Annals of Botany, 2012, 110, 703-712.	1.4	24
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109	Phylogenomic analysis of transcriptome data elucidates co-occurrence of a paleopolyploid event and the origin of bimodal karyotypes in Agavoideae (Asparagaceae). <i>American Journal of Botany</i> , 2012, 99, 397-406.	0.8	94
110	Assessing the monophyly of polyploid <i>Gossypium</i> species. <i>Plant Systematics and Evolution</i> , 2012, 298, 1177-1183.	0.3	44
111	Divergent evolution of oxidosqualene cyclases in plants. <i>New Phytologist</i> , 2012, 193, 1022-1038.	3.5	122
113	Genome and gene duplications and gene expression divergence: a view from plants. <i>Annals of the New York Academy of Sciences</i> , 2012, 1256, 1-14.	1.8	194
114	In silico archeogenomics unveils modern plant genome organisation, regulation and evolution. <i>Current Opinion in Plant Biology</i> , 2012, 15, 122-130.	3.5	68
115	Redundancy and rewiring of genetic networks following genome-wide duplication events. <i>Current Opinion in Plant Biology</i> , 2012, 15, 168-176.	3.5	118
116	Towards understanding how molecular networks evolve in plants. <i>Current Opinion in Plant Biology</i> , 2012, 15, 177-184.	3.5	61
117	Rarely successful polyploids and their legacy in plant genomes. <i>Current Opinion in Plant Biology</i> , 2012, 15, 140-146.	3.5	209
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124	Homoeolog expression bias and expression level dominance in allopolyploid cotton. <i>Heredity</i> , 2013, 110, 171-180.	1.2	366
125	The family of Dof transcription factors in pine. <i>Trees - Structure and Function</i> , 2013, 27, 1547-1557.	0.9	11
126	Phylogeny and evolutionary history of glycogen synthase kinase 3/SHAGGY-like kinase genes in land plants. <i>BMC Evolutionary Biology</i> , 2013, 13, 143.	3.2	21
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131	Evolution: He Who Grabs Too Much Loses All. <i>Current Biology</i> , 2013, 23, R961-R963.	1.8	2
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140	A multivalent three-point linkage analysis model of autotetraploids. <i>Briefings in Bioinformatics</i> , 2013, 14, 460-468.	3.2	14
142	Comprehensive analysis of expressed sequence tags from cultivated and wild radish (<i>Raphanus</i> spp.). <i>BMC Genomics</i> , 2013, 14, 721.	1.2	16
143	Whole genome duplication events in plant evolution reconstructed and predicted using myosin motor proteins. <i>BMC Evolutionary Biology</i> , 2013, 13, 202.	3.2	51
144	Rapid genomic and transcriptomic alterations induced by wide hybridization: <i>Chrysanthemum nankingense</i> and <i>Tanacetum vulgare</i> and <i>C. crassum</i> and <i>Crossostephium chinense</i> (Asteraceae). <i>BMC Genomics</i> , 2013, 14, 902.		20
145	A conifer genome spruces up plant phylogenomics. <i>Genome Biology</i> , 2013, 14, 122.	3.8	37
146	The promise of genomics in the study of plant-pollinator interactions. <i>Genome Biology</i> , 2013, 14, 207.	3.8	29

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148	Gene family evolution in green plants with emphasis on the origination and evolution of <i>rabidopsis thaliana</i> genes. <i>Plant Journal</i> , 2013, 73, 941-951.	2.8	117
149	RECONSTRUCTING THE COMPLEX EVOLUTIONARY ORIGIN OF WILD ALLOPOLYPLOID TOBACCOS (<i>NICOTIANA</i> SECTION <i>SUAVEOLENTES</i>). <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 80-94.	1.1	51
150	The Plant Nucleus at War and Peace: Genome Organization in the Interphase Nucleus. , 2013, , 13-31.		3
151	Meiosis: Recombination and the Control of Cell Division. , 2013, , 121-136.		1
152	Polyploidy and its effect on evolutionary success: old questions revisited with new tools. <i>Heredity</i> , 2013, 110, 99-104.	1.2	395
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154	Convergent gene loss following gene and genome duplications creates single-copy families in flowering plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 2898-2903.	3.3	351
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936	Plant Polyploidy: Origin, Evolution, and Its Influence on Crop Domestication. <i>Horticultural Plant Journal</i> , 2019, 5, 231-239.	2.3	85
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939	Enhanced ROS scavenging and sugar accumulation contribute to drought tolerance of naturally occurring autotetraploids in <i>Poncirus trifoliata</i> . <i>Plant Biotechnology Journal</i> , 2019, 17, 1394-1407.	4.1	100
940	A newly identified cluster of glutathione S-transferase genes provides <i>Verticillium</i> wilt resistance in cotton. <i>Plant Journal</i> , 2019, 98, 213-227.	2.8	44
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953	Nuclear genomes of two magnoliids. <i>Nature Plants</i> , 2019, 5, 6-7.	4.7	33
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971	Divergence of duplicated genes by repeated partitioning of splice forms and subcellular localization. <i>New Phytologist</i> , 2020, 225, 1011-1022.	3.5	27
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1015	Chromosome duplication causing geneâ€™dosageâ€™based effects on the gene expression level in <i>Gossypium hirsutum</i> â€™ <i>Gossypium australe</i> addition lines. <i>Plant Direct</i> , 2020, 4, e00247.	0.8	1
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1021	Genome-Wide Identification, Characterization, and Regulation of RWP-RK Gene Family in the Nitrogen-Fixing Clade. <i>Plants</i> , 2020, 9, 1178.	1.6	8
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1026	A chromosome-scale reference genome of <i>Lobularia maritima</i> , an ornamental plant with high stress tolerance. <i>Horticulture Research</i> , 2020, 7, 197.	2.9	6
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1040	A cotton β -1,3-/4-fucosyltransferase-encoding gene, FucT4, plays an important role in cell elongation and is significantly associated with fiber quality. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1141-1153.	1.0	3
1041	Molecular footprints of selection effects and whole genome duplication (WGD) events in three blueberry species: detected by transcriptome dataset. <i>BMC Plant Biology</i> , 2020, 20, 250.	1.6	15

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1044	The differential expression patterns of paralogs in response to stresses indicate expression and sequence divergences. <i>BMC Plant Biology</i> , 2020, 20, 277.	1.6	7
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1052	Different Patterns of Ecological Divergence Between Two Tetraploids and Their Diploid Counterpart in a Parapatric Linear Coastal Distribution Polyploid Complex. <i>Frontiers in Plant Science</i> , 2020, 11, 315.	1.7	27
1053	A Pan-plant Protein Complex Map Reveals Deep Conservation and Novel Assemblies. <i>Cell</i> , 2020, 181, 460-474.e14.	13.5	133
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1055	Polyploidy in liver development, homeostasis and disease. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2020, 17, 391-405.	8.2	111
1056	Genome-wide identification and expression analysis of the CBF/DREB1 gene family in lettuce. <i>Scientific Reports</i> , 2020, 10, 5733.	1.6	28
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1068	Mildew Locus O facilitates colonization by arbuscular mycorrhizal fungi in angiosperms. <i>New Phytologist</i> , 2020, 227, 343-351.	3.5	26
1069	Prickly waterlily and rigid hornwort genomes shed light on early angiosperm evolution. <i>Nature Plants</i> , 2020, 6, 215-222.	4.7	88
1070	Polyploidization-driven differentiation of freezing tolerance in <i>Solidago canadensis</i> . <i>Plant, Cell and Environment</i> , 2020, 43, 1394-1403.	2.8	16
1071	Recurrent gene duplication in the angiosperm tribe Delphinieae (Ranunculaceae) inferred from intracellular gene transfer events and heteroplasmic mutations in the plastid <i>matK</i> gene. <i>Scientific Reports</i> , 2020, 10, 2720.	1.6	15
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1581	Expression Analysis of TCP Transcription Factor Family in Autopolyploids of <i>Chrysanthemum nankingense</i> . <i>Frontiers in Plant Science</i> , 2022, 13, .	1.7	3
1582	The chromosome-level genome for <i>Toxicodendron vernicifluum</i> provides crucial insights into Anacardiaceae evolution and urushiol biosynthesis. <i>IScience</i> , 2022, 25, 104512.	1.9	6
1583	Extensive polyploid clonality was a successful strategy for seagrass to expand into a newly submerged environment. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, .	1.2	27
1586	A Population-Genetic Lens into the Process of Gene Loss Following Whole-Genome Duplication. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	16
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1596	Genome-wide identification, expression and evolution analysis of OVATE family proteins in cotton (<i>Gossypium</i> spp.). <i>Gene</i> , 2022, 834, 146653.	1.0	1
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1604	Comparative Transcriptomic, Anatomical and Phytohormone Analyses Provide New Insights Into Hormone-Mediated Tetraploid Dwarfing in Hybrid Sweetgum (<i>Liquidambar styraciflua</i> A— <i>L. formosana</i>). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
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1612	Key regulatory pathways, microRNAs, and target genes participate in adventitious root formation of <i>Acer rubrum</i> L. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
1613	Genome-wide identification and characterization of the abiotic-stress-responsive lipoxygenase gene family in diploid woodland strawberry (<i>Fragaria vesca</i>). <i>Journal of Integrative Agriculture</i> , 2022, 21, 1982-1996.	1.7	2
1614	Altered Developmental and Metabolic Gene Expression in Basil Interspecific Hybrids. <i>Plants</i> , 2022, 11, 1873.	1.6	1
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1624	ï»¿A monograph of the genus <i>Polylepis</i> (Rosaceae). <i>PhytoKeys</i> , 0, 203, 1-274.	0.4	5

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1626	Convergent evolution of AP2/ERF III and IX subfamilies through recurrent polyploidization and tandem duplication during eudicot adaptation to paleoenvironmental changes. <i>Plant Communications</i> , 2022, 3, 100420.	3.6	14
1627	<i>Idaho</i> and <i>Subularia</i> : Hidden polyploid origins of two enigmatic genera of crucifers. <i>American Journal of Botany</i> , 0, , .	0.8	4
1628	Identification of OSCA gene family in <i>Solanum habrochaites</i> and its function analysis under stress. <i>BMC Genomics</i> , 2022, 23, .	1.2	9
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1631	Establishment of an allotetraploid fern species, <i>Lepisorus yamaokae</i> Seriz., between two highly niche-differentiated parental species. <i>American Journal of Botany</i> , 2022, 109, 1456-1471.	0.8	2
1633	Methylome and transcriptome analysis of alters leaf phenotype with autotetraploid in grape. <i>Scientia Horticulturae</i> , 2023, 307, 111534.	1.7	3
1634	Evolution of complex genome architecture in gymnosperms. <i>GigaScience</i> , 2022, 11, .	3.3	8
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1637	Research Advances in Oxidosqualene Cyclase in Plants. <i>Forests</i> , 2022, 13, 1382.	0.9	2
1638	Deep evaluation of the evolutionary history of the Heat Shock Factor (HSF) gene family and its expansion pattern in seed plants. <i>PeerJ</i> , 0, 10, e13603.	0.9	3
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1640	Does polyploidy inhibit sex chromosome evolution in angiosperms?. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
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1642	A spatiotemporal atlas of organogenesis in the development of orchid flowers. <i>Nucleic Acids Research</i> , 2022, 50, 9724-9737.	6.5	20
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1645	The role of CDPKs in plant development, nutrient and stress signaling. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	12
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1648	Uniparentality: advantages for range expansion in diploid and diploid-autopolyploid species. <i>Botanical Journal of the Linnean Society</i> , 2022, 200, 563-585.	0.8	4
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1653	The Implications of Coalescent Conspecific Genetic Samples in Plants. , 2022, , 197-212.		2
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1656	Phylogenomics and Systematics of Overlooked Mesoamerican and South American Polyploid Broad-Leaved <i>Festuca</i> Grasses Differentiate <i>F.</i> sects. <i>Glabricarpae</i> and <i>Ruprechtia</i> and <i>F.</i> subgen. <i>Asperifolia</i> , <i>Erosiflorae</i> , <i>Mallopetalon</i> and <i>Coironhuecu</i> (subgen. nov.). <i>Plants</i> , 2022, 11, 2303.	1.6	3
1657	Inconsistent expression of the gigas effect in polyploid <i>Oxalis</i> . <i>American Journal of Botany</i> , 2022, 109, 1607-1621.	0.8	1
1658	Early stages of sympatric homoploid hybrid speciation in crater lake cichlid fishes. <i>Nature Communications</i> , 2022, 13, .	5.8	8
1659	A high-quality <i>Buxus austro-yunnanensis</i> (Buxales) genome provides new insights into karyotype evolution in early eudicots. <i>BMC Biology</i> , 2022, 20, .	1.7	12
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1672	Sublinear scaling of the cellular proteome with ploidy. <i>Nature Communications</i> , 2022, 13, .	5.8	16
1673	Genomic imbalance modulates transposable element expression in maize. <i>Plant Communications</i> , 2023, 4, 100467.	3.6	2
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1675	Thirteen Dipterocarpoideae genomes provide insights into their evolution and borneol biosynthesis. <i>Plant Communications</i> , 2022, 3, 100464.	3.6	6
1676	Compensatory Genetic and Transcriptional Cytonuclear Coordination in Allopolyploid Lager Yeast (<i>Saccharomyces pastorianus</i>). <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	1
1677	Alteration of synonymous codon usage bias accompanies polyploidization in wheat. <i>Frontiers in Genetics</i> , 0, 13, .	1.1	0
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1679	Genome-wide characterization and expression analysis of the growth-regulating factor family in <i>Saccharum</i> . <i>BMC Plant Biology</i> , 2022, 22, .	1.6	2
1680	The dynamics of lncRNAs transcription in interspecific F1 allotriploid hybrids between Brassica species. <i>Genomics</i> , 2022, 114, 110505.	1.3	3
1681	A likely autotetraploidization event shaped the Chinese mahogany (<i>Toona sinensis</i>) genome. <i>Horticultural Plant Journal</i> , 2022, , .	2.3	1
1682	Transposable elements orchestrate subgenome-convergent and -divergent transcription in common wheat. <i>Nature Communications</i> , 2022, 13, .	5.8	16
1683	Potential allopolyploid origin of Ericales revealed with gene-tree reconciliation. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3
1684	Revisiting ancient polyploidy in leptosporangiate ferns. <i>New Phytologist</i> , 2023, 237, 1405-1417.	3.5	4

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1687	Phylogenomics and the flowering plant tree of life. <i>Journal of Integrative Plant Biology</i> , 2023, 65, 299-323.	4.1	25
1688	Genome-Scale Investigation of GARP Family Genes Reveals Their Pivotal Roles in Nutrient Stress Resistance in Allotetraploid Rapeseed. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14484.	1.8	3
1689	Redox homeostasis at SAM: a new role of HINT protein. <i>Planta</i> , 2023, 257, .	1.6	1
1690	Subgenome-biased expression and functional diversification of a Na ⁺ /H ⁺ antiporter homoeologs in salt tolerance of polyploid wheat. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
1691	Genome-Wide Characterization and Evolutionary Expansion of Poplar NAC Transcription Factors and Their Tissue-Specific Expression Profiles under Drought. <i>International Journal of Molecular Sciences</i> , 2023, 24, 253.	1.8	3
1693	How to survive in the world's third poplar: Insights from the genome of the highest altitude woody plant, <i>Hippophae tibetana</i> (Elaeagnaceae). <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	2
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1695	Kinase regulators evolved into two families by gain and loss of ability to bind plant steroid receptors. <i>Plant Physiology</i> , 0, , .	2.3	2
1696	Polyploidization was not involved in the origin of five endemic species from southern Europe but is otherwise frequent in <i>Euphorbia</i> section <i>Esula</i> (Euphorbiaceae). <i>Botanical Journal of the Linnean Society</i> , 2023, 201, 260-285.	0.8	4
1697	Allotetraploidization event of <i>Coptis chinensis</i> shared by all Ranunculales. <i>Horticultural Plant Journal</i> , 2023, , .	2.3	0
1698	Genome-scale angiosperm phylogenies based on nuclear, plastome, and mitochondrial datasets. <i>Journal of Integrative Plant Biology</i> , 2023, 65, 1479-1489.	4.1	5
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1700	Multi-Omics Approaches for Breeding in Medicinal Plants. , 2023, , 165-191.		1
1701	Genome-wide characterization of the inositol transporters gene family in <i>Populus</i> and functional characterization of PtINT1b in response to salt stress. <i>International Journal of Biological Macromolecules</i> , 2023, 228, 197-206.	3.6	1
1702	Homoploid hybrids are common but evolutionary dead ends, whereas polyploidy is not linked to hybridization in a group of Pyrenean saxifrages. <i>Molecular Phylogenetics and Evolution</i> , 2023, 180, 107703.	1.2	2
1703	Constraining Whole-Genome Duplication Events in Geological Time. <i>Methods in Molecular Biology</i> , 2023, , 139-154.	0.4	1
1704	Chromosome-scale genomics, metabolomics, and transcriptomics provide insight into the synthesis and regulation of phenols in <i>Vitis adenocladia</i> grapes. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	1

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1708	Comparative gene retention analysis in barley, wild emmer, and bread wheat pangenome lines reveals factors affecting gene retention following gene duplication. <i>BMC Biology</i> , 2023, 21, .	1.7	9
1709	The genome sequence and demographic history of <i>Przewalskia tangutica</i> (Solanaceae), an endangered alpine plant on the Qinghai-Tibet Plateau. <i>DNA Research</i> , 2023, 30, .	1.5	1
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1713	Inference of Ancient Polyploidy from Genomic Data. <i>Methods in Molecular Biology</i> , 2023, , 3-18.	0.4	2
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1715	Fewer chromosomes, more co-occurring species within plant lineages: A likely effect of local survival and colonization. <i>American Journal of Botany</i> , 2023, 110, .	0.8	1
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1717	Characterization and expression profiles of the B-box gene family during plant growth and under low-nitrogen stress in <i>Saccharum</i> . <i>BMC Genomics</i> , 2023, 24, .	1.2	0
1718	Creating and <i>De Novo</i> Improvement of New Allopolyploid Crops for Future Agriculture. <i>Critical Reviews in Plant Sciences</i> , 2023, 42, 53-64.	2.7	0
1719	Depression and Its Phytopharmacotherapy—A Narrative Review. <i>International Journal of Molecular Sciences</i> , 2023, 24, 4772.	1.8	9
1720	Phylogenomic analyses of Sapindales support new family relationships, rapid Mid-Cretaceous Hothouse diversification, and heterogeneous histories of gene duplication. <i>Frontiers in Plant Science</i> , 0, 14, .	1.7	6
1721	Evolutionary analysis of KED-rich proteins in plants. <i>PLoS ONE</i> , 2023, 18, e0279772.	1.1	1
1722	Resynthesized Rapeseed (<i>Brassica napus</i>): Breeding and Genomics. <i>Critical Reviews in Plant Sciences</i> , 2023, 42, 65-92.	2.7	3
1723	The first chromosome-level <i>Fallopia multiflora</i> genome assembly provides insights into stilbene biosynthesis. <i>Horticulture Research</i> , 2023, 10, .	2.9	1
1724	Understanding protein import in diverse non-green plastids. <i>Frontiers in Genetics</i> , 0, 14, .	1.1	0

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1726	Uncovering gene-family founder events during major evolutionary transitions in animals, plants and fungi using GenEra. <i>Genome Biology</i> , 2023, 24, .	3.8	9
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1728	Nuclear phylogeny and insights into whole-genome duplications and reproductive development of Solanaceae plants. <i>Plant Communications</i> , 2023, 4, 100595.	3.6	8
1729	Genome balance and dosage effect drive allopolyploid formation in <i>Brassica</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	12
1730	Does competitive asymmetry confer polyploid advantage under changing environments?. <i>Journal of Ecology</i> , 2023, 111, 1327-1339.	1.9	3
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1732	Genomics of plant speciation. <i>Plant Communications</i> , 2023, 4, 100599.	3.6	4
1733	Phylogenetic placement of whole genome duplications in yeasts through quantitative analysis of hierarchical orthologous groups. <i>F1000Research</i> , 0, 12, 382.	0.8	0
1734	Evolution and expression analysis of the caffeoyl-CoA 3-O-methyltransferase (CCoAOMT) gene family in jute (<i>Corchorus L.</i>). <i>BMC Genomics</i> , 2023, 24, .	1.2	3
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