High Rate of Chimeric Gene Origination by Retropositio

Plant Cell 18, 1791-1802 DOI: 10.1105/tpc.106.041905

Citation Report

#	Article	IF	CITATIONS
1	Plant Biology Research Comes of Age in China. Plant Cell, 2006, 18, 2855-2864.	3.1	20
2	FGF: A web tool for Fishing Gene Family in a whole genome database. Nucleic Acids Research, 2007, 35, W121-W125.	6.5	6
3	Origins of New Male Germ-line Functions from X-Derived Autosomal Retrogenes in the Mouse. Molecular Biology and Evolution, 2007, 24, 2242-2253.	3.5	28
4	Retrosequence formation restructures the yeast genome. Genes and Development, 2007, 21, 3308-3318.	2.7	30
5	Quantifying the major mechanisms of recent gene duplications in the human and mouse genomes: a novel strategy to estimate gene duplication rates. Genome Biology, 2007, 8, R158.	13.9	35
6	A genome-wide transcriptional activity survey of rice transposable element-related genes. Genome Biology, 2007, 8, R28.	13.9	47
7	Novel sex pheromone desaturases in the genomes of corn borers generated through gene duplication and retroposon fusion. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 4467-4472.	3.3	54
8	Patterns of gene duplication in the plant SKP1 gene family in angiosperms: evidence for multiple mechanisms of rapid gene birth. Plant Journal, 2007, 50, 873-885.	2.8	361
9	A Microarray Based Genomic Hybridization Method for Identification of New Genes in Plants: Case Analyses of Arabidopsis and Oryza. Journal of Integrative Plant Biology, 2007, 49, 915-926.	4.1	10
10	Novel exon combinations generated by alternative splicing of gene fragments mobilized by a CACTA transposon in Glycine max. BMC Plant Biology, 2007, 7, 38.	1.6	37
11	Transposable elements and the plant pan-genomes. Current Opinion in Plant Biology, 2007, 10, 149-155.	3.5	220
12	A role for convergent evolution in the secretory life of cells. Trends in Cell Biology, 2007, 17, 157-164.	3.6	22
13	Analysis of genes associated with retrotransposons in the rice genome. Genetica, 2008, 134, 297-310.	0.5	20
14	AtCopeg1, the unique gene originated from AtCopia95 retrotransposon family, is sensitive to external hormones and abiotic stresses. Plant Cell Reports, 2008, 27, 1065-1073.	2.8	20
15	LTR retrotransposon landscape in Medicago truncatula: more rapid removal than in rice. BMC Genomics, 2008, 9, 382.	1.2	51
16	Retrocopy contributions to the evolution of the human genome. BMC Genomics, 2008, 9, 466.	1.2	93
17	Gene conversion in the rice genome. BMC Genomics, 2008, 9, 93.	1.2	42
18	On the origin and evolution of new genes—a genomic and experimental perspective. Journal of Genetics and Genomics, 2008, 35, 639-648.	1.7	44

TATION REPO

#	Article	IF	CITATIONS
19	Phylogenetic determination of the pace of transposable element proliferation in plants: <i>copia</i> and LINE-like elements in <i>Gossypium</i> . Genome, 2008, 51, 11-18.	0.9	52
20	Transcriptome-Based Examination of Putative Pollen Allergens of Rice (Oryza sativa ssp. japonica). Molecular Plant, 2008, 1, 751-759.	3.9	27
21	The evolution of courtship behaviors through the origination of a new gene in <i>Drosophila</i> . Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 7478-7483.	3.3	76
22	Bioinformatics in China: A Personal Perspective. PLoS Computational Biology, 2008, 4, e1000020.	1.5	18
23	The Subtelomere of Oryza sativa Chromosome 3 Short Arm as a Hot Bed of New Gene Origination in Rice. Molecular Plant, 2008, 1, 839-850.	3.9	36
24	On the origin of new genes in <i>Drosophila</i> . Genome Research, 2008, 18, 1446-1455.	2.4	240
25	Selection on Major Components of Angiosperm Genomes. Science, 2008, 320, 484-486.	6.0	62
26	Replication of Nonautonomous Retroelements in Soybean Appears to Be Both Recent and Common Â. Plant Physiology, 2008, 148, 1760-1771.	2.3	57
27	Exceptional Diversity, Non-Random Distribution, and Rapid Evolution of Retroelements in the B73 Maize Genome. PLoS Genetics, 2009, 5, e1000732.	1.5	322
28	Expansion Mechanisms and Functional Annotations of Hypothetical Genes in the Rice Genome. Plant Physiology, 2009, 150, 1997-2008.	2.3	19
29	The Functional Role of Pack-MULEs in Rice Inferred from Purifying Selection and Expression Profile. Plant Cell, 2009, 21, 25-38.	3.1	91
30	Extensive Structural Renovation of Retrogenes in the Evolution of the Populus Genome. Plant Physiology, 2009, 151, 1943-1951.	2.3	66
31	Structure-based discovery and description of plant and animal <i>Helitrons</i> . Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12832-12837.	3.3	102
32	A New Family of Ty1-copia-Like Retrotransposons Originated in the Tomato Genome by a Recent Horizontal Transfer Event. Genetics, 2009, 181, 1183-1193.	1.2	56
33	Formation and Longevity of Chimeric and Duplicate Genes in <i>Drosophila melanogaster</i> . Genetics, 2009, 181, 313-322.	1.2	58
34	More than just orphans: are taxonomically-restricted genes important in evolution?. Trends in Genetics, 2009, 25, 404-413.	2.9	399
35	Identification and characterization of pseudogenes in the rice gene complement. BMC Genomics, 2009, 10, 317.	1.2	56
36	Evolutionary Process of the Genomic Sequence Around the 100 Map Unit of Chromosome 1 in Arabidopsis thaliana. Journal of Plant Biology, 2009, 52, 616-624.	0.9	3

#	Article	IF	CITATIONS
37	The Contribution of Transposable Elements to Expressed Coding Sequence in Arabidopsis thaliana. Journal of Molecular Evolution, 2009, 68, 80-89.	0.8	68
38	Genome organization of the tomato <i>sun</i> locus and characterization of the unusual retrotransposon <i>Rider</i> . Plant Journal, 2009, 60, 181-193.	2.8	64
39	RNA-based gene duplication: mechanistic and evolutionary insights. Nature Reviews Genetics, 2009, 10, 19-31.	7.7	374
40	Gene duplication and evolutionary novelty in plants. New Phytologist, 2009, 183, 557-564.	3.5	725
41	Evolution of a Novel Phenolic Pathway for Pollen Development. Science, 2009, 325, 1688-1692.	6.0	148
42	Evolutionary Origin and Functions of Retrogene Introns. Molecular Biology and Evolution, 2009, 26, 2147-2156.	3.5	53
43	Evolutionary and Expression Signatures of Pseudogenes in Arabidopsis and Rice Â. Plant Physiology, 2009, 151, 3-15.	2.3	118
44	Identification of LTR retrotransposons in eukaryotic genomes: supports from structure and evolution. International Journal of Bioinformatics Research and Applications, 2009, 5, 365.	0.1	2
45	Unique evolutionary pattern of numbers of gramineous NBS–LRR genes. Molecular Genetics and Genomics, 2010, 283, 427-438.	1.0	147
46	Evolutionary history and stress regulation of the lectin superfamily in higher plants. BMC Evolutionary Biology, 2010, 10, 79.	3.2	129
47	Genome-wide computational prediction of tandem gene arrays: application in yeasts. BMC Genomics, 2010, 11, 56.	1.2	13
48	The rapid generation of chimerical genes expanding protein diversity in zebrafish. BMC Genomics, 2010, 11, 657.	1.2	36
49	Genetically modified myths and realities. New Biotechnology, 2010, 27, 545-551.	2.4	26
50	Gene duplications and the time thereafter - examples from plant secondary metabolism. Plant Biology, 2010, 12, 570-7.	1.8	41
51	Adaptive impact of the chimeric gene <i>Quetzalcoatl</i> in <i>Drosophila melanogaster</i> . Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10943-10948.	3.3	37
52	<i>Bs1</i> , a New Chimeric Gene Formed by Retrotransposon-Mediated Exon Shuffling in Maize Â. Plant Physiology, 2010, 153, 1413-1424.	2.3	48
53	Origins, evolution, and phenotypic impact of new genes. Genome Research, 2010, 20, 1313-1326.	2.4	665
54	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

		CITATION REPORT	
#	Article	IF	Citations
55	A triptych of the evolution of plant transposable elements. Trends in Plant Science, 2010, 15, 47	1-478. 4.3	254
56	Comparative analysis of intronless genes in teleost fish genomes: Insights into their evolution an molecular function. Marine Genomics, 2011, 4, 109-119.	nd 0.4	21
57	Evolution of alternative splicing in newly evolved genes of Drosophila. Gene, 2011, 470, 1-6.	1.0	7
58	Genomeâ€wide Expansion and Expression Divergence of the Basic Leucine Zipper Transcription F Higher Plants with an Emphasis on Sorghum ^F . Journal of Integrative Plant Biology, 2 53, 212-231.	Factors in 2011, 4.1	157
59	A CASEâ€BYâ€CASE EVOLUTIONARY ANALYSIS OF FOUR IMPRINTED RETROGENES. Evolution; Ir Journal of Organic Evolution, 2011, 65, 1413-1427.	nternational 1.1	26
60	Evolutionary origins of Brassicaceae specific genes in Arabidopsis thaliana. BMC Evolutionary Biology, 2011, 11, 47.	3.2	161
61	Phylogenetics and evolution of Su(var)3-9 SET genes in land plants: rapid diversification in struct and function. BMC Evolutionary Biology, 2011, 11, 63.	ture 3.2	15
62	Functional characterization of a class III acid endochitinase from the traps of the carnivorous pitcher plant genus, Nepenthes. Journal of Experimental Botany, 2011, 62, 4639-4647.	2.4	58
63	Retrogenes in Rice (Oryza sativa L. ssp. japonica) Exhibit Correlated Expression with Their Source Genes. Genome Biology and Evolution, 2011, 3, 1357-1368.	2 1.1	62
64	Different Gene Families in Arabidopsis thaliana Transposed in Different Epochs and at Different Frequencies throughout the Rosids. Plant Cell, 2011, 23, 4241-4253.	3.1	41
65	Combining Comparative Sequence and Genomic Data to Ascertain Phylogenetic Relationships ar Explore the Evolution of the Large GDSL-Lipase Family in Land Plants. Molecular Biology and Evolution, 2011, 28, 551-565.	nd 3.5	76
66	Chimeric Genes as a Source of Rapid Evolution in Drosophila melanogaster. Molecular Biology ar Evolution, 2012, 29, 517-529.	nd 3.5	57
67	MCScanX: a toolkit for detection and evolutionary analysis of gene synteny and collinearity. Nuc Acids Research, 2012, 40, e49-e49.	leic 6.5	4,252
68	Editor's Choice: Crop Genome Plasticity and Its Relevance to Food and Feed Safety of Genet Engineered Breeding Stacks. Plant Physiology, 2012, 160, 1842-1853.	ically 2.3	68
69	Comparative Analysis of Syntenic Genes in Grass Genomes Reveals Accelerated Rates of Gene St and Coding Sequence Evolution in Polyploid Wheat Â. Plant Physiology, 2012, 161, 252-265.	ructure 2.3	113
70	In with the Old, in with the New: The Promiscuity of the Duplication Process Engenders Diverse Pathways for Novel Gene Creation. International Journal of Evolutionary Biology, 2012, 2012, 1-2	24. 1.0	35
71	Evolution at the Subgene Level: Domain Rearrangements in the Drosophila Phylogeny. Molecular Biology and Evolution, 2012, 29, 689-705.	3.5	42
72	Life at the extreme: lessons from the genome. Genome Biology, 2012, 13, .	3.8	53

#	Article	IF	CITATIONS
73	Characterization and functional annotation of nested transposable elements in eukaryotic genomes. Genomics, 2012, 100, 222-230.	1.3	37
74	Phylogenetics and evolution of Trx SET genes in fully sequenced land plants. Genome, 2012, 55, 269-280.	0.9	4
75	Origins of New Genes and Evolution of Their Novel Functions. Annual Review of Ecology, Evolution, and Systematics, 2012, 43, 345-363.	3.8	75
76	Evolution of Genome Content: Population Dynamics of Transposable Elements in Flies and Humans. Methods in Molecular Biology, 2012, 855, 361-383.	0.4	41
77	Origin, Diversity, Expansion History, and Functional Evolution of the Plant Receptor-Like Kinase/Pelle Family. Signaling and Communication in Plants, 2012, , 1-22.	0.5	17
78	Origin of a novel protein-coding gene family with similar signal sequence in Schistosoma japonicum. BMC Genomics, 2012, 13, 260.	1.2	1
79	The SLEEPERgenes: a transposase-derived angiosperm-specific gene family. BMC Plant Biology, 2012, 12, 192.	1.6	34
80	Evolutionary patterns of RNA-based gene duplicates in Caenorhabditis nematodes coincide with their genomic features. BMC Research Notes, 2012, 5, 398.	0.6	7
81	Rider Transposon Insertion and Phenotypic Change in Tomato. Topics in Current Genetics, 2012, , 297-312.	0.7	11
82	The Origin and Evolution of New Genes. Methods in Molecular Biology, 2012, 856, 161-186.	0.4	23
83	Plant Genome Diversity Volume 1. , 2012, , .		15
84	The Mitochondrial Genome of the Lycophyte Huperzia squarrosa: The Most Archaic Form in Vascular Plants. PLoS ONE, 2012, 7, e35168.	1.1	42
85	The Impact of Transposable Elements on Gene and Genome Evolution. , 2012, , 35-58.		19
86	Newly evolved genes: Moving from comparative genomics to functional studies in model systems. BioEssays, 2012, 34, 477-483.	1.2	28
87	The turbulent life of Sirevirus retrotransposons and the evolution of the maize genome: more than ten thousand elements tell the story. Plant Journal, 2012, 69, 475-488.	2.8	36
88	The Ca ²⁺ â€dependent DNases are Involved in Secondary Xylem Development in <i>Eucommia ulmoides</i> . Journal of Integrative Plant Biology, 2012, 54, 456-470.	4.1	18
89	Grande retrotransposons contain an accessory gene in the unusually long 3′-internal region that encodes a nuclear protein transcribed from its own promoter. Plant Molecular Biology, 2013, 81, 541-551.	2.0	7
90	Patterns of Gene Duplication and Their Contribution to Expansion of Gene Families in Grapevine. Plant Molecular Biology Reporter, 2013, 31, 852-861.	1.0	39

#	ARTICLE	IF	CITATIONS
92	Insights into the role of DNA methylation in diatoms by genome-wide profiling in Phaeodactylum tricornutum. Nature Communications, 2013, 4, 2091.	5.8	113
93	New Gene Evolution: Little Did We Know. Annual Review of Genetics, 2013, 47, 307-333.	3.2	249
94	How important are transposons for plant evolution?. Nature Reviews Genetics, 2013, 14, 49-61.	7.7	711
96	Novel receptorâ€like kinases in cacao contain <scp>PR</scp> â€1 extracellular domains. Molecular Plant Pathology, 2013, 14, 602-609.	2.0	12
97	Co-evolution of plant LTR-retrotransposons and their host genomes. Protein and Cell, 2013, 4, 493-501.	4.8	42
98	High Occurrence of Functional New Chimeric Genes in Survey of Rice Chromosome 3 Short Arm Genome Sequences. Genome Biology and Evolution, 2013, 5, 1038-1048.	1.1	11
99	Genome-Wide Analysis Reveals Origin of Transfer RNA Genes from tRNA Halves. Molecular Biology and Evolution, 2013, 30, 2087-2098.	3.5	20
100	Transposable Elements: Powerful Contributors to Angiosperm Evolution and Diversity. Genome Biology and Evolution, 2013, 5, 1886-1901.	1.1	195
101	Selective Acquisition and Retention of Genomic Sequences by Pack- <i>Mutator</i> -Like Elements Based on Guanine-Cytosine Content and the Breadth of Expression. Plant Physiology, 2013, 163, 1419-1432.	2.3	25
102	Genome-Wide Survey on Genomic Variation, Expression Divergence, and Evolution in Two Contrasting Rice Genotypes under High Salinity Stress. Genome Biology and Evolution, 2013, 5, 2032-2050.	1.1	22
103	Genomic rearrangements and the evolution of clusters of locally adaptive loci. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E1743-51.	3.3	299
104	Life at the extreme: lessons from the genome. Genome Biology, 2013, 13, 241.	3.8	72
105	Genome-Wide Survey and Comparative Analysis of LTR Retrotransposons and Their Captured Genes in Rice and Sorghum. PLoS ONE, 2013, 8, e71118.	1.1	33
107	Evolution of Gene Structural Complexity: An Alternative-Splicing-Based Model Accounts for Intron-Containing Retrogenes Â. Plant Physiology, 2014, 165, 412-423.	2.3	19
108	"Out of Pollen―Hypothesis for Origin of New Genes in Flowering Plants: Study from Arabidopsis thaliana. Genome Biology and Evolution, 2014, 6, 2822-2829.	1.1	28
109	Rolling-Circle Transposons Catalyze Genomic Innovation in a Mammalian Lineage. Genome Biology and Evolution, 2014, 6, 2595-2610.	1.1	53
110	The Contributions of Transposable Elements to the Structure, Function, and Evolution of Plant Genomes. Annual Review of Plant Biology, 2014, 65, 505-530.	8.6	436
111	Pollen-Specific Activation of Arabidopsis Retrogenes Is Associated with Global Transcriptional Reprogramming Â. Plant Cell, 2014, 26, 3299-3313.	3.1	23

ARTICLE IF CITATIONS # Genomic localization of AtRE1 and AtRE2, copia-type retrotransposons, in natural variants of 112 1.0 2 Arabidopsis thaliana. Molecular Genetics and Genomics, 2014, 289, 821-835. Sucrose metabolism gene families and their biological functions. Scientific Reports, 2015, 5, 17583. 1.6 Evolutionary fate and implications of retrocopies in the African coelacanth genome. BMC Genomics, 114 1.2 4 2015, 16, 915. Small-scale gene duplications played a major role in the recent evolution of wheat chromosome 3B. Genome Biology, 2015, 16, 188. Diversity, abundance, and evolutionary dynamics of Pong-like transposable elements in Triticeae. 116 1.2 7 Molecular Phylogenetics and Evolution, 2015, 93, 318-330. Alternative Transposition Generates New Chimeric Genes and Segmental Duplications at the Maize <i>p1</i> Locus. Genetics, 2015, 201, 925-935. 1.2 Identification and analysis of retrogenes in the East Asian nematode Caenorhabditis sp. 5 genome. 118 0.9 2 Genome, 2015, 58, 349-355. Genome Evolution in Maize: From Genomes Back to Genes. Annual Review of Plant Biology, 2015, 66, 119 8.6 329-343. Rapid evolutionary dynamics in a 2.8â€Mb chromosomal region containing multiple prolamin and 120 2.8 33 resistance gene families in <i>Aegilops tauschii</i>. Plant Journal, 2016, 87, 495-506. An Intronless β-amyrin Synthase Gene is More Efficient in Oleanolic Acid Accumulation than its Paralog 1.6 in Gentiana straminea. Scientific Reports, 2016, 6, 33364. Bioinformatic analysis of Arabidopsis reverse transcriptases with a zinc-finger domain. Biologia 122 3 0.8 (Poland), 2016, 71, 1223-1229. DNA methylation changes facilitated evolution of genes derived from Mutator-like transposable 3.8 elements. Genome Biology, 2016, 17, 92. Altered Transcription and Neofunctionalization of Duplicated Genes Rescue the Harmful Effects of a 124 3.1 28 Chimeric Gene in <i>Brassica napus</i>. Plant Cell, 2016, 28, 2060-2078. Are We There Yet? Reliably Estimating the Completeness of Plant Genome Sequences. Plant Cell, 2016, 3.1 89 28, 1759-1768. Comparative genomic analysis of retrogene repertoire in two green algae Volvox carteri and 126 1.9 11 Chlamydomonas reinhardtii. Biology Direct, 2016, 11, 35. LTR-mediated retroposition as a mechanism of RNA-based duplication in metazoans. Genome Research, 127 2.4 2016, 26, 1663-1675. LINE-1-like retrotransposons contribute to RNA-based gene duplication in dicots. Scientific Reports, 128 1.6 13 2016, 6, 24755. 129 Evolution of Gene Duplication in Plants. Plant Physiology, 2016, 171, 2294-2316. 2.3 1,094

#	Article	IF	CITATIONS
130	Characterization of apple NADPH oxidase genes and their expression associated with oxidative stress in shoot culture in vitro. Plant Cell, Tissue and Organ Culture, 2016, 124, 621-633.	1.2	20
131	Genome Reduction Uncovers a Large Dispensable Genome and Adaptive Role for Copy Number Variation in Asexually Propagated <i>Solanum tuberosum</i> . Plant Cell, 2016, 28, 388-405.	3.1	163
132	What makes up plant genomes: The vanishing line between transposable elements and genes. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2016, 1859, 366-380.	0.9	67
133	The Role of Microsatellites in Streptophyta Gene Evolution. Journal of Molecular Evolution, 2017, 84, 144-148.	0.8	0
134	The fate of retrotransposed processed genes in Arabidopsis thaliana. Gene, 2017, 609, 1-8.	1.0	4
135	The Genomic Impact of Gene Retrocopies: What Have We Learned from Comparative Genomics, Population Genomics, and Transcriptomic Analyses?. Genome Biology and Evolution, 2017, 9, 1351-1373.	1.1	77
136	Emergence of a Novel Chimeric Gene Underlying Grain Number in Rice. Genetics, 2017, 205, 993-1002.	1.2	15
137	Integrative analysis of DNA methylation, mRNAs, and small RNAs during maize embryo dedifferentiation. BMC Plant Biology, 2017, 17, 105.	1.6	16
138	A Comprehensive Analysis of Transcript-Supported De Novo Genes in Saccharomyces sensu stricto Yeasts. Molecular Biology and Evolution, 2017, 34, 2823-2838.	3.5	28
139	PlantRGDB: A Database of Plant Retrocopied Genes. Plant and Cell Physiology, 2017, 58, pcw210.	1.5	6
140	Living Organisms Author Their Read-Write Genomes in Evolution. Biology, 2017, 6, 42.	1.3	44
141	Transcriptional activity of PIF and Pong-like Class II transposable elements in Triticeae. BMC Evolutionary Biology, 2017, 17, 178.	3.2	2
142	New reference genome sequences of hot pepper reveal the massive evolution of plant disease-resistance genes by retroduplication. Genome Biology, 2017, 18, 210.	3.8	255
143	Protein-Coding Genes' Retrocopies and Their Functions. Viruses, 2017, 9, 80.	1.5	57
144	Oryza nivara Sharma et Shastry. Compendium of Plant Genomes, 2018, , 207-238.	0.3	10
145	DNA methylation changes and evolution of RNA-based duplication inSus scrofa: based on a two-step strategy. Epigenomics, 2018, 10, 199-218.	1.0	6
146	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus Oryza. Nature Genetics, 2018, 50, 285-296.	9.4	413
147	The unique epigenetic features of Pack-MULEs and their impact on chromosomal base composition and expression spectrum. Nucleic Acids Research, 2018, 46, 2380-2397.	6.5	14

#	Article	IF	CITATIONS
148	Identification of Pseudogenes in Brachypodium distachyon Chromosomes. Methods in Molecular Biology, 2018, 1667, 149-171.	0.4	1
149	Evolutionary Impacts of Alternative Transposition. , 2018, , 113-130.		6
150	A Comprehensive Survey on the Terpene Synthase Gene Family Provides New Insight into Its Evolutionary Patterns. Genome Biology and Evolution, 2019, 11, 2078-2098.	1.1	78
151	Analysis of new retrogenes provides insight into dog adaptive evolution. Ecology and Evolution, 2019, 9, 11185-11197.	0.8	6
152	The Gene Structure and Expression Level Changes of the GH3 Gene Family in Brassica napus Relative to Its Diploid Ancestors. Genes, 2019, 10, 58.	1.0	15
153	LtrDetector: A tool-suite for detecting long terminal repeat retrotransposons de-novo. BMC Genomics, 2019, 20, 450.	1.2	19
154	Parallelism and convergence in post-domestication adaptation in cereal grasses. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180245.	1.8	16
155	In the name of the rose: a roadmap for rose research in the genome era. Horticulture Research, 2019, 6, 65.	2.9	53
156	Expansion of PmBEAT genes in the Prunus mume genome induces characteristic floral scent production. Horticulture Research, 2019, 6, 24.	2.9	24
157	AtFusionDB: a database of fusion transcripts inArabidopsis thaliana. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	8
158	Evolutionary patterns of chimeric retrogenes in Oryza species. Scientific Reports, 2019, 9, 17733.	1.6	3
159	A member of wheat class III peroxidase gene family, TaPRX-2A, enhanced the tolerance of salt stress. BMC Plant Biology, 2020, 20, 392.	1.6	48
160	An Overview of Duplicated Gene Detection Methods: Why the Duplication Mechanism Has to Be Accounted for in Their Choice. Genes, 2020, 11, 1046.	1.0	65
161	A Novel Mutation of the NARROW LEAF 1 Gene Adversely Affects Plant Architecture in Rice (Oryza) Tj ETQq1 1 ().784314 ı 1.8	gBJ /Overloc
162	Pan-Genome of Wild and Cultivated Soybeans. Cell, 2020, 182, 162-176.e13.	13.5	508
163	The new chimeric chiron genes evolved essential roles in zebrafish embryonic development by regulating NAD+ levels. Science China Life Sciences, 2021, 64, 1929-1948.	2.3	6
164	Interpopulation differences of retroduplication variations (RDVs) in rice retrogenes and their phenotypic correlations. Computational and Structural Biotechnology Journal, 2021, 19, 600-611.	1.9	1
165	In Silico Identification of Stress-Associated Transposable Elements in Arabidopsis thaliana Using Public Transcriptome Data. Methods in Molecular Biology, 2021, 2250, 15-30.	0.4	0

#	Article	IF	Citations
166	How should we think about evolution in the age of genomics?. , 2021, , 1-44.		1
167	Impact of short-read sequencing on the misassembly of a plant genome. BMC Genomics, 2021, 22, 99.	1.2	5
168	Structural characterization and duplication modes of pseudogenes in plants. Scientific Reports, 2021, 11, 5292.	1.6	14
169	Gauging the trends of pseudogenes in plants. Critical Reviews in Biotechnology, 2021, 41, 1114-1129.	5.1	4
170	Full-length LTR retroelements in Capsicum annuum revealed a few species-specific family bursts with insertional preferences. Chromosome Research, 2021, 29, 261-284.	1.0	7
171	The Dispensable Roles of X-Linked Ubl4a and Its Autosomal Counterpart Ubl4b in Spermatogenesis Represent a New Evolutionary Type of X-Derived Retrogenes. Frontiers in Genetics, 2021, 12, 689902.	1.1	0
172	The Structural, Functional and Evolutionary Impact of Transposable Elements in Eukaryotes. Genes, 2021, 12, 918.	1.0	31
176	Maize Genome Structure and Evolution. , 2009, , 179-199.		8
177	Transposable Element Dynamics in Rice and Its Wild Relatives. , 2013, , 55-69.		9
178	Eukaryotic Pangenomes. , 2020, , 253-291.		5
179	A Novel Gene Family Controls Species-Specific Morphological Traits in Hydra. PLoS Biology, 2008, 6, e278.	2.6	85
180	Maize opaque10 Encodes a Cereal-Specific Protein That Is Essential for the Proper Distribution of Zeins in Endosperm Protein Bodies. PLoS Genetics, 2016, 12, e1006270.	1.5	43
181	Evolutionary Patterns of RNA-Based Duplication in Non-Mammalian Chordates. PLoS ONE, 2011, 6, e21466.	1.1	13
182	Comparative Sequence Analysis of the Ghd7 Orthologous Regions Revealed Movement of Ghd7 in the Grass Genomes. PLoS ONE, 2012, 7, e50236.	1.1	14
183	Divergent Evolutionary and Expression Patterns between Lineage Specific New Duplicate Genes and Their Parental Paralogs in Arabidopsis thaliana. PLoS ONE, 2013, 8, e72362.	1.1	19
191	CicerSpTEdb: A web-based database for high-resolution genome-wide identification of transposable elements in Cicer species. PLoS ONE, 2021, 16, e0259540.	1.1	5
192	Rapid Genome Evolution and Adaptation of Thlaspi arvense Mediated by Recurrent RNA-Based and Tandem Gene Duplications. Frontiers in Plant Science, 2021, 12, 772655.	1.7	8
193	Phylotranscriptomics Resolves the Phylogeny of Pooideae and Uncovers Factors for Their Adaptive Evolution. Molecular Biology and Evolution, 2022, 39, .	3.5	31

#	Article	IF	CITATIONS
194	Gene duplication and rate variation in the evolution of plastid ACCase and Clp genes in angiosperms. Molecular Phylogenetics and Evolution, 2022, 168, 107395.	1.2	2
195	A recent burst of gene duplications in Triticeae. Plant Communications, 2022, 3, 100268.	3.6	18
196	Construction and characterization of a de novo draft genome of garden cress (Lepidium sativum L.). Functional and Integrative Genomics, 2022, 22, 879-889.	1.4	2
197	Gene fusion as an important mechanism to generate new genes in the genus Oryza. Genome Biology, 2022, 23, .	3.8	7
198	The nearly complete assembly of the Cercis chinensis genome and Fabaceae phylogenomic studies provide insights into new gene evolution. Plant Communications, 2023, 4, 100422.	3.6	4
199	Retroviruses: Reversing the dogma of life - A review. Journal of Clinical Microbiology and Biochemical Technology, 2022, 8, 018-028.	0.4	0
200	Trends in the evolution of intronless genes in Poaceae. Frontiers in Plant Science, 0, 14, .	1.7	0
201	Mutational Bias and Natural Selection Driving the Synonymous Codon Usage of Single-Exon Genes in Rice (Oryza sativa L.). Rice, 2023, 16, .	1.7	4
202	PlantLTRdb: An interactive database for 195 plant species LTR-retrotransposons. Frontiers in Plant Science, 0, 14, .	1.7	7
206	CicerSpTEdb2.0: An Upgrade of Cicer Species Transposable Elements Database. Methods in Molecular Biology, 2023, , 71-82.	0.4	1