Jonathan F Wendel

List of Publications by Year
in descending order

184 papers	22,894 citations	10986 71 h-index	9345 143 g-index
201 all docs	201 docs citations	201 times ranked	12607 citing authors

#	Article	IF	Citations
1	Genomic and GWAS analyses demonstrate phylogenomic relationships of <i>Gossypium barbadense</i> in China and selection for fibre length, lint percentage and <i>Fusarium wilt</i> resistance. Plant Biotechnology Journal, 2022, 20, 691-710.	8.3	33
2	Deleterious Mutations Accumulate Faster in Allopolyploid Than Diploid Cotton (<i>Gossypium</i>) and Unequally between Subgenomes. Molecular Biology and Evolution, 2022, 39, .	8.9	16
3	Genetic diversity of Malagasy baobabs: implications for conservation. Adansonia, 2022, 44, .	0.2	1
4	Reshuffling of the ancestral core-eudicot genome shaped chromatin topology and epigenetic modification in Panax. Nature Communications, 2022, 13, 1902.	12.8	30
5	Global Patterns of Subgenome Evolution in Organelle-Targeted Genes of Six Allotetraploid Angiosperms. Molecular Biology and Evolution, 2022, 39, .	8.9	17
6	Parental legacy versus regulatory innovation in salt stress responsiveness of allopolyploid cotton (<i>Gossypium</i>) species. Plant Journal, 2022, 111, 872-887.	5.7	8
7	Homoeologous gene expression and co-expression network analyses and evolutionary inference in allopolyploids. Briefings in Bioinformatics, 2021, 22, 1819-1835.	6.5	23
8	Genomic mosaicism due to homoeologous exchange generates extensive phenotypic diversity in nascent allopolyploids. National Science Review, 2021, 8, nwaa277.	9.5	42
9	Evolution and Diversity of the Cotton Genome. , 2021, , 25-78.		21
10	Parallel and Intertwining Threads of Domestication in Allopolyploid Cotton. Advanced Science, 2021, 8, 2003634.	11.2	45
11	The <i>Gossypium stocksii</i> genome as a novel resource for cotton improvement. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	8
12	Homoploid F1 hybrids and segmental allotetraploids of japonica and indica rice subspecies show similar and enhanced tolerance to nitrogen deficiency than parental lines. Journal of Experimental Botany, 2021, 72, 5612-5624.	4.8	1
13	Comparative Genome Analyses Highlight Transposon-Mediated Genome Expansion and the Evolutionary Architecture of 3D Genomic Folding in Cotton. Molecular Biology and Evolution, 2021, 38, 3621-3636.	8.9	41
14	pSONIC: Ploidy-aware Syntenic Orthologous Networks Identified via Collinearity. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	8
15	Nuclearâ€“cytoplasmic balance: whole genome duplications induce elevated organellar genome copy number. Plant Journal, 2021, 108, 219-230.	5.7	22
16	Reciprocal allopolyploid grasses (<i>Festuca</i> Ã— <i>Lolium</i>) display stable patterns of genome dominance. Plant Journal, 2021, 107, 1166-1182.	5.7	14
17	Embryogenic Calli Induction and Salt Stress Response Revealed by RNA-Seq in Diploid Wild Species Gossypium sturtianum and Gossypium raimondii. Frontiers in Plant Science, 2021, 12, 715041.	3.6	3
18	The<i>Gossypium anomalum</i>genome as a resource for cotton improvement and evolutionary analysis of hybrid incompatibility. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	13

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19	A Calmodulin-Like Gene (GbCML7) for Fiber Strength and Yield Improvement Identified by Resequencing Core Accessions of a Pedigree in Gossypium barbadense. Frontiers in Plant Science, 2021, 12, 815648.	3.6	4
20	Reticulate Evolution Helps Explain Apparent Homoplasy in Floral Biology and Pollination in Baobabs (Adansonia; Bombacoideae; Malvaceae). Systematic Biology, 2020, 69, 462-478.	5.6	32
21	Saltâ€tolerance diversity in diploid and polyploid cotton (<i>Gossypium</i>) species. Plant Journal, 2020, 101, 1135-1151.	5.7	34
22	The grand sweep of chromosomal evolution in angiosperms. New Phytologist, 2020, 228, 805-808.	7.3	19
23	Genomics of Evolutionary Novelty in Hybrids and Polyploids. Frontiers in Genetics, 2020, 11, 792.	2.3	103
24	Genome-wide characterization of the GRF family and their roles in response to salt stress in Gossypium. BMC Genomics, 2020, 21, 575.	2.8	23
25	Homoeologous Exchanges, Segmental Allopolyploidy, and Polyploid Genome Evolution. Frontiers in Genetics, 2020, 11, 1014.	2.3	124
26	The miR319-Targeted GhTCP4 Promotes the Transition from Cell Elongation to Wall Thickening in Cotton Fiber. Molecular Plant, 2020, 13, 1063-1077.	8.3	79
27	The <i>Gossypium longicalyx</i> Genome as a Resource for Cotton Breeding and Evolution. G3: Genes, Genomes, Genetics, 2020, 10, 1457-1467.	1.8	32
28	Comparative analysis of codon usage between Gossypium hirsutum and G. barbadense mitochondrial genomes. Mitochondrial DNA Part B: Resources, 2020, 5, 2500-2506.	0.4	4
29	The Utility of Graph Clustering of 5S Ribosomal DNA Homoeologs in Plant Allopolyploids, Homoploid Hybrids, and Cryptic Introgressants. Frontiers in Plant Science, 2020, 11, 41.	3.6	28
30	Coevolution in Hybrid Genomes: Nuclear-Encoded Rubisco Small Subunits and Their Plastid-Targeting Translocons Accompanying Sequential Allopolyploidy Events in<i>Triticum</i>. Molecular Biology and Evolution, 2020, 37, 3409-3422.	8.9	11
31	Conservation and Divergence in Duplicated Fiber Coexpression Networks Accompanying Domestication of the Polyploid <i>Gossypium hirsutum</i> L. G3: Genes, Genomes, Genetics, 2020, 10, 2879-2892.	1.8	30
32	Genomic diversifications of five Gossypium allopolyploid species and their impact on cotton improvement. Nature Genetics, 2020, 52, 525-533.	21.4	249
33	Genetic Analysis of the Transition from Wild to Domesticated Cotton (<i>Gossypium hirsutum</i>L.). G3: Genes, Genomes, Genetics, 2020, 10, 731-754.	1.8	14
34	The chromosome-scale reference genome of black pepper provides insight into piperine biosynthesis. Nature Communications, 2019, 10, 4702.	12.8	115
35	Intergenomic gene transfer in diploid and allopolyploid Gossypium. BMC Plant Biology, 2019, 19, 492.	3.6	14
36	The Genome Sequence of Gossypioides kirkii Illustrates a Descending Dysploidy in Plants. Frontiers in Plant Science, 2019, 10, 1541.	3.6	41

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37	DNA methylation repatterning accompanying hybridization, whole genome doubling and homoeolog exchange in nascent segmental rice allotetraploids. New Phytologist, 2019, 223, 979-992.	7.3	56
38	<i>De Novo</i> Genome Sequence Assemblies of <i>Gossypium raimondii</i> and <i>Gossypium turneri</i>. G3: Genes, Genomes, Genetics, 2019, 9, 3079-3085.	1.8	72
39	Unraveling cis and trans regulatory evolution during cotton domestication. Nature Communications, 2019, 10, 5399.	12.8	58
40	A Malvaceae mystery: A mallow maelstrom of genome multiplications and maybe misleading methods?. Journal of Integrative Plant Biology, 2019, 61, 12-31.	8.5	25
41	Cytonuclear Coevolution following Homoploid Hybrid Speciation in<i>Aegilops tauschii</i>. Molecular Biology and Evolution, 2019, 36, 341-349.	8.9	22
42	Insights into the Evolution of the New World Diploid Cottons (<i>Gossypium</i>,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 547 Td (Subger 53-71.	2.5	45
43	<i>Cis</i>â€“<i>trans</i> controls and regulatory novelty accompanying allopolyploidization. New Phytologist, 2019, 221, 1691-1700.	7.3	68
44	Core <i>cis</i>â€element variation confers subgenomeâ€biased expression of a transcription factor that functions in cotton fiber elongation. New Phytologist, 2018, 218, 1061-1075.	7.3	56
45	Gene Expression Dominance in Allopolyploids: Hypotheses and Models. Trends in Plant Science, 2018, 23, 393-402.	8.8	81
46	The long and short of doubling down: polyploidy, epigenetics, and the temporal dynamics of genome fractionation. Current Opinion in Genetics and Development, 2018, 49, 1-7.	3.3	186
47	Designations for individual genomes and chromosomes in Gossypium. Journal of Cotton Research, 2018, 1, .	2.5	66
48	Molecular evolution of the plastid genome during diversification of the cotton genus. Molecular Phylogenetics and Evolution, 2017, 112, 268-276.	2.7	52
49	Nucleotide diversity in the two co-resident genomes of allopolyploid cotton. Plant Systematics and Evolution, 2017, 303, 1021-1042.	0.9	4
50	A New Species of Cotton from Wake Atoll, <i>Gossypium stephensii</i> (Malvaceae). Systematic Botany, 2017, 42, 115-123.	0.5	94
51	Segmental allotetraploidy generates extensive homoeologous expression rewiring and phenotypic diversity at the population level in rice. Molecular Ecology, 2017, 26, 5451-5466.	3.9	35
52	Cytonuclear responses to genome doubling. American Journal of Botany, 2017, 104, 1277-1280.	1.7	62
53	Evolution of DMSP (dimethylsulfoniopropionate) biosynthesis pathway: Origin and phylogenetic distribution in polyploid Spartina (Poaceae, Chloridoideae). Molecular Phylogenetics and Evolution, 2017, 114, 401-414.	2.7	8
54	Gene-body CG methylation and divergent expression of duplicate genes in rice. Scientific Reports, 2017, 7, 2675.	3.3	25

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55	Plant Mitochondrial Genome Evolution and Cytoplasmic Male Sterility. Critical Reviews in Plant Sciences, 2017, 36, 55-69.	5.7	105
56	Diversity analysis of cotton (Gossypium hirsutum L.) germplasm using the CottonSNP63K Array. BMC Plant Biology, 2017, 17, 37.	3.6	56
57	Comparative Genomics of an Unusual Biogeographic Disjunction in the Cotton Tribe (Gossypieae) Yields Insights into Genome Downsizing. Genome Biology and Evolution, 2017, 9, 3328-3344.	2.5	26
58	Chloroplast DNA Structural Variation, Phylogeny, and Age of Divergence among Diploid Cotton Species. PLoS ONE, 2016, 11, e0157183.	2.5	58
59	Rapid proliferation and nucleolar organizer targeting centromeric retrotransposons in cotton. Plant Journal, 2016, 88, 992-1005.	5.7	33
60	Independent Domestication of Two Old World Cotton Species. Genome Biology and Evolution, 2016, 8, 1940-1947.	2.5	40
61	Evolution of plant genome architecture. Genome Biology, 2016, 17, 37.	8.8	331
62	Evolution of Plant Phenotypes, from Genomes to Traits. G3: Genes, Genomes, Genetics, 2016, 6, 775-778.	1.8	16
63	Insights into the Ecology and Evolution of Polyploid Plants through Network Analysis. Molecular Ecology, 2016, 25, 2644-2660.	3.9	35
64	Evolutionary Conservation and Divergence of Gene Coexpression Networks in<i>Gossypium</i>(Cotton) Seeds. Genome Biology and Evolution, 2016, 8, evw280.	2.5	40
65	Candidate Gene Identification of Flowering Time Genes in Cotton. Plant Genome, 2015, 8, eplantgenome2014.12.0098.	2.8	14
66	Rapid evolutionary divergence of Gossypium barbadense and G. hirsutum mitochondrial genomes. BMC Genomics, 2015, 16, 770.	2.8	42
67	A Transcriptome Profile for Developing Seed of Polyploid Cotton. Plant Genome, 2015, 8, eplantgenome2014.08.0041.	2.8	30
68	Re-evaluating the phylogeny of allopolyploid Gossypium L.. Molecular Phylogenetics and Evolution, 2015, 92, 45-52.	2.7	110
69	Gene-Expression Novelty in Allopolyploid Cotton: A Proteomic Perspective. Genetics, 2015, 200, 91-104.	2.9	37
70	Multiple rounds of ancient and recent hybridizations have occurred within the <i>Aegilops</i>â€“<i>Triticum</i> complex. New Phytologist, 2015, 208, 11-12.	7.3	19
71	The wondrous cycles of polyploidy in plants. American Journal of Botany, 2015, 102, 1753-1756.	1.7	363
72	Persistence of Subgenomes in Paleopolyploid Cotton after 60 My of Evolution. Molecular Biology and Evolution, 2015, 32, 1063-1071.	8.9	85

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73	A reâ€evaluation of the homoploid hybrid origin of <i><scp>A</scp>egilops tauschii</i>, the donor of the wheat Dâ€subgenome. New Phytologist, 2015, 208, 4-8.	7.3	43
74	<i>Gossypium anapoides</i>(Malvaceae), a New Species from Western Australia. Novon, 2015, 23, 447-451.	0.3	22
75	Unraveling the fabric of polyploidy. Nature Biotechnology, 2015, 33, 491-493.	17.5	17
76	A Cluster of Recently Inserted Transposable Elements Associated with siRNAs in Gossypium raimondii. Plant Genome, 2015, 8, eplantgenome2014.11.0088.	2.8	7
77	Genome-Wide Disruption of Gene Expression in Allopolyploids but Not Hybrids of Rice Subspecies. Molecular Biology and Evolution, 2014, 31, 1066-1076.	8.9	74
78	Comparative Evolutionary and Developmental Dynamics of the Cotton (Gossypium hirsutum) Fiber Transcriptome. PLoS Genetics, 2014, 10, e1004073.	3.5	149
79	Control of cotton fibre elongation by a homeodomain transcription factor GhHOX3. Nature Communications, 2014, 5, 5519.	12.8	205
80	Evolution of the BBAA Component of Bread Wheat during Its History at the Allohexaploid Level. Plant Cell, 2014, 26, 2761-2776.	6.6	77
81	CenH3 evolution in diploids and polyploids of three angiosperm genera. BMC Plant Biology, 2014, 14, 383.	3.6	16
82	Polyploid Speciation and Genome Evolution: Lessons from Recent Allopolyploids. , 2014, , 87-113.		16
83	Cytonuclear Evolution of Rubisco in Four Allopolyploid Lineages. Molecular Biology and Evolution, 2014, 31, 2624-2636.	8.9	57
84	Ancient Gene Duplicates in Gossypium (Cotton) Exhibit Near-Complete Expression Divergence. Genome Biology and Evolution, 2014, 6, 559-571.	2.5	72
85	Contemporary and future studies in plant speciation, morphological/floral evolution and polyploidy: honouring the scientific contributions of Leslie D. Gottlieb to plant evolutionary biology. Philosophical Transactions of the Royal Society B: Biological Sciences, 2014, 369, 20130341.	4.0	6
86	Proteomics profiling of fiber development and domestication in upland cotton (Gossypium hirsutum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	3.2	25
87	Doubling down on genomes: Polyploidy and crop plants. American Journal of Botany, 2014, 101, 1711-1725.	1.7	336
88	The legacy of diploid progenitors in allopolyploid gene expression patterns. Philosophical Transactions of the Royal Society B: Biological Sciences, 2014, 369, 20130354.	4.0	111
89	A Bountiful Harvest: Genomic Insights into Crop Domestication Phenotypes. Annual Review of Plant Biology, 2013, 64, 47-70.	18.7	326
90	Proteomic profiling of developing cotton fibers from wild and domesticated <i><scp>G</scp>ossypium barbadense</i>. New Phytologist, 2013, 200, 570-582.	7.3	72

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91	Crop plants as models for understanding plant adaptation and diversification. Frontiers in Plant Science, 2013, 4, 290.	3.6	80
92	Composition and Expression of Conserved MicroRNA Genes in Diploid Cotton (Gossypium) Species. Genome Biology and Evolution, 2013, 5, 2449-2459.	2.5	35
93	Insights into the Evolution of Cotton Diploids and Polyploids from Whole-Genome Re-sequencing. G3: Genes, Genomes, Genetics, 2013, 3, 1809-1818.	1.8	73
94	Proteomic profiling of developing cotton fibers from wild and domesticated Gossypium barbadense. , 2013, 200, 570.		1
95	The Cytonuclear Dimension of Allopolyploid Evolution: An Example from Cotton Using Rubisco. Molecular Biology and Evolution, 2012, 29, 3023-3036.	8.9	59
96	Targeted sequence capture as a powerful tool for evolutionary analysis¹. American Journal of Botany, 2012, 99, 312-319.	1.7	146
97	Targeted Capture of Homoeologous Coding and Noncoding Sequence in Polyploid Cotton. G3: Genes, Genomes, Genetics, 2012, 2, 921-930.	1.8	48
98	Duplicate gene evolution, homoeologous recombination, and transcriptome characterization in allopolyploid cotton. BMC Genomics, 2012, 13, 302.	2.8	102
99	Jeans, Genes, and Genomes: Cotton as a Model for Studying Polyploidy. , 2012, , 181-207.		50
100	Repeated polyploidization of Gossypium genomes and the evolution of spinnable cotton fibres. Nature, 2012, 492, 423-427.	27.8	1,204
101	The hairy problem of epigenetics in evolution. New Phytologist, 2011, 191, 7-9.	7.3	9
102	Parallel up-regulation of the profilin gene family following independent domestication of diploid and allopolyploid cotton (<i>Gossypium</i>). Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 21152-21157.	7.1	61
103	Genomically Biased Accumulation of Seed Storage Proteins in Allopolyploid Cotton. Genetics, 2011, 189, 1103-1115.	2.9	53
104	Sequencing and Utilization of the Gossypium Genomes. Tropical Plant Biology, 2010, 3, 71-74.	1.9	6
105	A draft physical map of a D-genome cotton species (Gossypium raimondii). BMC Genomics, 2010, 11, 395.	2.8	48
106	Multiple patterns of rDNA evolution following polyploidy in Oryza. Molecular Phylogenetics and Evolution, 2010, 55, 136-142.	2.7	32
107	Gene expression in developing fibres of Upland cotton (Gossypium hirsutum L.) was massively altered by domestication. BMC Biology, 2010, 8, 139.	3.8	87
108	Homoeologous nonreciprocal recombination in polyploid cotton. New Phytologist, 2010, 186, 123-134.	7.3	136

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109	Evolutionary rate variation, genomic dominance and duplicate gene expression evolution during allotetraploid cotton speciation. New Phytologist, 2010, 186, 184-193.	7.3	223
110	Phylogenetically Distinct Cellulose Synthase Genes Support Secondary Wall Thickening in Arabidopsis Shoot Trichomes and Cotton Fiber. Journal of Integrative Plant Biology, 2010, 52, 205-220.	8.5	84
111	Recent Insights into Mechanisms of Genome Size Change in Plants. Journal of Botany, 2010, 2010, 1-8.	1.2	86
112	The Origin and Evolution of Gossypium. , 2010, , 1-18.		92
113	The history and disposition of transposable elements in polyploid Gossypium. Genome, 2010, 53, 599-607.	2.0	43
114	Reproductive and Pollination Biology of the Endemic Hawaiian Cotton, <i>Gossypium tomentosum</i> (Malvaceae). Pacific Science, 2010, 64, 45-55.	0.6	18
115	Reciprocal Silencing, Transcriptional Bias and Functional Divergence of Homeologs in Polyploid Cotton (Gossypium). Genetics, 2009, 182, 503-517.	2.9	212
116	Rapid DNA loss as a counterbalance to genome expansion through retrotransposon proliferation in plants. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 17811-17816.	7.1	164
117	Coordinated and Fine-Scale Control of Homoeologous Gene Expression in Allotetraploid Cotton. Journal of Heredity, 2009, 100, 487-490.	2.4	34
118	Evolution and Natural History of the Cotton Genus. , 2009, , 3-22.		169
119	Parallel expression evolution of oxidative stress-related genes in fiber from wild and domesticated diploid and polyploid cotton (Gossypium). BMC Genomics, 2009, 10, 378.	2.8	87
120	Genomic expression dominance in allopolyploids. BMC Biology, 2009, 7, 18.	3.8	232
121	Gene duplication and evolutionary novelty in plants. New Phytologist, 2009, 183, 557-564.	7.3	725
122	Duplicate gene expression in allopolyploid Gossypiumreveals two temporally distinct phases of expression evolution. BMC Biology, 2008, 6, 16.	3.8	235
123	Global analysis of gene expression in cotton fibers from wild and domesticated <i>Gossypium barbadense</i>. Evolution & Development, 2008, 10, 567-582.	2.0	77
124	Evolutionary Genetics of Genome Merger and Doubling in Plants. Annual Review of Genetics, 2008, 42, 443-461.	7.6	618
125	The Evolution of Spinnable Cotton Fiber Entailed Prolonged Development and a Novel Metabolism. PLoS Genetics, 2008, 4, e25.	3.5	93
126	Parallel Domestication, Convergent Evolution and Duplicated Gene Recruitment in Allopolyploid Cotton. Genetics, 2008, 179, 1725-1733.	2.9	57

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127	A Phylogenetic Analysis of Indel Dynamics in the Cotton Genus. Molecular Biology and Evolution, 2008, 25, 1415-1428.	8.9	57
128	Partitioned expression of duplicated genes during development and evolution of a single cell in a polyploid plant. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6191-6195.	7.1	143
129	Meta-analysis of Polyploid Cotton QTL Shows Unequal Contributions of Subgenomes to a Complex Network of Genes and Gene Clusters Implicated in Lint Fiber Development. Genetics, 2007, 176, 2577-2588.	2.9	240
130	Toward Sequencing Cotton (<i>Gossypium</i>) Genomes: Figure 1.. Plant Physiology, 2007, 145, 1303-1310.	4.8	390
131	Microcolinearity and genome evolution in the AdhA region of diploid and polyploid cotton (Gossypium). Plant Journal, 2007, 50, 995-1006.	5.7	89
132	A majority of cotton genes are expressed in single-celled fiber. Planta, 2007, 227, 319-329.	3.2	97
133	Differential lineage-specific amplification of transposable elements is responsible for genome size variation in <i>Gossypium</i>. Genome Research, 2006, 16, 1252-1261.	5.5	378
134	A Novel Approach for Characterizing Expression Levels of Genes Duplicated by Polyploidy. Genetics, 2006, 173, 1823-1827.	2.9	74
135	A global assembly of cotton ESTs. Genome Research, 2006, 16, 441-450.	5.5	138
136	Polyploidy and Crop Improvement. Crop Science, 2006, 46, S-3.	1.8	178
137	Epigenetics and plant evolution. New Phytologist, 2005, 168, 81-91.	7.3	361
138	Genetic and epigenetic consequences of recent hybridization and polyploidy in <i>Spartina</i> (Poaceae). Molecular Ecology, 2005, 14, 1163-1175.	3.9	399
139	Novel patterns of gene expression in polyploid plants. Trends in Genetics, 2005, 21, 539-543.	6.7	316
140	Polyploidy and genome evolution in plants. Current Opinion in Plant Biology, 2005, 8, 135-141.	7.1	1,160
141	Molecular Confirmation of the Position of Gossypium trifurcatum Vollesen. Genetic Resources and Crop Evolution, 2005, 52, 749-753.	1.6	4
142	Organ-Specific Silencing of Duplicated Genes in a Newly Synthesized Cotton Allotetraploid. Genetics, 2004, 168, 2217-2226.	2.9	242
143	Tradeâ€offs among antiâ€herbivore resistance traits: insights from Gossypieae (Malvaceae). American Journal of Botany, 2004, 91, 871-880.	1.7	87
144	Incongruent Patterns of Local and Global Genome Size Evolution in Cotton. Genome Research, 2004, 14, 1474-1482.	5.5	80

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145	Cryptic trysts, genomic mergers, and plant speciation. New Phytologist, 2004, 161, 133-142.	7.3	124
146	Plant speciation â€“ rise of the poor cousins. New Phytologist, 2004, 161, 3-8.	7.3	52
147	Polyploidy and the evolutionary history of cotton. Advances in Agronomy, 2003, 78, 139-186.	5.2	694
148	Rate Variation Among Nuclear Genes and the Age of Polyploidy in Gossypium. Molecular Biology and Evolution, 2003, 20, 633-643.	8.9	325
149	Genes duplicated by polyploidy show unequal contributions to the transcriptome and organ-specific reciprocal silencing. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 4649-4654.	7.1	793
150	Rapid diversification of the cotton genus (<i>Gossypium</i>: Malvaceae) revealed by analysis of sixteen nuclear and chloroplast genes. American Journal of Botany, 2002, 89, 707-725.	1.7	249
151	Feast and famine in plant genomes. Genetica, 2002, 115, 37-47.	1.1	135
152	Intersimple sequence repeat (ISSR) polymorphisms as a genetic marker system in cotton. Molecular Ecology Notes, 2001, 1, 205-208.	1.7	69
153	Comparative development of fiber in wild and cultivated cotton. Evolution & Development, 2001, 3, 3-17.	2.0	145
154	Genome evolution in polyploids. Plant Molecular Biology, 2000, 42, 225-249.	3.9	1,439
155	Ty1-copia-retrotransposon behavior in a polyploid cotton. Chromosome Research, 2000, 8, 73-76.	2.2	55
156	Divergent Evolution of Plant NBS-LRR Resistance Gene Homologues in Dicot and Cereal Genomes. Journal of Molecular Evolution, 2000, 50, 203-213.	1.8	352
157	Copy Number Lability and Evolutionary Dynamics of the <i>Adh</i> Gene Family in Diploid and Tetraploid Cotton (Gossypium). Genetics, 2000, 155, 1913-1926.	2.9	83
158	The tortoise and the hare: choosing between noncoding plastome and nuclear Adh sequences for phylogeny reconstruction in a recently diverged plant group. American Journal of Botany, 1998, 85, 1301-1315.	1.7	423
159	Dispersed Repetitive DNA Has Spread to New Genomes Since Polyploid Formation inâ€‰Cotton. Genome Research, 1998, 8, 479-492.	5.5	234
160	Cladistic biogeography of Gleditsia (Leguminosae) based on ndh F and rpl16 chloroplast gene sequences. American Journal of Botany, 1998, 85, 1753-1765.	1.7	91
161	Toward a unified genetic map of higher plants, transcending the monocotâ€“dicot divergence. Nature Genetics, 1996, 14, 380-382.	21.4	200
162	W<scp>eedy adaptation in</scp><i>S<scp>etaria</scp></i><scp>spp</scp>. II. G<scp>enetic diversity and population genetic structure in</scp><i>S. <scp>glauca</scp>, S</i>. <scp><i>geniculata</i></scp>, <scp>and</scp><i>S. <scp>faberii</scp></i> (P<scp>oaceae</scp>). American Journal of Botany, 1995, 82, 1031-1039.	1.7	34

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163	WEEDY ADAPTATION IN <i>SETARIA</i> SPP. I. ISOZYME ANALYSIS OF GENETIC DIVERSITY AND POPULATION GENETIC STRUCTURE IN <i>SETARIA VIRIDIS</i>. American Journal of Botany, 1995, 82, 308-317.	1.7	45
164	Weedy Adaptation in Setaria spp. I. Isozyme Analysis of Genetic Diversity and Population Genetic Structure in Setaria viridis. American Journal of Botany, 1995, 82, 308.	1.7	47
165	Weedy Adaptation in Setaria spp. II. Genetic Diversity and Population Genetic Structure in S. glauca, S. geniculata, and S. faberii (Poaceae). American Journal of Botany, 1995, 82, 1031.	1.7	19
166	Morphological Diversity and Relationships in the Aâ€Genome Cottons, Gossypium arboreum and G. herbaceum. Crop Science, 1994, 34, 519-527.	1.8	26
167	R eevaluating the origin of domesticated cotton (G ossypium hirsutum ; M alvaceae) using nuclear restriction fragment length polymorphisms (RFLP s). American Journal of Botany, 1994, 81, 1309-1326.	1.7	144
168	Genetic diversity in and phylogenetic relationships of the Brazilian endemic cotton,Gossypium mustelinum (Malvaceae). Plant Systematics and Evolution, 1994, 192, 49-59.	0.9	53
169	Reevaluating the Origin of Domesticated Cotton (Gossypium hirsutum; Malvaceae) Using Nuclear Restriction Fragment Length Polymorphisms (RFLPs). American Journal of Botany, 1994, 81, 1309.	1.7	98
170	Bidirectional cytoplasmic and nuclear introgression in the New World cottons <i>Gossypium barbadense</i> and <i>G. Hirsutum</i> (Malvaceae). American Journal of Botany, 1993, 80, 1203-1208.	1.7	44
171	Bidirectional Cytoplasmic and Nuclear Introgression in the New World Cottons, Gossypium barbadense and G. hirsutum (Malvaceae). American Journal of Botany, 1993, 80, 1203.	1.7	17
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