

# Peter Morrell

## List of Publications by Year in descending order

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Version: 2024-02-01

60  
papers

6,767  
citations

126708

33  
h-index

143772

57  
g-index

72  
all docs

72  
docs citations

72  
times ranked

7548  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide comparative diversity uncovers multiple targets of selection for improvement in hexaploid wheat landraces and cultivars. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 8057-8062.	3.3	1,065
2	Comparative population genomics of maize domestication and improvement. <i>Nature Genetics</i> , 2012, 44, 808-811.	9.4	816
3	Crop genomics: advances and applications. <i>Nature Reviews Genetics</i> , 2012, 13, 85-96.	7.7	439
4	Plant domestication, a unique opportunity to identify the genetic basis of adaptation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 8641-8648.	3.3	385
5	Genetic evidence for a second domestication of barley ( <i>Hordeum vulgare</i> ) east of the Fertile Crescent. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 3289-3294.	3.3	331
6	Is self-fertilization an evolutionary dead end? Revisiting an old hypothesis with genetic theories and a macroevolutionary approach. <i>American Journal of Botany</i> , 2001, 88, 1143-1150.	0.8	321
7	Barley whole exome capture: a tool for genomic research in the genus <i>Hordeum</i> and beyond. <i>Plant Journal</i> , 2013, 76, 494-505.	2.8	260
8	Exome sequencing highlights the role of wild-relative introgression in shaping the adaptive landscape of the wheat genome. <i>Nature Genetics</i> , 2019, 51, 896-904.	9.4	225
9	Genome comparisons reveal a dominant mechanism of chromosome number reduction in grasses and accelerated genome evolution in Triticeae. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15780-15785.	3.3	190
10	Nucleotide diversity maps reveal variation in diversity among wheat genomes and chromosomes. <i>BMC Genomics</i> , 2010, 11, 702.	1.2	189
11	Low levels of linkage disequilibrium in wild barley ( <i>Hordeum vulgare</i> ssp. <i>spontaneum</i> ) despite high rates of self-fertilization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2442-2447.	3.3	184
12	Genetic diversity and structure in semiwild and domesticated chiles ( <i>Capsicum annum</i> ); Tj ETQqO 0 0 rgBT /Overlock 10 Tf 50 30	0.8	163
13	Genetic Costs of Domestication and Improvement. <i>Journal of Heredity</i> , 2018, 109, 103-116.	1.0	149
14	Genomics and the Contrasting Dynamics of Annual and Perennial Domestication. <i>Trends in Genetics</i> , 2015, 31, 709-719.	2.9	145
15	MULTILOCUS INTERACTIONS RESTRICT GENE INTROGRESSION IN INTERSPECIFIC POPULATIONS OF POLYPLOID GOSSYPIUM (COTTON). <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 798-814.	1.1	133
16	Tracing the Geographic Origins of Major Avocado Cultivars. <i>Journal of Heredity</i> , 2008, 100, 56-65.	1.0	126
17	Barley landraces are characterized by geographically heterogeneous genomic origins. <i>Genome Biology</i> , 2015, 16, 173.	3.8	117
18	Crop-to-weed introgression has impacted allelic composition of johnsongrass populations with and without recent exposure to cultivated sorghum. <i>Molecular Ecology</i> , 2005, 14, 2143-2154.	2.0	111

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19	Distinct geographic patterns of genetic diversity are maintained in wild barley ( <i>Hordeum vulgare</i> ssp.) Tj ETQq1 1 of America, 2003, 100, 10812-10817.	0.784314 3.3	rgBT /Ove 94
20	Megabase-Scale Inversion Polymorphism in the Wild Ancestor of Maize. <i>Genetics</i> , 2012, 191, 883-894.	1.2	94
21	The Role of Deleterious Substitutions in Crop Genomes. <i>Molecular Biology and Evolution</i> , 2016, 33, 2307-2317.	3.5	83
22	Toward Integration of Comparative Genetic, Physical, Diversity, and Cytomolecular Maps for Grasses and Grains, Using the Sorghum Genome as a Foundation. <i>Plant Physiology</i> , 2001, 125, 1325-1341.	2.3	81
23	Genes that determine flower color: the role of regulatory changes in the evolution of phenotypic adaptations. <i>Molecular Phylogenetics and Evolution</i> , 2003, 29, 507-518.	1.2	73
24	Development and Genetic Characterization of an Advanced Backcross-Nested Association Mapping (AB-NAM) Population of Wild Å– Cultivated Barley. <i>Genetics</i> , 2016, 203, 1453-1467.	1.2	73
25	Determination and Applications of Environmental Costs at Different Sized Airports “ Aircraft Noise and Engine Emissions. <i>Transportation</i> , 2006, 33, 45-61.	2.1	70
26	Deleterious variants in Asian rice and the potential cost of domestication. <i>Molecular Biology and Evolution</i> , 2017, 34, msw296.	3.5	68
27	Plant Genome Editing and the Relevance of Off-Target Changes. <i>Plant Physiology</i> , 2020, 183, 1453-1471.	2.3	68
28	Estimating the Contribution of Mutation, Recombination and Gene Conversion in the Generation of Haplotypic Diversity. <i>Genetics</i> , 2006, 173, 1705-1723.	1.2	44
29	Nucleotide Diversity and Linkage Disequilibrium in Wild Avocado ( <i>Persea americana</i> Mill.). <i>Journal of Heredity</i> , 2008, 99, 382-389.	1.0	44
30	Resequencing Data Indicate a Modest Effect of Domestication on Diversity in Barley: A Cultigen With Multiple Origins. <i>Journal of Heredity</i> , 2014, 105, 253-264.	1.0	42
31	The Influence of Linkage and Inbreeding on Patterns of Nucleotide Sequence Diversity at Duplicate Alcohol Dehydrogenase Loci in Wild Barley ( <i>Hordeum vulgare</i> ssp. <i>spontaneum</i> ). <i>Genetics</i> , 2002, 162, 2007-2015.	1.2	41
32	Evidence of Positive Selection for a Glycogen Synthase ( <i>GYS1</i> ) Mutation in Domestic Horse Populations. <i>Journal of Heredity</i> , 2014, 105, 163-172.	1.0	40
33	Environmental Association Analyses Identify Candidates for Abiotic Stress Tolerance in <i>Glycine soja</i> , the Wild Progenitor of Cultivated Soybeans. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 835-843.	0.8	39
34	Two Genomic Regions Contribute Disproportionately to Geographic Differentiation in Wild Barley. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1193-1203.	0.8	38
35	Intercontinental dispersal: The origin of the widespread South American plant species <i>Gilia laciniata</i> (Polemoniaceae) from a rare California and Oregon coastal endemic. <i>Plant Systematics and Evolution</i> , 2000, 224, 13-32.	0.3	36
36	Comparative Genomics Approaches Accurately Predict Deleterious Variants in Plants. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3321-3329.	0.8	36

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37	Molecular tests of the proposed diploid hybrid origin of <i>Gilia achilleifolia</i> (Polemoniaceae). <i>American Journal of Botany</i> , 1998, 85, 1439-1453.	0.8	33
38	The environmental cost implication of hub–hub versus hub by-pass flight networks. <i>Transportation Research, Part D: Transport and Environment</i> , 2007, 12, 143-157.	3.2	33
39	Genomic variants affecting homoeologous gene expression dosage contribute to agronomic trait variation in allopolyploid wheat. <i>Nature Communications</i> , 2022, 13, 826.	5.8	31
40	Development of a Multiparent Population for Genetic Mapping and Allele Discovery in Six-Row Barley. <i>Genetics</i> , 2019, 213, 595-613.	1.2	23
41	Evaluating an interspecific <i>Helianthus annuus</i> – <i>Helianthus tuberosus</i> population for use in a perennial sunflower breeding program. <i>Field Crops Research</i> , 2014, 155, 254-264.	2.3	21
42	The Effects of Both Recent and Long-Term Selection and Genetic Drift Are Readily Evident in North American Barley Breeding Populations. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 609-622.	0.8	21
43	MULTILOCUS INTERACTIONS RESTRICT GENE INTROGRESSION IN INTERSPECIFIC POPULATIONS OF POLYPLOID <i>GOSSYPIUM</i> (COTTON). <i>Evolution; International Journal of Organic Evolution</i> , 2000, 54, 798.	1.1	20
44	<sc>angsd</sc> wrapper: utilities for analysing next-generation sequencing data. <i>Molecular Ecology Resources</i> , 2016, 16, 1449-1454.	2.2	18
45	Environmental Association Identifies Candidates for Tolerance to Low Temperature and Drought. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3423-3438.	0.8	18
46	Domestication: Polyploidy boosts domestication. <i>Nature Plants</i> , 2016, 2, 16116.	4.7	16
47	<i>Hordeum</i> . , 2011, , 309-319.		12
48	Tracing the Geographic Origins of Weedy <i>Ipomoea purpurea</i> in the Southeastern United States. <i>Journal of Heredity</i> , 2013, 104, 666-677.	1.0	12
49	The Fate of Deleterious Variants in a Barley Genomic Prediction Population. <i>Genetics</i> , 2019, 213, 1531-1544.	1.2	12
50	Evaluation and implications of environmental charges on commercial flights. <i>Transport Reviews</i> , 2001, 21, 377-395.	4.7	11
51	Error detection in SNP data by considering the likelihood of recombinational history implied by three-site combinations. <i>Bioinformatics</i> , 2007, 23, 1807-1814.	1.8	11
52	Comparative Analyses Identify the Contributions of Exotic Donors to Disease Resistance in a Barley Experimental Population. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1945-1953.	0.8	11
53	<sc>SNPM</sc>: <sc>SNP</sc> annotation and <sc>SNP</sc> metadata collection without a reference genome. <i>Molecular Ecology Resources</i> , 2014, 14, 419-425.	2.2	11
54	Nucleotide Sequence Diversity and Linkage Disequilibrium of Four Nuclear Loci in Foxtail Millet ( <i>Setaria italica</i> ). <i>PLoS ONE</i> , 2015, 10, e0137088.	1.1	6

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55	Allele-specific PCR can improve the efficiency of experimental resolution of heterozygotes in resequencing studies. <i>Molecular Ecology Resources</i> , 2010, 10, 647-658.	2.2	4
56	Nucleotide Sequence Diversity of Floral Pigment Genes in Mexican Populations of <i>Ipomoea purpurea</i> (Morning Glory) Accord with a Neutral Model of Evolution. <i>Journal of Heredity</i> , 2012, 103, 863-872.	1.0	4
57	Fast neutron mutagenesis in soybean enriches for small indels and creates frameshift mutations. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	4
58	The evolutionary patterns of barley pericentromeric chromosome regions, as shaped by linkage disequilibrium and domestication. <i>Plant Journal</i> , 0, , .	2.8	3
59	Mutational Processes. , 2004, , 760-762.		2
60	Utilizing whole genome sequences to study population genomics of gene networks: a case study of the <i>Arabidopsis thaliana</i> immune-signaling network. <i>Genome Biology</i> , 2011, 12, .	13.9	0