

# Michael S Barker

## List of Articles by Year in descending order

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citing authors

#	ARTICLE	IF	CITATIONS
1	Complementing model species with model clades. <i>Plant Cell</i> , 2024, 36, 1205-1226.	7.6	12
2	A de novo long-read genome assembly of the sacred datura plant ( <i>Datura wrightii</i> ) reveals a role of tandem gene duplications in the evolution of herbivore-defense response. <i>BMC Genomics</i> , 2024, 25, .	3.3	3
3	Speciesâ€tree topology impacts the inference of ancient wholeâ€genome duplications across the angiosperm phylogeny. <i>American Journal of Botany</i> , 2024, 111, .	2.2	10
4	Doubling down on polyploid discoveries: Global advances in genomics and ecological impacts of polyploidy. <i>American Journal of Botany</i> , 2024, 111, .	2.2	6
5	Chromosome-scale Reference Genome and RAD-based Genetic Map of Yellow Starthistle ( <i>Taraxacum officinale</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 <i>Biology and Evolution</i> , 2024, 16, .	2.4	2
6	Demographic history inference and the polyploid continuum. <i>Genetics</i> , 2023, 224, .	4.2	24
7	GOgetter: A pipeline for summarizing and visualizing GO slim annotations for plant genetic data. <i>Applications in Plant Sciences</i> , 2023, 11, .	1.8	6
8	Chromosome-Scale Genome Assembly of <i>Gilia yorkii</i> Enables Genetic Mapping of Floral Traits in an Interspecies Cross. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.4	7
9	Genome size evolution in the diverse insect order Trichoptera. <i>GigaScience</i> , 2022, 11, .	3.2	58
10	Dynamic genome evolution in a model fern. <i>Nature Plants</i> , 2022, 8, 1038-1051.	11.4	174
11	Pilot RNAâ€seq data from 24 species of vascular plants at Harvard Forest. <i>Applications in Plant Sciences</i> , 2021, 9, .	1.8	6
12	Genes derived from ancient polyploidy have higher genetic diversity and are associated with domestication in <i>Brassica rapa</i> . <i>New Phytologist</i> , 2021, 230, 372-386.	8.1	43
13	The contributions from the progenitor genomes of the mesopolyploid Brassiceae are evolutionarily distinct but functionally compatible. <i>Genome Research</i> , 2021, 31, 799-810.	4.6	30
14	Analysis of the <i>Coptis chinensis</i> genome reveals the diversification of protoberberine-type alkaloids. <i>Nature Communications</i> , 2021, 12, .	13.7	128
15	Patterns and Processes of Diploidization in Land Plants. <i>Annual Review of Plant Biology</i> , 2021, 72, 387-410.	24.5	149
16	Animal chromosome counts reveal a similar range of chromosome numbers but with less polyploidy in animals compared to flowering plants. <i>Journal of Evolutionary Biology</i> , 2021, 34, 1333-1339.	1.9	27
17	Modelling of gene loss propensity in the pangenomes of three Brassica species suggests different mechanisms between polyploids and diploids. <i>Plant Biotechnology Journal</i> , 2021, 19, 2488-2500.	8.8	77
18	Underwater CAM photosynthesis elucidated by <i>Isoetes</i> genome. <i>Nature Communications</i> , 2021, 12, .	13.7	94

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19	Polyloid plants have faster rates of multivariate niche differentiation than their diploid relatives. <i>Ecology Letters</i> , 2020, 23, 68-78.	7.5	153
20	Sequencing and Analyzing the Transcriptomes of a Thousand Species Across the Tree of Life for Green Plants. <i>Annual Review of Plant Biology</i> , 2020, 71, 741-765.	24.5	54
21	Polyploids increase overall diversity despite higher turnover than diploids in the Brassicaceae. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20200962.	2.4	23
22	Phylogeny and multiple independent whole-genome duplication events in the Brassicales. <i>American Journal of Botany</i> , 2020, 107, 1148-1164.	2.2	54
23	TagSeq for gene expression in non-model plants: A pilot study at the Santa Rita Experimental Range NEON core site. <i>Applications in Plant Sciences</i> , 2020, 8, .	1.8	7
24	The <i>Chimonanthus salicifolius</i> genome provides insight into magnoliid evolution and flavonoid biosynthesis. <i>Plant Journal</i> , 2020, 103, 1910-1923.	6.2	60
25	<i>Anthoceros</i> genomes illuminate the origin of land plants and the unique biology of hornworts. <i>Nature Plants</i> , 2020, 6, 259-272.	11.4	328
26	Inferring putative ancient whole-genome duplications in the 1000 Plants (1KP) initiative: access to gene family phylogenies and age distributions. <i>GigaScience</i> , 2020, 9, .	3.2	64
27	Inferring the Demographic History of Inbred Species from Genome-Wide SNP Frequency Data. <i>Molecular Biology and Evolution</i> , 2020, 37, 2124-2136.	4.7	40
28	Transcriptome and organellar sequencing highlights the complex origin and diversification of allotetraploid <i>Brassica napus</i> . <i>Nature Communications</i> , 2019, 10, .	13.7	102
29	Access to RNA-sequencing data from 1,173 plant species: The 1000 Plant transcriptomes initiative (1KP). <i>GigaScience</i> , 2019, 8, .	3.2	156
30	Reply to Nakatani and McLysaght: Analyzing deep duplication events. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 1819-1820.	7.5	19
31	Nuclear Genome Size is Positively Correlated with Median LTR-RT Insertion Time in Fern and Lycophyte Genomes. <i>American Fern Journal</i> , 2019, 109, 248.	0.7	21
32	Current Status and Future Prospects for Fern and Lycophyte Genomics: Introduction to an American Fern Journal Special Issue. <i>American Fern Journal</i> , 2019, 109, 177.	0.7	1
33	Multiple large-scale gene and genome duplications during the evolution of hexapods. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4713-4718.	7.5	192
34	Impact of whole-genome duplication events on diversification rates in angiosperms. <i>American Journal of Botany</i> , 2018, 105, 348-363.	2.2	346
35	Fern genomes elucidate land plant evolution and cyanobacterial symbioses. <i>Nature Plants</i> , 2018, 4, 460-472.	11.4	501
36	Genomic inferences of domestication events are corroborated by written records in <i>Brassica rapa</i> . <i>Molecular Ecology</i> , 2017, 26, 3373-3388.	3.7	81

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37	Diverse genome organization following 13 independent mesopolyploid events in Brassicaceae contrasts with convergent patterns of gene retention. <i>Plant Journal</i> , 2017, 91, 3-21.	6.2	118
38	Multilocus phylogenetic reconstruction informing polyploid relationships of <i>Aconitum</i> subgenus <i>Lycoctonum</i> (Ranunculaceae) in China. <i>Plant Systematics and Evolution</i> , 2017, 303, 727-744.	1.1	12
39	A Successful <i>in vitro</i> Propagation Technique for Resurrection Plants of the Selaginellaceae. <i>American Fern Journal</i> , 2017, 107, 96-104.	0.7	6
40	The Compositae Tree of Life in the age of phylogenomics. <i>Journal of Systematics and Evolution</i> , 2017, 55, 405-410.	3.2	72
41	On the relative abundance of autopolyploids and allopolyploids. <i>New Phytologist</i> , 2016, 210, 391-398.	8.1	417
42	Is hybridization driving the evolution of climatic niche in <i>Alyssum montanum</i> . <i>American Journal of Botany</i> , 2016, 103, 1348-1357.	2.2	47
43	Spreading Wings and flying high: The evolutionary importance of polyploidy after a century of study. <i>American Journal of Botany</i> , 2016, 103, 1139-1145.	2.2	93
44	Transcriptome-derived evidence supports recent polyploidization and a major phylogeographic division in <i>Trithuria submersa</i> (Hydatellaceae, Nymphaeales). <i>New Phytologist</i> , 2016, 210, 310-323.	8.1	14
45	The Small Nuclear Genomes of <i>Selaginella</i> Are Associated with a Low Rate of Genome Size Evolution. <i>Genome Biology and Evolution</i> , 2016, 8, 1516-1525.	2.4	34
46	Most Compositae (Asteraceae) are descendants of a paleohexaploid and all share a paleotetraploid ancestor with the Calyceraceae. <i>American Journal of Botany</i> , 2016, 103, 1203-1211.	2.2	111
47	Methods for studying polyploid diversification and the dead end hypothesis: a reply to Soltis et al. (2014). <i>New Phytologist</i> , 2015, 206, 27-35.	8.1	96
48	The butterfly plant arms-race escalated by gene and genome duplications. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8362-8366.	7.5	524
49	Early genome duplications in conifers and other seed plants. <i>Science Advances</i> , 2015, 1, .	10.9	271
50	Between Two Fern Genomes. <i>GigaScience</i> , 2014, 3, .	3.2	73
51	Data access for the 1,000 Plants (1KP) project. <i>GigaScience</i> , 2014, 3, .	3.2	603
52	Genomics of Compositae crops: reference transcriptome assemblies and evidence of hybridization with wild relatives. <i>Molecular Ecology Resources</i> , 2014, 14, 166-177.	4.8	47
53	Phylotranscriptomic analysis of the origin and early diversification of land plants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, .	7.5	1,264
54	A total evidence approach to understanding phylogenetic relationships and ecological diversity in <i>Selaginella</i> subg. <i>Tetragonostachys</i> . <i>American Journal of Botany</i> , 2013, 100, 1672-1682.	2.2	54

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55	Quantitative visualization of biological data in Google Earth using R	4.8	5
56	Genomics of Compositae weeds: EST libraries, microarrays, and evidence of introgression. American Journal of Botany, 2012, 99, 209-218.	2.2	84
57	Development of an Ultra-Dense Genetic Map of the Sunflower Genome Based on Single-Feature Polymorphisms. PLoS ONE, 2012, 7, e51360.	2.3	13
58	Rarely successful polyploids and their legacy in plant genomes. Current Opinion in Plant Biology, 2012, 15, 140-146.	7.2	249
59	De novo characterization of the gametophyte transcriptome in bracken fern, Pteridium aquilinum. BMC Genomics, 2011, 12, .	3.3	116
60	Molecular Evolution across the Asteraceae: Micro- and Macroevolutionary Processes. Molecular Biology and Evolution, 2011, 28, 3225-3235.	4.7	19
61	Ancient genome duplications during the evolution of kiwifruit (Actinidia) and related Ericales. Annals of Botany, 2010, 106, 497-504.	3.1	99
62	Unfurling Fern Biology in the Genomics Age. BioScience, 2010, 60, 177-185.	3.9	96
63	Probabilistic Models of Chromosome Number Evolution and the Inference of Polyploidy. Systematic Biology, 2010, 59, 132-144.	5.0	210
64	Establishing genomic tools and resources for Guizotia abyssinica (L.f.) Cass.â€”the development of a library of expressed sequence tags, microsatellite loci, and the sequencing of its chloroplast genome. Molecular Ecology Resources, 2010, 10, 1048-1058.	4.8	54
65	The frequency of polyploid speciation in vascular plants. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 13875-13879.	7.5	1,315
66	Paleopolyploidy in the Brassicales: Analyses of the Cleome Transcriptome Elucidate the History of Genome Duplications in Arabidopsis and Other Brassicales. Genome Biology and Evolution, 2009, 1, 391-399.	2.4	241
67	SCARF: maximizing next-generation EST assemblies for evolutionary and population genomic analyses. Bioinformatics, 2009, 25, 535-536.	4.7	13
68	COMPARATIVE GENOMIC AND POPULATION GENETIC ANALYSES INDICATE HIGHLY POROUS GENOMES AND HIGH LEVELS OF GENE FLOW BETWEEN DIVERGENT HELIANTHUS SPECIES. Evolution; International Journal of Organic Evolution, 2009, 63, 2061-2075.	1.9	108
69	Contribution to The Pteridophyte Flora of Puerto Rico. American Fern Journal, 2008, 98, 107-111.	0.7	0
70	Multiple Paleopolyploidizations during the Evolution of the Compositae Reveal Parallel Patterns of Duplicate Gene Retention after Millions of Years. Molecular Biology and Evolution, 2008, 25, 2445-2455.	4.7	349
71	A TAXONOMIC REVISION OF CARIBBEAN ADIANTOPSIS (PTERIDACEAE) 1,2. Annals of the Missouri Botanical Garden, 2006, 93, 371-401.	0.7	9
72	Lepidopteran Soral Crispis on Caribbean Ferns 1. Biotropica, 2005, 37, 314-316.	1.5	12

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73	A Natural History of Ferns. American Fern Journal, 2005, 95, 128-129.	0.7	0
74	Maternal Expression Relaxes Constraint on Innovation of the Anterior Determinant, bicoid. PLoS Genetics, 2005, 1, e57.	3.2	56
75	An Adiantopsis Hybrid from Northeastern Argentina and Vicinity. American Fern Journal, 2003, 93, 42-44.	0.7	6
76	An Evaluation of Sceptridium dissectum (Ophioglossaceae) with ISSR Markers: Implications for Sceptridium Systematics. American Fern Journal, 2003, 93, 1-19.	0.7	17
77	Botrychium lanceolatum subsp. angustisegmentum in Ohio. American Fern Journal, 2003, 93, 93-94.	0.7	0
78	Assessing the performance of Ks plots for detecting ancient whole genome duplications. Genome Biology and Evolution, 0, , .	2.4	70
79	Phylogenomic synteny reveals paleohexaploid-derived genomic blocks across Asteraceae. Proceedings of the National Academy of Sciences of the United States of America, 0, 123, .	7.5	0