

# Xi-Yin Wang

## List of Publications by Year in descending order

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Version: 2024-02-01

76  
papers

22,031  
citations

70961

41  
h-index

79541

73  
g-index

88  
all docs

88  
docs citations

88  
times ranked

16543  
citing authors

#	ARTICLE	IF	CITATIONS
1	Chromosome-length genome assemblies of six legume species provide insights into genome organization, evolution, and agronomic traits for crop improvement. <i>Journal of Advanced Research</i> , 2022, 42, 315-329.	4.4	20
2	Genome structure and evolutionary history of frankincense producing <i>Boswellia sacra</i> . <i>IScience</i> , 2022, 25, 104574.	1.9	3
3	Integrative genomics analysis of the ever-shrinking pectin methylesterase (PME) gene family in foxtail		

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19	Coriander Genomics Database: a genomic, transcriptomic, and metabolic database for coriander. <i>Horticulture Research</i> , 2020, 7, 55.	2.9	35
20	Cotton Duplicated Genes Produced by Polyploidy Show Significantly Elevated and Unbalanced Evolutionary Rates, Overwhelmingly Perturbing Gene Tree Topology. <i>Frontiers in Genetics</i> , 2020, 11, 239.	1.1	14
21	Alignment of Rutaceae Genomes Reveals Lower Genome Fractionation Level Than Eudicot Genomes Affected by Extra Polyploidization. <i>Frontiers in Plant Science</i> , 2019, 10, 986.	1.7	6
22	The wax gourd genomes offer insights into the genetic diversity and ancestral cucurbit karyotype. <i>Nature Communications</i> , 2019, 10, 5158.	5.8	94
23	Polyploidy Index and Its Implications for the Evolution of Polyploids. <i>Frontiers in Genetics</i> , 2019, 10, 807.	1.1	29
24	Sequencing of Cultivated Peanut, <i>Arachis hypogaea</i> , Yields Insights into Genome Evolution and Oil Improvement. <i>Molecular Plant</i> , 2019, 12, 920-934.	3.9	185
25	The genome of cultivated peanut provides insight into legume karyotypes, polyploid evolution and crop domestication. <i>Nature Genetics</i> , 2019, 51, 865-876.	9.4	398
26	Reconstruction of evolutionary trajectories of chromosomes unraveled independent genomic repatterning between Triticeae and Brachypodium. <i>BMC Genomics</i> , 2019, 20, 180.	1.2	12
27	A newly identified cluster of glutathione <i>S</i> -transferase genes provides <i>Verticillium</i> wilt resistance in cotton. <i>Plant Journal</i> , 2019, 98, 213-227.	2.8	44
28	Recursive Paleohexaploidization Shaped the Durian Genome. <i>Plant Physiology</i> , 2019, 179, 209-219.	2.3	36
29	An Overlooked Paleotetraploidization in Cucurbitaceae. <i>Molecular Biology and Evolution</i> , 2018, 35, 16-26.	3.5	89
30	Discovery and annotation of a novel transposable element family in <i>Gossypium</i> . <i>BMC Plant Biology</i> , 2018, 18, 307.	1.6	6
31	Genomic, expressional, protein-protein interactional analysis of Trihelix transcription factor genes in <i>Setaria italica</i> and inference of their evolutionary trajectory. <i>BMC Genomics</i> , 2018, 19, 665.	1.2	14
32	Two Likely Auto-Tetraploidization Events Shaped Kiwifruit Genome and Contributed to Establishment of the Actinidiaceae Family. <i>iScience</i> , 2018, 7, 230-240.	1.9	44
33	Comprehensive analyses of the BES1 gene family in <i>Brassica napus</i> and examination of their evolutionary pattern in representative species. <i>BMC Genomics</i> , 2018, 19, 346.	1.2	45
34	Hierarchically Aligning 10 Legume Genomes Establishes a Family-Level Genomics Platform. <i>Plant Physiology</i> , 2017, 174, 284-300.	2.3	112
35	Two Highly Similar Poplar Paleo-subgenomes Suggest an Autotetraploid Ancestor of Salicaceae Plants. <i>Frontiers in Plant Science</i> , 2017, 08, 571.	1.7	20
36	Alignment of Common Wheat and Other Grass Genomes Establishes a Comparative Genomics Research Platform. <i>Frontiers in Plant Science</i> , 2017, 8, 1480.	1.7	11

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37	RNA-Seq Profiling Shows Divergent Gene Expression Patterns in Arabidopsis Grown under Different Densities. <i>Frontiers in Plant Science</i> , 2017, 8, 2001.	1.7	10
38	Comparative Genomics Analysis of Rice and Pineapple Contributes to Understand the Chromosome Number Reduction and Genomic Changes in Grasses. <i>Frontiers in Genetics</i> , 2016, 7, 174.	1.1	15
39	Origination, Expansion, Evolutionary Trajectory, and Expression Bias of AP2/ERF Superfamily in <i>Brassica napus</i> . <i>Frontiers in Plant Science</i> , 2016, 7, 1186.	1.7	36
40	Comparative genomic deconvolution of the cotton genome revealed a decaploid ancestor and widespread chromosomal fractionation. <i>New Phytologist</i> , 2016, 209, 1252-1263.	3.5	65
41	Draft genome of the peanut A-genome progenitor ( <i>Arachis duranensis</i> ) provides insights into geocarpy, oil biosynthesis, and allergens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 6785-6790.	3.3	235
42	Genome Alignment Spanning Major Poaceae Lineages Reveals Heterogeneous Evolutionary Rates and Alters Inferred Dates for Key Evolutionary Events. <i>Molecular Plant</i> , 2015, 8, 885-898.	3.9	131
43	Comparative Analysis of Gene Conversion Between Duplicated Regions in <i>Brassica rapa</i> and <i>B. oleracea</i> Genomes. <i>Compendium of Plant Genomes</i> , 2015, , 121-129.	0.3	3
44	Telomere-centric genome repatterning determines recurring chromosome number reductions during the evolution of eukaryotes. <i>New Phytologist</i> , 2015, 205, 378-389.	3.5	64
45	Insights into the Common Ancestor of Cereals. <i>Advances in Botanical Research</i> , 2014, 69, 175-194.	0.5	0
46	Comparative and Evolutionary Analysis of Major Peanut Allergen Gene Families. <i>Genome Biology and Evolution</i> , 2014, 6, 2468-2488.	1.1	15
47	Extensive and Biased Intergenomic Nonreciprocal DNA Exchanges Shaped a Nascent Polyploid Genome, <i>Gossypium</i> (Cotton). <i>Genetics</i> , 2014, 197, 1153-1163.	1.2	51
48	SNPhylo: a pipeline to construct a phylogenetic tree from huge SNP data. <i>BMC Genomics</i> , 2014, 15, 162.	1.2	410
49	Comparative Analysis of <i>Miscanthus</i> and <i>Saccharum</i> Reveals a Shared Whole-Genome Duplication but Different Evolutionary Fates. <i>Plant Cell</i> , 2014, 26, 2420-2429.	3.1	88
50	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	6.0	2,089
51	The <i>Brassica oleracea</i> genome reveals the asymmetrical evolution of polyploid genomes. <i>Nature Communications</i> , 2014, 5, 3930.	5.8	918
52	Transcriptome and methylome profiling reveals relics of genome dominance in the mesopolyploid <i>Brassica oleracea</i> . <i>Genome Biology</i> , 2014, 15, R77.	13.9	456
53	Gene body methylation shows distinct patterns associated with different gene origins and duplication modes and has a heterogeneous relationship with gene expression in <i>Oryza sativa</i> (rice). <i>New Phytologist</i> , 2013, 198, 274-283.	3.5	57
54	Comparative Genomic Analysis of C4 Photosynthesis Pathway Evolution in Grasses. , 2013, , 447-477.		4

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55	Genome Sequencing and Comparative Genomics in Cereals. , 2013, , 101-126.		0
56	Draft genome sequence of the mulberry tree <i>Morus notabilis</i> . Nature Communications, 2013, 4, 2445.	5.8	277
57	MCSanX: a toolkit for detection and evolutionary analysis of gene synteny and collinearity. Nucleic Acids Research, 2012, 40, e49-e49.	6.5	4,252
58	PGDD: a database of gene and genome duplication in plants. Nucleic Acids Research, 2012, 41, D1152-D1158.	6.5	544
59	Repeated polyploidization of <i>Gossypium</i> genomes and the evolution of spinnable cotton fibres. Nature, 2012, 492, 423-427.	13.7	1,204
60	Gene Conversion in Angiosperm Genomes with an Emphasis on Genes Duplicated by Polyploidization. Genes, 2011, 2, 1-20.	1.0	47
61	Modes of Gene Duplication Contribute Differently to Genetic Novelty and Redundancy, but Show Parallels across Divergent Angiosperms. PLoS ONE, 2011, 6, e28150.	1.1	139
62	Comparative analysis of peanut NBS-LRR gene clusters suggests evolutionary innovation among duplicated domains and erosion of gene microsynteny. New Phytologist, 2011, 192, 164-178.	3.5	63
63	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . Nature Genetics, 2011, 43, 1035-1039.	9.4	1,893
64	Seventy Million Years of Concerted Evolution of a Homoeologous Chromosome Pair, in Parallel, in Major Poaceae Lineages. Plant Cell, 2011, 23, 27-37.	3.1	80
65	Angiosperm genome comparisons reveal early polyploidy in the monocot lineage. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 472-477.	3.3	267
66	Comparative inference of illegitimate recombination between rice and sorghum duplicated genes produced by polyploidization. Genome Research, 2009, 19, 1026-1032.	2.4	83
67	The <i>Sorghum bicolor</i> genome and the diversification of grasses. Nature, 2009, 457, 551-556.	13.7	2,642
68	Comparative genomic analysis of C4 photosynthetic pathway evolution in grasses. Genome Biology, 2009, 10, R68.	13.9	144
69	The draft genome of the transgenic tropical fruit tree papaya ( <i>Carica papaya</i> Linnaeus). Nature, 2008, 452, 991-996.	13.7	964
70	Synteny and Collinearity in Plant Genomes. Science, 2008, 320, 486-488.	6.0	1,156
71	Unraveling ancient hexaploidy through multiply-aligned angiosperm gene maps. Genome Research, 2008, 18, 1944-1954.	2.4	515
72	Extensive Concerted Evolution of Rice Paralogs and the Road to Regaining Independence. Genetics, 2007, 177, 1753-1763.	1.2	85

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73	Evidence that Natural Selection is the Primary Cause of the Guanine-cytosine Content Variation in Rice Genes. <i>Journal of Integrative Plant Biology</i> , 2007, 49, 1393-1399.	4.1	10
74	Statistical inference of chromosomal homology based on gene colinearity and applications to Arabidopsis and rice. <i>BMC Bioinformatics</i> , 2006, 7, 447.	1.2	123
75	Duplication and DNA segmental loss in the rice genome: implications for diploidization. <i>New Phytologist</i> , 2005, 165, 937-946.	3.5	318
76	The Genomes of <i>Oryza sativa</i> : A History of Duplications. <i>PLoS Biology</i> , 2005, 3, e38.	2.6	808