

# Haibao Tang

## List of Publications by Year in descending order

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121  
papers

31,887  
citations

19636

61  
h-index

21521

114  
g-index

130  
all docs

130  
docs citations

130  
times ranked

25142  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic variation underlying kernel size, shape, and color in two interspecific <i>S. bicolor</i> – <i>S. halepense</i> subpopulations. <i>Genetic Resources and Crop Evolution</i> , 2022, 69, 1261-1281.	0.8	1
2	Two divergent haplotypes from a highly heterozygous lychee genome suggest independent domestication events for early and late-maturing cultivars. <i>Nature Genetics</i> , 2022, 54, 73-83.	9.4	88
3	GC content of plant genes is linked to past gene duplications. <i>PLoS ONE</i> , 2022, 17, e0261748.	1.1	6
4	A comparative genomics examination of desiccation tolerance and sensitivity in two sister grass species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	8
5	The spinach YY genome reveals sex chromosome evolution, domestication, and introgression history of the species. <i>Genome Biology</i> , 2022, 23, 75.	3.8	15
6	SunUp and Sunset genomes revealed impact of particle bombardment mediated transformation and domestication history in papaya. <i>Nature Genetics</i> , 2022, 54, 715-724.	9.4	26
7	Genomic insights into the recent chromosome reduction of autopolyploid sugarcane <i>Saccharum spontaneum</i> . <i>Nature Genetics</i> , 2022, 54, 885-896.	9.4	33
8	A high-quality <i>Brassica napus</i> genome reveals expansion of transposable elements, subgenome evolution and disease resistance. <i>Plant Biotechnology Journal</i> , 2021, 19, 615-630.	4.1	56
9	Genome sequence and evolution of <i>Betula platyphylla</i> . <i>Horticulture Research</i> , 2021, 8, 37.	2.9	53
10	Chromosome-level genome assembly of a regenerable maize inbred line A188. <i>Genome Biology</i> , 2021, 22, 175.	3.8	32
11	Haplotype-resolved genome assembly provides insights into evolutionary history of the tea plant <i>Camellia sinensis</i> . <i>Nature Genetics</i> , 2021, 53, 1250-1259.	9.4	157
12	Unzipping haplotypes in diploid and polyploid genomes. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 66-72.	1.9	57
13	The water lily genome and the early evolution of flowering plants. <i>Nature</i> , 2020, 577, 79-84.	13.7	238
14	Genomes of the Banyan Tree and Pollinator Wasp Provide Insights into Fig-Wasp Coevolution. <i>Cell</i> , 2020, 183, 875-889.e17.	13.5	71
15	Factorial estimating assembly base errors using k-mer abundance difference (KAD) between short reads and genome assembled sequences. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa075.	1.5	8
16	<i>Nymphaea colorata</i> (Blue-Petal Water Lily). <i>Trends in Genetics</i> , 2020, 36, 718-719.	2.9	3
17	Comparative analysis of sucrose phosphate synthase (SPS) gene family between <i>Saccharum officinarum</i> and <i>Saccharum spontaneum</i> . <i>BMC Plant Biology</i> , 2020, 20, 422.	1.6	27
18	A phased <i>Vanilla planifolia</i> genome enables genetic improvement of flavour and production. <i>Nature Food</i> , 2020, 1, 811-819.	6.2	52

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19	Transmission Genetics of a Sorghum bicolor × S. halepense Backcross Populations. <i>Frontiers in Plant Science</i> , 2020, 11, 467.	1.7	10
20	Genome-Wide Characterization of DNase I-Hypersensitive Sites and Cold Response Regulatory Landscapes in Grasses. <i>Plant Cell</i> , 2020, 32, 2457-2473.	3.1	29
21	Precision medicine integrating whole-genome sequencing, comprehensive metabolomics, and advanced imaging. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 3053-3062.	3.3	85
22	The evolutionary origin and domestication history of goldfish ( <i>Carassius auratus</i> ). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 29775-29785.	3.3	47
23	Recent polyploidization events in three <i>Saccharum</i> founding species. <i>Plant Biotechnology Journal</i> , 2019, 17, 264-274.	4.1	40
24	Models for Similarity Distributions of Syntenic Homologs and Applications to Phylogenomics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 727-737.	1.9	11
25	Assembly of allele-aware, chromosomal-scale autopolyploid genomes based on Hi-C data. <i>Nature Plants</i> , 2019, 5, 833-845.	4.7	292
26	Single-pollen-cell sequencing for gamete-based phased diploid genome assembly in plants. <i>Genome Research</i> , 2019, 29, 1889-1899.	2.4	28
27	Effector gene reshuffling involves dispensable mini-chromosomes in the wheat blast fungus. <i>PLoS Genetics</i> , 2019, 15, e1008272.	1.5	103
28	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
29	Haplotype-phased genome and evolution of phytonutrient pathways of tetraploid blueberry. <i>GigaScience</i> , 2019, 8, .	3.3	167
30	Single-base resolution map of evolutionary constraints and annotation of conserved elements across major grass genomes. <i>Genome Biology and Evolution</i> , 2018, 10, 473-488.	1.1	11
31	Comparative Genomics of Pineapple and Other Angiosperm Genomes. <i>Plant Genetics and Genomics: Crops and Models</i> , 2018, , 131-153.	0.3	0
32	Allele-defined genome of the autopolyploid sugarcane <i>Saccharum spontaneum</i> L.. <i>Nature Genetics</i> , 2018, 50, 1565-1573.	9.4	463
33	From Alpha-Duplication to Triplication and Sextuplication. <i>Compendium of Plant Genomes</i> , 2018, , 99-109.	0.3	0
34	PGD: Pineapple Genomics Database. <i>Horticulture Research</i> , 2018, 5, 66.	2.9	25
35	The Sequenced Angiosperm Genomes and Genome Databases. <i>Frontiers in Plant Science</i> , 2018, 9, 418.	1.7	110
36	Genotype-Corrector: improved genotype calls for genetic mapping in F2 and RIL populations. <i>Scientific Reports</i> , 2018, 8, 10088.	1.6	22

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37	GOATOOLS: A Python library for Gene Ontology analyses. <i>Scientific Reports</i> , 2018, 8, 10872.	1.6	717
38	Cataloging Plant Genome Structural Variations. <i>Current Issues in Molecular Biology</i> , 2018, 27, 181-194.	1.0	6
39	Long-read sequencing uncovers the adaptive topography of a carnivorous plant genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E4435-E4441.	3.3	95
40	Wild tobacco genomes reveal the evolution of nicotine biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 6133-6138.	3.3	160
41	Water lilies as emerging models for Darwin's abominable mystery. <i>Horticulture Research</i> , 2017, 4, 17051.	2.9	30
42	The asparagus genome sheds light on the origin and evolution of a young Y chromosome. <i>Nature Communications</i> , 2017, 8, 1279.	5.8	240
43	Profiling of Short-Tandem-Repeat Disease Alleles in 12,632 Human Whole Genomes. <i>American Journal of Human Genetics</i> , 2017, 101, 700-715.	2.6	142
44	PacBio Sequencing Reveals Transposable Elements as a Key Contributor to Genomic Plasticity and Virulence Variation in <i>Magnaporthe oryzae</i> . <i>Molecular Plant</i> , 2017, 10, 1465-1468.	3.9	100
45	Identification of individuals by trait prediction using whole-genome sequencing data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10166-10171.	3.3	118
46	Disentangling a polyploid genome. <i>Nature Plants</i> , 2017, 3, 688-689.	4.7	15
47	The <i>Kalanchoë</i> genome provides insights into convergent evolution and building blocks of crassulacean acid metabolism. <i>Nature Communications</i> , 2017, 8, 1899.	5.8	159
48	The pomegranate ( <i>Punica granatum</i> L.) genome and the genomics of punicalagin biosynthesis. <i>Plant Journal</i> , 2017, 91, 1108-1128.	2.8	109
49	Cataloging Plant Genome Structural Variations. , 2017, , .		0
50	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
51	The Genome of a Southern Hemisphere Seagrass Species ( <i>Zostera muelleri</i> ). <i>Plant Physiology</i> , 2016, 172, 272-283.	2.3	88
52	Rapid proliferation and nucleolar organizer targeting centromeric retrotransposons in cotton. <i>Plant Journal</i> , 2016, 88, 992-1005.	2.8	33
53	Two Paleo-Hexaploidies Underlie Formation of Modern Solanaceae Genome Structure. <i>Compendium of Plant Genomes</i> , 2016, , 201-216.	0.3	0
54	The Evolution of Photoperiod-Insensitive Flowering in Sorghum, A Genomic Model for Panicoid Grasses. <i>Molecular Biology and Evolution</i> , 2016, 33, 2417-2428.	3.5	42

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55	The pangenome of an agronomically important crop plant <i>Brassica oleracea</i> . <i>Nature Communications</i> , 2016, 7, 13390.	5.8	375
56	Directional Selection from Host Plants Is a Major Force Driving Host Specificity in <i>Magnaporthe</i> Species. <i>Scientific Reports</i> , 2016, 6, 25591.	1.6	62
57	Insight into the evolution of the Solanaceae from the parental genomes of <i>Petunia hybrida</i> . <i>Nature Plants</i> , 2016, 2, 16074.	4.7	311
58	A phylogenomic assessment of ancient polyploidy and genome evolution across the Poales. <i>Genome Biology and Evolution</i> , 2016, 8, evw060.	1.1	117
59	The Trees in the Peaks. <i>Lecture Notes in Computer Science</i> , 2016, , 3-14.	1.0	4
60	Structure of the germline genome of <i>Tetrahymena thermophila</i> and relationship to the massively rearranged somatic genome. <i>ELife</i> , 2016, 5, .	2.8	130
61	Polyribosomal RNA-Seq Reveals the Decreased Complexity and Diversity of the Arabidopsis Translatome. <i>PLoS ONE</i> , 2015, 10, e0117699.	1.1	40
62	SynFind: Compiling Syntenic Regions across Any Set of Genomes on Demand. <i>Genome Biology and Evolution</i> , 2015, 7, 3286-3298.	1.1	70
63	Single-molecule sequencing of the desiccation-tolerant grass <i>Oropetium thomaeum</i> . <i>Nature</i> , 2015, 527, 508-511.	13.7	291
64	Optical mapping in plant comparative genomics. <i>GigaScience</i> , 2015, 4, 3.	3.3	41
65	ALLMAPS: robust scaffold ordering based on multiple maps. <i>Genome Biology</i> , 2015, 16, 3.	3.8	340
66	The pineapple genome and the evolution of CAM photosynthesis. <i>Nature Genetics</i> , 2015, 47, 1435-1442.	9.4	472
67	MTGD: The <i>Medicago truncatula</i> Genome Database. <i>Plant and Cell Physiology</i> , 2015, 56, e1-e1.	1.5	83
68	Consequences of Whole-Genome Triplication as Revealed by Comparative Genomic Analyses of the Wild Radish <i>Raphanus raphanistrum</i> and Three Other Brassicaceae Species. <i>Plant Cell</i> , 2014, 26, 1925-1937.	3.1	137
69	A novel approach for multi-domain and multi-gene family identification provides insights into evolutionary dynamics of disease resistance genes in core eudicot plants. <i>BMC Genomics</i> , 2014, 15, 966.	1.2	29
70	Insights into the Common Ancestor of Eudicots. <i>Advances in Botanical Research</i> , 2014, 69, 137-174.	0.5	1
71	Early History of the Angiosperms. <i>Advances in Botanical Research</i> , 2014, 69, 195-222.	0.5	6
72	Integrated Syntenic and Phylogenomic Analyses Reveal an Ancient Genome Duplication in Monocots. <i>Plant Cell</i> , 2014, 26, 2792-2802.	3.1	220

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73	An improved genome release (version Mt4.0) for the model legume <i>Medicago truncatula</i> . <i>BMC Genomics</i> , 2014, 15, 312.	1.2	381
74	Early allopolyploid evolution in the post-Neolithic <i>Brassica napus</i> oilseed genome. <i>Science</i> , 2014, 345, 950-953.	6.0	2,089
75	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
76	Syntenic Sequence Conservation Between and Within Papaya Genes. , 2014, , 205-224.		0
77	The <i>Amborella</i> Genome and the Evolution of Flowering Plants. <i>Science</i> , 2013, 342, 1241089.	6.0	743
78	The dynamics of functional classes of plant genes in rediploidized ancient polyploids. <i>BMC Bioinformatics</i> , 2013, 14, S19.	1.2	17
79	Genome of the long-living sacred lotus ( <i>Nelumbo nucifera</i> Gaertn.). <i>Genome Biology</i> , 2013, 14, R41.	13.9	329
80	Comparative Genomics of Grasses: A Saccharinae-Centric View. , 2013, , 429-445.		1
81	Seed shattering in a wild sorghum is conferred by a locus unrelated to domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 15824-15829.	3.3	59
82	Unleashing the Genome of <i>Brassica Rapa</i> . <i>Frontiers in Plant Science</i> , 2012, 3, 172.	1.7	44
83	MCScanX: 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
84	PGDD: a database of gene and genome duplication in plants. <i>Nucleic Acids Research</i> , 2012, 41, D1152-D1158.	6.5	544
85	Profiling of gene duplication patterns of sequenced teleost genomes: evidence for rapid lineage-specific genome expansion mediated by recent tandem duplications. <i>BMC Genomics</i> , 2012, 13, 246.	1.2	100
86	Ancient and Recent Polyploidy in Monocots. , 2012, , 93-108.		18
87	Repeated polyploidization of <i>Gossypium</i> genomes and the evolution of spinnable cotton fibres. <i>Nature</i> , 2012, 492, 423-427.	13.7	1,204
88	The tomato genome sequence provides insights into fleshy fruit evolution. <i>Nature</i> , 2012, 485, 635-641.	13.7	2,860
89	Altered Patterns of Fractionation and Exon Deletions in <i>Brassica rapa</i> Support a Two-Step Model of Paleohexaploidy. <i>Genetics</i> , 2012, 190, 1563-1574.	1.2	163
90	The Evolution of Genome Structure. <i>International Journal of Evolution</i> , 2012, 01, .	0.5	1

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91	The Medicago genome provides insight into the evolution of rhizobial symbioses. <i>Nature</i> , 2011, 480, 520-524.	13.7	1,166
92	A physical map for the <i>Amborella trichopoda</i> genome sheds light on the evolution of angiosperm genome structure. <i>Genome Biology</i> , 2011, 12, R48.	13.9	28
93	Comparative analysis of <i>Gossypium</i> and <i>Vitis</i> genomes indicates genome duplication specific to the <i>Gossypium</i> lineage. <i>Genomics</i> , 2011, 97, 313-320.	1.3	20
94	Modes of Gene Duplication Contribute Differently to Genetic Novelty and Redundancy, but Show Parallels across Divergent Angiosperms. <i>PLoS ONE</i> , 2011, 6, e28150.	1.1	139
95	Comparative analysis of peanut NBS-LRR gene clusters suggests evolutionary innovation among duplicated domains and erosion of gene microsynteny. <i>New Phytologist</i> , 2011, 192, 164-178.	3.5	63
96	The genome of the mesopolyploid crop species <i>Brassica rapa</i> . <i>Nature Genetics</i> , 2011, 43, 1035-1039.	9.4	1,893
97	Screening synteny blocks in pairwise genome comparisons through integer programming. <i>BMC Bioinformatics</i> , 2011, 12, 102.	1.2	142
98	Gobe: an interactive, web-based tool for comparative genomic visualization. <i>Bioinformatics</i> , 2011, 27, 1015-1016.	1.8	7
99	Seventy Million Years of Concerted Evolution of a Homoeologous Chromosome Pair, in Parallel, in Major Poaceae Lineages. <i>Plant Cell</i> , 2011, 23, 27-37.	3.1	80
100	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
101	Domestication and plant genomes. <i>Current Opinion in Plant Biology</i> , 2010, 13, 160-166.	3.5	89
102	Microcollinearity between autopolyploid sugarcane and diploid sorghum genomes. <i>BMC Genomics</i> , 2010, 11, 261.	1.2	175
103	A draft physical map of a D-genome cotton species ( <i>Gossypium raimondii</i> ). <i>BMC Genomics</i> , 2010, 11, 395.	1.2	48
104	Angiosperm genome comparisons reveal early polyploidy in the monocot lineage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 472-477.	3.3	267
105	Insights from the Comparison of Plant Genome Sequences. <i>Annual Review of Plant Biology</i> , 2010, 61, 349-372.	8.6	202
106	Comparative inference of illegitimate recombination between rice and sorghum duplicated genes produced by polyploidization. <i>Genome Research</i> , 2009, 19, 1026-1032.	2.4	83
107	Sixty Million Years in Evolution of Soft Grain Trait in Grasses: Emergence of the Softness Locus in the Common Ancestor of Pooideae and Ehrhartoideae, after their Divergence from Panicoideae. <i>Molecular Biology and Evolution</i> , 2009, 26, 1651-1661.	3.5	46
108	Comparative Genomics of Grasses Promises a Bountiful Harvest. <i>Plant Physiology</i> , 2009, 149, 125-131.	2.3	42

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109	QUBIC: a qualitative biclustering algorithm for analyses of gene expression data. <i>Nucleic Acids Research</i> , 2009, 37, e101-e101.	6.5	222
110	Duplication and Divergence of Grass Genomes: Integrating the Chloridoids. <i>Tropical Plant Biology</i> , 2009, 2, 51-62.	1.0	23
111	Evolutionary fate of rhizome-specific genes in a non-rhizomatous Sorghum genotype. <i>Heredity</i> , 2009, 102, 266-273.	1.2	30
112	The Sorghum bicolor genome and the diversification of grasses. <i>Nature</i> , 2009, 457, 551-556.	13.7	2,642
113	Comparative genomic analysis of C4 photosynthetic pathway evolution in grasses. <i>Genome Biology</i> , 2009, 10, R68.	13.9	144
114	Haplotype inference using a genetic algorithm. , 2009, , .		1
115	The draft genome of the transgenic tropical fruit tree papaya ( <i>Carica papaya</i> Linnaeus). <i>Nature</i> , 2008, 452, 991-996.	13.7	964
116	Synteny and Collinearity in Plant Genomes. <i>Science</i> , 2008, 320, 486-488.	6.0	1,156
117	Unraveling ancient hexaploidy through multiply-aligned angiosperm gene maps. <i>Genome Research</i> , 2008, 18, 1944-1954.	2.4	515
118	Finding and Comparing Syntenic Regions among Arabidopsis and the Outgroups Papaya, Poplar, and Grape: CoGe with Rosids. <i>Plant Physiology</i> , 2008, 148, 1772-1781.	2.3	376
119	Extensive Concerted Evolution of Rice Paralogs and the Road to Regaining Independence. <i>Genetics</i> , 2007, 177, 1753-1763.	1.2	85
120	Phylogenetic relationships in Elymus (Poaceae: Triticeae) based on the nuclear ribosomal internal transcribed spacer and chloroplast trnL $\epsilon$ F sequences. <i>New Phytologist</i> , 2006, 170, 411-420.	3.5	148
121	Comparative physical mapping links conservation of microsynteny to chromosome structure and recombination in grasses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 13206-13211.	3.3	141