

Extensive introgression in a malaria vector species com

Science

347, 1258524

DOI: [10.1126/science.1258524](https://doi.org/10.1126/science.1258524)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Research highlights for issue 2: recent applications in molecular evolution. <i>Evolutionary Applications</i> , 2015, 8, 119-120.	1.5	0
2	Insect phylogenomics. <i>Insect Molecular Biology</i> , 2015, 24, 403-411.	1.0	17
3	A maximum pseudo-likelihood approach for phylogenetic networks. <i>BMC Genomics</i> , 2015, 16, S10.	1.2	164
4	Reticulate Speciation and Barriers to Introgression in the <i>Anopheles gambiae</i> Species Complex. <i>Genome Biology and Evolution</i> , 2015, 7, 3116-3131.	1.1	32
5	Divergence and gene flow among Darwin's finches: A genome-wide view of adaptive radiation driven by interspecies allele sharing. <i>BioEssays</i> , 2015, 37, 968-974.	1.2	16
6	Negligible nuclear introgression despite complete mitochondrial capture between two species of chipmunks. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 1961-1972.	1.1	88
7	Heterosis Increases Fertility, Fecundity, and Survival of Laboratory-Produced F1 Hybrid Males of the Malaria Mosquito <i>Anopheles coluzzii</i> . <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2693-2709.	0.8	27
8	Does extreme asymmetric dominance promote hybridization between <i>Anopheles coluzzii</i> and <i>Anopheles gambiae</i> s.s. in seasonal malaria mosquito communities of West Africa?. <i>Parasites and Vectors</i> , 2015, 8, 586.	1.0	16
9	DNA Barcode Development for Three Recent Exotic Whitefly (Hemiptera: Aleyrodidae) Invaders in Florida. <i>Florida Entomologist</i> , 2015, 98, 473-478.	0.2	16
10	Diversification of the Genus <i>Anopheles</i> and a Neotropical Clade from the Late Cretaceous. <i>PLoS ONE</i> , 2015, 10, e0134462.	1.1	29
11	Hybridization in Parasites: Consequences for Adaptive Evolution, Pathogenesis, and Public Health in a Changing World. <i>PLoS Pathogens</i> , 2015, 11, e1005098.	2.1	108
12	Hybrid zones: windows on climate change. <i>Trends in Ecology and Evolution</i> , 2015, 30, 398-406.	4.2	178
13	A Genome-Scale Investigation of Incongruence in Culicidae Mosquitoes. <i>Genome Biology and Evolution</i> , 2015, 7, 3463-3471.	1.1	8
14	Conundrum of jumbled mosquito genomes. <i>Science</i> , 2015, 347, 27-28.	6.0	29
15	Whole-genome sequencing reveals absence of recent gene flow and separate demographic histories for <i>Anopheles punctulatus</i> mosquitoes in Papua New Guinea. <i>Molecular Ecology</i> , 2015, 24, 1263-1274.	2.0	13
16	Evolving the world's most dangerous animal. <i>Trends in Parasitology</i> , 2015, 31, 39-40.	1.5	5
17	Connecting genotypes to medically relevant phenotypes in major vector mosquitoes. <i>Current Opinion in Insect Science</i> , 2015, 10, 59-64.	2.2	0
18	A maturing understanding of the composition of the insect gene repertoire. <i>Current Opinion in Insect Science</i> , 2015, 7, 15-23.	2.2	24

#	ARTICLE	IF	CITATIONS
19	Detection and Polarization of Introgression in a Five-Taxon Phylogeny. <i>Systematic Biology</i> , 2015, 64, 651-662.	2.7	244
20	Genome-wide QTL mapping of saltwater tolerance in sibling species of <i>Anopheles</i> (malaria vector) mosquitoes. <i>Heredity</i> , 2015, 115, 471-479.	1.2	17
21	Analysis of phylogenomic datasets reveals conflict, concordance, and gene duplications with examples from animals and plants. <i>BMC Evolutionary Biology</i> , 2015, 15, 150.	3.2	350
22	Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. <i>Science</i> , 2015, 347, 1258522.	6.0	492
23	Inferring Phylogenetic Networks with Maximum Pseudolikelihood under Incomplete Lineage Sorting. <i>PLoS Genetics</i> , 2016, 12, e1005896.	1.5	348
24	The Genetic Basis of Host Preference and Resting Behavior in the Major African Malaria Vector, <i>Anopheles arabiensis</i> . <i>PLoS Genetics</i> , 2016, 12, e1006303.	1.5	76
25	Genomic heterogeneity of historical gene flow between two species of newts inferred from transcriptome data. <i>Ecology and Evolution</i> , 2016, 6, 4513-4525.	0.8	21
26	Becoming pure: identifying generational classes of admixed individuals within lesser and greater saucup populations. <i>Molecular Ecology</i> , 2016, 25, 661-674.	2.0	37
27	Evolution of <i>GOUNDRY</i> , a cryptic subgroup of <i>Anopheles gambiae</i> s.l., and its impact on susceptibility to <i>Plasmodium</i> infection. <i>Molecular Ecology</i> , 2016, 25, 1494-1510.	2.0	18
28	A genomic perspective on hybridization and speciation. <i>Molecular Ecology</i> , 2016, 25, 2337-2360.	2.0	458
29	Identifying targets of selection in mosaic genomes with machine learning: applications in <i>Anopheles gambiae</i> for detecting sites within locally adapted chromosomal inversions. <i>Molecular Ecology</i> , 2016, 25, 2226-2243.	2.0	7
30	Powerful methods for detecting introgressed regions from population genomic data. <i>Molecular Ecology</i> , 2016, 25, 2387-2397.	2.0	78
31	Shift in species composition in the <i>Anopheles gambiae</i> complex after implementation of long-lasting insecticidal nets in Dielmo, Senegal. <i>Medical and Veterinary Entomology</i> , 2016, 30, 365-368.	0.7	35
32	Challenges in Species Tree Estimation Under the Multispecies Coalescent Model. <i>Genetics</i> , 2016, 204, 1353-1368.	1.2	137
33	Radical remodeling of the Y chromosome in a recent radiation of malaria mosquitoes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2114-23.	3.3	92
34	On Tree-Based Phylogenetic Networks. <i>Journal of Computational Biology</i> , 2016, 23, 553-565.	0.8	41
35	Chromosome evolution in malaria mosquitoes inferred from physically mapped genome assemblies. <i>Journal of Bioinformatics and Computational Biology</i> , 2016, 14, 1630003.	0.3	8
36	Recent advances in malaria genomics and epigenomics. <i>Genome Medicine</i> , 2016, 8, 92.	3.6	37

#	ARTICLE	IF	CITATIONS
37	The last bastion? X chromosome genotyping of <i>Anopheles gambiae</i> species pair males from a hybrid zone reveals complex recombination within the major candidate genomic island of speciation™. <i>Molecular Ecology</i> , 2016, 25, 5719-5731.	2.0	15
38	Distinguishing contemporary hybridization from past introgression with postgenomic ancestry-informative SNPs in strongly differentiated <i>Ciona</i> species. <i>Molecular Ecology</i> , 2016, 25, 5527-5542.	2.0	50
39	Maximum Likelihood Implementation of an Isolation-with-Migration Model for Three Species. <i>Systematic Biology</i> , 2017, 66, syw063.	2.7	45
40	How reticulated are species?. <i>BioEssays</i> , 2016, 38, 140-149.	1.2	449
41	hybridcheck: software for the rapid detection, visualization and dating of recombinant regions in genome sequence data. <i>Molecular Ecology Resources</i> , 2016, 16, 534-539.	2.2	52
42	Irrational exuberance for resolved species trees. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 7-17.	1.1	177
43	Hidden histories of gene flow in highland birds revealed with genomic markers. <i>Molecular Ecology</i> , 2016, 25, 5144-5157.	2.0	64
44	Gene Tree Discordance Can Generate Patterns of Diminishing Convergence over Time. <i>Molecular Biology and Evolution</i> , 2016, 33, 3299-3307.	3.5	58
45	Distribution of coalescent histories under the coalescent model with gene flow. <i>Molecular Phylogenetics and Evolution</i> , 2016, 105, 177-192.	1.2	11
46	Genomics of speciation and introgression in Princess cichlid fishes from Lake Tanganyika. <i>Molecular Ecology</i> , 2016, 25, 6143-6161.	2.0	68
47	Sequencing of the genus <i>Arabidopsis</i> identifies a complex history of nonbifurcating speciation and abundant trans-specific polymorphism. <i>Nature Genetics</i> , 2016, 48, 1077-1082.	9.4	198
48	Reticulation, divergence, and the phylogeography phylogenetics continuum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8025-8032.	3.3	130
49	Mosquito Vectors and the Globalization of <i>Plasmodium falciparum</i> Malaria. <i>Annual Review of Genetics</i> , 2016, 50, 447-465.	3.2	51
50	Advances using molecular data in insect systematics. <i>Current Opinion in Insect Science</i> , 2016, 18, 40-47.	2.2	13
51	Genome-Wide Divergence in the West-African Malaria Vector <i>Anopheles melas</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2867-2879.	0.8	10
52	Speciation Continuum. , 2016, , 159-165.		24
53	Split Scores: A Tool to Quantify Phylogenetic Signal in Genome-Scale Data. <i>Systematic Biology</i> , 2017, 66, syw103.	2.7	21
54	Chromosomal inversions and ecotypic differentiation in <i>Anopheles gambiae</i> : the perspective from whole-genome sequencing. <i>Molecular Ecology</i> , 2016, 25, 5889-5906.	2.0	35

#	ARTICLE	IF	CITATIONS
55	In the light of deep coalescence: revisiting trees within networks. BMC Bioinformatics, 2016, 17, 415.	1.2	45
56	Exploring phylogenetic hypotheses via Gibbs sampling on evolutionary networks. BMC Genomics, 2016, 17, 784.	1.2	2
57	Reticulate evolutionary history and extensive introgression in mosquito species revealed by phylogenetic network analysis. Molecular Ecology, 2016, 25, 2361-2372.	2.0	98
58	Evaluation of DISCOVAR de novo using a mosquito sample for cost-effective short-read genome assembly. BMC Genomics, 2016, 17, 187.	1.2	60
59	Genome-wide introgression among distantly related Heliconius butterfly species. Genome Biology, 2016, 17, 25.	3.8	115
60	Maintenance of Species Boundaries Despite Ongoing Gene Flow in Ragworts. Genome Biology and Evolution, 2016, 8, 1038-1047.	1.1	18
61	Disease vectors in the era of next generation sequencing. Genome Biology, 2016, 17, 95.	3.8	25
62	Transcriptomic differences between euryhaline and stenohaline malaria vector sibling species in response to salinity stress. Molecular Ecology, 2016, 25, 2210-2225.	2.0	17
63	Plant-Herbivore Interactions in the Era of Big Data. , 2016, , 3-48.		2
64	Genomics at the evolving species boundary. Current Opinion in Insect Science, 2016, 13, 7-15.	2.2	9
65	Balancing push and pull in Confuga, an active storage cluster file system for scientific workflows. Concurrency Computation Practice and Experience, 2017, 29, e3834.	1.4	0
66	The Evolution of Genome Structure by Natural and Sexual Selection. Journal of Heredity, 2017, 108, 3-11.	1.0	72
67	Extensive genetic diversity among populations of the malaria mosquito Anopheles moucheti revealed by population genomics. Infection, Genetics and Evolution, 2017, 48, 27-33.	1.0	23
68	A morphological and phylogenetic investigation into divergence among sympatric Australian southern bull kelps (<i>Durvillaea potatorum</i> and <i>D. amatheiae</i> sp. nov.). Molecular Phylogenetics and Evolution, 2017, 107, 630-643.	1.2	16
69	Chromosome inversions and ecological plasticity in the main African malaria mosquitoes. Evolution; International Journal of Organic Evolution, 2017, 71, 686-701.	1.1	51
70	Phylogenomics provides new insight into evolutionary relationships and genealogical discordance in the reef-building coral genus <i>Acropora</i> . Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20162182.	1.2	30
71	Whole genome sequencing data and de novo draft assemblies for 66 teleost species. Scientific Data, 2017, 4, 160132.	2.4	67
72	Anopheline salivary protein genes and gene families: an evolutionary overview after the whole genome sequence of sixteen Anopheles species. BMC Genomics, 2017, 18, 153.	1.2	59

#	ARTICLE	IF	CITATIONS
73	Molecular and morphometric data suggest the presence of a neglected species in the marine gastropod family Conidae. <i>Molecular Phylogenetics and Evolution</i> , 2017, 109, 421-429.	1.2	8
74	Bounds to parapatric speciation: A Dobzhansky-Muller incompatibility model involving autosomes, X chromosomes, and mitochondria. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 1366-1380.	1.1	24
75	When COI barcodes deceive: complete genomes reveal introgression in hairstreaks. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20161735.	1.2	39
76	Watching speciation in action. <i>Science</i> , 2017, 355, 910-911.	6.0	18
77	Genome content analysis yields new insights into the relationship between the human malaria parasite <i>Plasmodium falciparum</i> and its anopheline vectors. <i>BMC Genomics</i> , 2017, 18, 205.	1.2	2
78	Homology-aware Phylogenomics at Gigabase Scales. <i>Systematic Biology</i> , 2017, 66, syw104.	2.7	34
79	Pollutants and Insecticides Drive Local Adaptation in African Malaria Mosquitoes. <i>Molecular Biology and Evolution</i> , 2017, 34, 1261-1275.	3.5	50
80	Pan-American Similarities in Genetic Structures of <i>Helicoverpa armigera</i> and <i>Helicoverpa zea</i> (Lepidoptera: Noctuidae) With Implications for Hybridization. <i>Environmental Entomology</i> , 2017, 46, 1024-1034.	0.7	21
81	Massive introgression drives species radiation at the range limit of <i>Anopheles gambiae</i> . <i>Scientific Reports</i> , 2017, 7, 46451.	1.6	28
82	Rapid radiations of both kiwifruit hybrid lineages and their parents shed light on a two-layer mode of species diversification. <i>New Phytologist</i> , 2017, 215, 877-890.	3.5	52
83	Can genomic data alone tell us whether speciation happened with gene flow?. <i>Molecular Ecology</i> , 2017, 26, 2845-2849.	2.0	43
84	The impact of GC bias on phylogenetic accuracy using targeted enrichment phylogenomic data. <i>Molecular Phylogenetics and Evolution</i> , 2017, 111, 149-157.	1.2	50
85	Exploring Evolutionary Relationships Across the Genome Using Topology Weighting. <i>Genetics</i> , 2017, 206, 429-438.	1.2	193
86	Genomic evidence for convergent evolution of a key trait underlying divergence in island birds. <i>Molecular Ecology</i> , 2017, 26, 3760-3774.	2.0	20
87	Interspecific hybridization causes long-term phylogenetic discordance between nuclear and mitochondrial genomes in freshwater fishes. <i>Molecular Ecology</i> , 2017, 26, 3116-3127.	2.0	61
88	The value of new genome references. <i>Experimental Cell Research</i> , 2017, 358, 433-438.	1.2	19
89	Genomewide variation provides insight into evolutionary relationships in a monkeyflower species complex (<i>Mimulus</i> sect. <i>Diplacus</i>). <i>American Journal of Botany</i> , 2017, 104, 1510-1521.	0.8	18
90	Genomics of natural populations: Evolutionary forces that establish and maintain gene arrangements in <i>Drosophila pseudoobscura</i> . <i>Molecular Ecology</i> , 2017, 26, 6539-6562.	2.0	37

#	ARTICLE	IF	CITATIONS
91	Genome-Guided Phylo-Transcriptomic Methods and the Nuclear Phylogenetic Tree of the Paniceae Grasses. <i>Scientific Reports</i> , 2017, 7, 13528.	1.6	27
92	Extensive gene tree discordance and hemiplasy shaped the genomes of North American columnar cacti. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12003-12008.	3.3	90
93	Genome-wide signatures of complex introgression and adaptive evolution in the big cats. <i>Science Advances</i> , 2017, 3, e1700299.	4.7	142
94	Interpreting the genomic landscape of introgression. <i>Current Opinion in Genetics and Development</i> , 2017, 47, 69-74.	1.5	186
95	Cross-Species Y Chromosome Function Between Malaria Vectors of the <i>Anopheles gambiae</i> Species Complex. <i>Genetics</i> , 2017, 207, 729-740.	1.2	18
96	Patterns of divergence across the geographic and genomic landscape of a butterfly hybrid zone associated with a climatic gradient. <i>Molecular Ecology</i> , 2017, 26, 4725-4742.	2.0	44
98	Dissecting functional components of reproductive isolation among closely related sympatric species of the <i>Anopheles gambiae</i> complex. <i>Evolutionary Applications</i> , 2017, 10, 1102-1120.	1.5	39
99	Wing Morphometry and Genetic Variability Between <i>Culex coronator</i> and <i>Culex usquatus</i> (Diptera: Tj ETQq1 1 0.784314 rgBT /Overl 0.9 7 901-908.	0.9	7
100	No evidence for maintenance of a sympatric <i>Heliconius</i> species barrier by chromosomal inversions. <i>Evolution Letters</i> , 2017, 1, 138-154.	1.6	90
101	Genomic insights into adaptive divergence and speciation among malaria vectors of the <i>Anopheles nili</i> group. <i>Evolutionary Applications</i> , 2017, 10, 897-906.	1.5	14
102	Evolution of novel mimicry rings facilitated by adaptive introgression in tropical butterflies. <i>Molecular Ecology</i> , 2017, 26, 5160-5172.	2.0	70
103	Speciation as a sieve for ancestral polymorphism. <i>Molecular Ecology</i> , 2017, 26, 5362-5368.	2.0	88
104	Rapid neo-sex chromosome evolution and incipient speciation in a major forest pest. <i>Nature Communications</i> , 2017, 8, 1593.	5.8	59
105	Widespread paleopolyploidy, gene tree conflict, and recalcitrant relationships among the carnivorous Caryophyllales. <i>American Journal of Botany</i> , 2017, 104, 858-867.	0.8	62
106	A program to compute the soft Robinson-Foulds distance between phylogenetic networks. <i>BMC Genomics</i> , 2017, 18, 111.	1.2	11
107	A whole genome gene content phylogenetic analysis of anopheline mosquitoes. <i>Molecular Phylogenetics and Evolution</i> , 2017, 107, 266-269.	1.2	6
108	<i>Solanum insanum</i> L. (subgenus <i>Leptostemonum</i> Bitter, Solanaceae), the neglected wild progenitor of eggplant (<i>S. melongena</i> L.): a review of taxonomy, characteristics and uses aimed at its enhancement for improved eggplant breeding. <i>Genetic Resources and Crop Evolution</i> , 2017, 64, 1707-1722.	0.8	39
109	Hybrids and horizontal transfer: introgression allows adaptive allele discovery. <i>Journal of Experimental Botany</i> , 2017, 68, 5453-5470.	2.4	24

#	ARTICLE	IF	CITATIONS
110	Admixture and Ancestry Inference from Ancient and Modern Samples through Measures of Population Genetic Drift. <i>Human Biology</i> , 2017, 89, 21.	0.4	30
111	Stable feature ranking with logistic regression ensembles. , 2017, , .		1
112	Chromosomal Speciation in the Genomics Era: Disentangling Phylogenetic Evolution of Rock-wallabies. <i>Frontiers in Genetics</i> , 2017, 8, 10.	1.1	78
113	The implementation of long-lasting insecticidal bed nets has differential effects on the genetic structure of the African malaria vectors in the <i>Anopheles gambiae</i> complex in Dielmo, Senegal. <i>Malaria Journal</i> , 2017, 16, 337.	0.8	16
114	New prospects in the detection and comparative analysis of hybridization in the tree of life. <i>American Journal of Botany</i> , 2018, 105, 364-375.	0.8	150
115	Genomic evidence of speciation reversal in ravens. <i>Nature Communications</i> , 2018, 9, 906.	5.8	105
116	Engineered Reciprocal Chromosome Translocations Drive High Threshold, Reversible Population Replacement in <i>Drosophila</i> . <i>ACS Synthetic Biology</i> , 2018, 7, 1359-1370.	1.9	72
117	Coestimating Reticulate Phylogenies and Gene Trees from Multilocus Sequence Data. <i>Systematic Biology</i> , 2018, 67, 439-457.	2.7	124
118	Genomes of Diptera. <i>Current Opinion in Insect Science</i> , 2018, 25, 116-124.	2.2	26
119	Ancient genomic variation underlies repeated ecological adaptation in young stickleback populations. <i>Evolution Letters</i> , 2018, 2, 9-21.	1.6	127
120	Genomes of 13 domesticated and wild rice relatives highlight genetic conservation, turnover and innovation across the genus <i>Oryza</i> . <i>Nature Genetics</i> , 2018, 50, 285-296.	9.4	413
121	A genomic map of clinal variation across the European rabbit hybrid zone. <i>Molecular Ecology</i> , 2018, 27, 1457-1478.	2.0	30
122	Variation and constraints in hybrid genome formation. <i>Nature Ecology and Evolution</i> , 2018, 2, 549-556.	3.4	69
123	Rapid evolution in insect pests: the importance of space and time in population genomics studies. <i>Current Opinion in Insect Science</i> , 2018, 26, 8-16.	2.2	58
124	BUSCO Applications from Quality Assessments to Gene Prediction and Phylogenomics. <i>Molecular Biology and Evolution</i> , 2018, 35, 543-548.	3.5	1,844
125	Human Interventions: Driving Forces of Mosquito Evolution. <i>Trends in Parasitology</i> , 2018, 34, 127-139.	1.5	20
126	Analysis of natural female post-mating responses of <i>Anopheles gambiae</i> and <i>Anopheles coluzzii</i> unravels similarities and differences in their reproductive ecology. <i>Scientific Reports</i> , 2018, 8, 6594.	1.6	17
127	Gene flow analysis method, the D-statistic, is robust in a wide parameter space. <i>BMC Bioinformatics</i> , 2018, 19, 10.	1.2	68

#	ARTICLE	IF	CITATIONS
128	Partial-arm translocations in evolution of malaria mosquitoes revealed by high-coverage physical mapping of the <i>Anopheles atroparvus</i> genome. <i>BMC Genomics</i> , 2018, 19, 278.	1.2	18
129	The Neutral Theory in Light of Natural Selection. <i>Molecular Biology and Evolution</i> , 2018, 35, 1366-1371.	3.5	180
130	A matter of phylogenetic scale: Distinguishing incomplete lineage sorting from lateral gene transfer as the cause of gene tree discord in recent versus deep diversification histories. <i>American Journal of Botany</i> , 2018, 105, 376-384.	0.8	45
131	ALPHA: a toolkit for Automated Local PHylogenomic Analyses. <i>Bioinformatics</i> , 2018, 34, 2848-2850.	1.8	0
132	Detecting Chromosomal Inversions from Dense SNPs by Combining PCA and Association Tests. , 2018, , .		4
133	The fate of genes that cross species boundaries after a major hybridization event in a natural mosquito population. <i>Molecular Ecology</i> , 2018, 27, 4978-4990.	2.0	23
134	Adjusted likelihood-ratio test for variants with unknown genotypes. <i>Journal of Bioinformatics and Computational Biology</i> , 2018, 16, 1840020.	0.3	2
135	Pathway to Deployment of Gene Drive Mosquitoes as a Potential Biocontrol Tool for Elimination of Malaria in Sub-Saharan Africa: Recommendations of a Scientific Working Group. <i>American Journal of Tropical Medicine and Hygiene</i> , 2018, 98, 1-49.	0.6	165
136	Quantifying the risk of hemiplasy in phylogenetic inference. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 12787-12792.	3.3	49
138	Three new genome assemblies support a rapid radiation in <i>Musa acuminata</i> (wild banana). <i>Genome Biology and Evolution</i> , 2018, 10, 3129-3140.	1.1	29
139	Role of sexual imprinting in assortative mating and premating isolation in Darwin's finches. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10879-E10887.	3.3	30
140	Evolutionary and Medical Consequences of Archaic Introgression into Modern Human Genomes. <i>Genes</i> , 2018, 9, 358.	1.0	28
141	Inference of species phylogenies from bi-allelic markers using pseudo-likelihood. <i>Bioinformatics</i> , 2018, 34, i376-i385.	1.8	26
142	Natura Fecit Saltum: Punctualism Pervades the Natural Sciences. , 2018, , 341-361.		0
143	Supervised machine learning reveals introgressed loci in the genomes of <i>Drosophila simulans</i> and <i>D. sechellia</i> . <i>PLoS Genetics</i> , 2018, 14, e1007341.	1.5	97
144	Dissecting the basis of novel trait evolution in a radiation with widespread phylogenetic discordance. <i>Molecular Ecology</i> , 2018, 27, 3301-3316.	2.0	59
145	Ancestral polymorphisms explain the role of chromosomal inversions in speciation. <i>PLoS Genetics</i> , 2018, 14, e1007526.	1.5	67
146	The genomic impact of historical hybridization with massive mitochondrial DNA introgression. <i>Genome Biology</i> , 2018, 19, 91.	3.8	71

#	ARTICLE	IF	CITATIONS
147	Detecting introgression despite phylogenetic uncertainty: The case of the South American siskins. <i>Molecular Ecology</i> , 2018, 27, 4350-4367.	2.0	18
148	Phylogenetic signal from rearrangements in 18 <i>Anopheles</i> species by joint scaffolding extant and ancestral genomes. <i>BMC Genomics</i> , 2018, 19, 96.	1.2	10
149	Cryptic diversity in an Atlantic Forest malaria vector from the mountains of South-East Brazil. <i>Parasites and Vectors</i> , 2018, 11, 36.	1.0	17
150	From cacti to carnivores: Improved phylotranscriptomic sampling and hierarchical homology inference provide further insight into the evolution of Caryophyllales. <i>American Journal of Botany</i> , 2018, 105, 446-462.	0.8	87
151	Coalescent Analysis of Phylogenomic Data Confidently Resolves the Species Relationships in the <i>Anopheles gambiae</i> Species Complex. <i>Molecular Biology and Evolution</i> , 2018, 35, 2512-2527.	3.5	76
152	Reduced-representation sequencing identifies small effective population sizes of <i>Anopheles gambiae</i> in the north-western Lake Victoria basin, Uganda. <i>Malaria Journal</i> , 2018, 17, 285.	0.8	7
153	Unraveling historical introgression and resolving phylogenetic discord within <i>Catostomus</i> (Osteichthys: Catostomidae). <i>BMC Evolutionary Biology</i> , 2018, 18, 86.	3.2	24
154	The Effect of Hybridization on Dosage Compensation in Member Species of the <i>Anopheles gambiae</i> Species Complex. <i>Genome Biology and Evolution</i> , 2018, 10, 1663-1672.	1.1	8
155	Bayesian inference of phylogenetic networks from bi-allelic genetic markers. <i>PLoS Computational Biology</i> , 2018, 14, e1005932.	1.5	43
156	Inversions are bigger on the X chromosome. <i>Molecular Ecology</i> , 2019, 28, 1238-1245.	2.0	13
157	Dissecting the role of a large chromosomal inversion in life history divergence throughout the <i>Mimulus guttatus</i> species complex. <i>Molecular Ecology</i> , 2019, 28, 1343-1357.	2.0	53
158	Putting the genome in insect phylogenomics. <i>Current Opinion in Insect Science</i> , 2019, 36, 111-117.	2.2	19
159	Genetic homogeneity of <i>Anopheles maculatus</i> in Indonesia and origin of a novel species present in Central Java. <i>Parasites and Vectors</i> , 2019, 12, 351.	1.0	2
160	Speciation, gene flow, and seasonal migration in <i>Catharus</i> thrushes (Aves:Turdidae). <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106564.	1.2	21
161	Admixture between Ancient Lineages, Selection, and the Formation of Sympatric Stickleback Species-Pairs. <i>Molecular Biology and Evolution</i> , 2019, 36, 2481-2497.	3.5	19
162	A new species in the major malaria vector complex sheds light on reticulated species evolution. <i>Scientific Reports</i> , 2019, 9, 14753.	1.6	56
163	Evolutionary Models for the Diversification of Placental Mammals Across the KPg Boundary. <i>Frontiers in Genetics</i> , 2019, 10, 1241.	1.1	41
164	Genomic architecture and introgression shape a butterfly radiation. <i>Science</i> , 2019, 366, 594-599.	6.0	365

#	ARTICLE	IF	CITATIONS
165	Selection, Linkage, and Population Structure Interact To Shape Genetic Variation Among Threespine Stickleback Genomes. <i>Genetics</i> , 2019, 212, 1367-1382.	1.2	6
166	Characterization of the complete mitogenome of <i>Anopheles aquasalis</i> , and phylogenetic divergences among <i>Anopheles</i> from diverse geographic zones. <i>PLoS ONE</i> , 2019, 14, e0219523.	1.1	20
167	Premeiotic and meiotic failures lead to hybrid male sterility in the <i>Anopheles gambiae</i> complex. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20191080.	1.2	13
168	Insights from genomes into the evolutionary importance and prevalence of hybridization in nature. <i>Nature Ecology and Evolution</i> , 2019, 3, 170-177.	3.4	348
169	The Timing and Direction of Introgression Under the Multispecies Network Coalescent. <i>Genetics</i> , 2019, 211, 1059-1073.	1.2	38
170	Recent Advances in the Inference of Gene Flow from Population Genomic Data. <i>Current Molecular Biology Reports</i> , 2019, 5, 107-115.	0.8	1
171	Sequence-based identification of <i>Anopheles</i> species in eastern Ethiopia. <i>Malaria Journal</i> , 2019, 18, 135.	0.8	24
172	Recombination-Aware Phylogenomics Reveals the Structured Genomic Landscape of Hybridizing Cat Species. <i>Molecular Biology and Evolution</i> , 2019, 36, 2111-2126.	3.5	98
173	Searching for Sympatric Speciation in the Genomic Era. <i>BioEssays</i> , 2019, 41, e1900047.	1.2	61
174	The perils of intralocus recombination for inferences of molecular convergence. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180244.	1.8	33
175	Editorial overview: Revisiting Dobzhansky and the "modern synthesis"™ in light of insect evolutionary genomics. <i>Current Opinion in Insect Science</i> , 2019, 31, iii-vi.	2.2	1
176	Estimates of introgression as a function of pairwise distances. <i>BMC Bioinformatics</i> , 2019, 20, 207.	1.2	21
177	Clusters, Trees, and Phylogenetic Network Classes. <i>Computational Biology</i> , 2019, , 277-315.	0.1	10
178	Advances in Computational Methods for Phylogenetic Networks in the Presence of Hybridization. <i>Computational Biology</i> , 2019, , 317-360.	0.1	55
179	Gene Selection and Evolutionary Modeling Affect Phylogenomic Inference of Neuropterida Based on Transcriptome Data. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1072.	1.8	8
180	Recombination rate variation shapes barriers to introgression across butterfly genomes. <i>PLoS Biology</i> , 2019, 17, e2006288.	2.6	253
181	In Silico Karyotyping of Chromosomally Polymorphic Malaria Mosquitoes in the <i>Anopheles gambiae</i> Complex. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3249-3262.	0.8	24
182	Transcontinental dispersal of <i>Anopheles gambiae</i> occurred from West African origin via serial founder events. <i>Communications Biology</i> , 2019, 2, 473.	2.0	13

#	ARTICLE	IF	CITATIONS
183	No barrier breakdown between human and cattle schistosome species in the Senegal River Basin in the face of hybridisation. <i>International Journal for Parasitology</i> , 2019, 49, 1039-1048.	1.3	20
184	Eukaryote hybrid genomes. <i>PLoS Genetics</i> , 2019, 15, e1008404.	1.5	77
185	Translineage polymorphism and nonbifurcating diversification of the genus <i>Picea</i> . <i>New Phytologist</i> , 2019, 222, 576-587.	3.5	29
186	Genome Sequence of <i>Jaltomata</i> Addresses Rapid Reproductive Trait Evolution and Enhances Comparative Genomics in the Hyper-Diverse Solanaceae. <i>Genome Biology and Evolution</i> , 2019, 11, 335-349.	1.1	17
187	Of Genes and Genomes: Mosquito Evolution and Diversity. <i>Trends in Parasitology</i> , 2019, 35, 32-51.	1.5	35
188	The extent of adaptive wild introgression in crops. <i>New Phytologist</i> , 2019, 221, 1279-1288.	3.5	75
189	Delineating species in the speciation continuum: A proposal. <i>Evolutionary Applications</i> , 2019, 12, 657-663.	1.5	61
190	The Unreasonable Effectiveness of Convolutional Neural Networks in Population Genetic Inference. <i>Molecular Biology and Evolution</i> , 2019, 36, 220-238.	3.5	151
191	Genomic transitions during host race and species formation. <i>Current Opinion in Insect Science</i> , 2019, 31, 84-92.	2.2	7
192	Speciation with gene flow via cycles of isolation and migration: insights from multiple mangrove taxa. <i>National Science Review</i> , 2019, 6, 275-288.	4.6	97
193	Association mapping desiccation resistance within chromosomal inversions in the African malaria vector <i>Anopheles gambiae</i> . <i>Molecular Ecology</i> , 2019, 28, 1333-1342.	2.0	51
194	Patterns of Genomic Differentiation in the <i>Drosophila nasuta</i> Species Complex. <i>Molecular Biology and Evolution</i> , 2020, 37, 208-220.	3.5	26
195	Rapid and Predictable Evolution of Admixed Populations Between Two <i>Drosophila</i> Species Pairs. <i>Genetics</i> , 2020, 214, 211-230.	1.2	42
196	Global evaluation of taxonomic relationships and admixture within the <i>Culex pipiens</i> complex of mosquitoes. <i>Parasites and Vectors</i> , 2020, 13, 8.	1.0	25
197	Evolutionary superscaffolding and chromosome anchoring to improve <i>Anopheles</i> genome assemblies. <i>BMC Biology</i> , 2020, 18, 1.	1.7	177
198	A Bayesian Implementation of the Multispecies Coalescent Model with Introgression for Phylogenomic Analysis. <i>Molecular Biology and Evolution</i> , 2020, 37, 1211-1223.	3.5	109
199	The Earth BioGenome project: opportunities and challenges for plant genomics and conservation. <i>Plant Journal</i> , 2020, 102, 222-229.	2.8	35
200	Genomic data reveal a protracted window of introgression during the diversification of a neotropical woodcreeper radiation*. <i>Evolution; International Journal of Organic Evolution</i> , 2020, 74, 842-858.	1.1	32

#	ARTICLE	IF	CITATIONS
201	The Genetic Architecture of Post-Zygotic Reproductive Isolation Between <i>Anopheles coluzzii</i> and <i>An. quadriannulatus</i> . <i>Frontiers in Genetics</i> , 2020, 11, 925.	1.1	2
202	Divergence-Based Introgression Polarization. <i>Genome Biology and Evolution</i> , 2020, 12, 463-478.	1.1	9
203	Biased Gene Retention in the Face of Introgression Obscures Species Relationships. <i>Genome Biology and Evolution</i> , 2020, 12, 1646-1663.	1.1	24
204	Adequacy and sufficiency evaluation of existing EFSA guidelines for the molecular characterisation, environmental risk assessment and post-market environmental monitoring of genetically modified insects containing engineered gene drives. <i>EFSA Journal</i> , 2020, 18, e06297.	0.9	23
205	Deep Convergence, Shared Ancestry, and Evolutionary Novelty in the Genetic Architecture of <i>Heliconius</i> Mimicry. <i>Genetics</i> , 2020, 216, 765-780.	1.2	13
206	Culicidae evolutionary history focusing on the Culicinae subfamily based on mitochondrial phylogenomics. <i>Scientific Reports</i> , 2020, 10, 18823.	1.6	37
207	Impact of homologous recombination on core genome phylogenies. <i>BMC Genomics</i> , 2020, 21, 829.	1.2	17
208	Unveiling mosquito cryptic species and their reproductive isolation. <i>Insect Molecular Biology</i> , 2020, 29, 499-510.	1.0	8
209	Gene flow and species delimitation in fishes of Western North America: Flannelmouth (<i>Catostomus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 6477-6493.	0.8	12
210	Climate and Urbanization Drive Mosquito Preference for Humans. <i>Current Biology</i> , 2020, 30, 3570-3579.e6.	1.8	153
211	Genomics of Evolutionary Novelty in Hybrids and Polyploids. <i>Frontiers in Genetics</i> , 2020, 11, 792.	1.1	103
212	Alternative views of biological species: reproductively isolated units or genotypic clusters?. <i>National Science Review</i> , 2020, 7, 1401-1407.	4.6	17
213	Evaluating the probability of CRISPR-based gene drive contaminating another species. <i>Evolutionary Applications</i> , 2020, 13, 1888-1905.	1.5	17
214	Mitochondrial genomics reveals the evolutionary history of the porpoises (Phocoenidae) across the speciation continuum. <i>Scientific Reports</i> , 2020, 10, 15190.	1.6	13
215	A phylogenomic study of Steganinae fruit flies (Diptera: Drosophilidae): strong gene tree heterogeneity and evidence for monophyly. <i>BMC Evolutionary Biology</i> , 2020, 20, 141.	3.2	4
216	Female-biased gene flow between two species of Darwin's finches. <i>Nature Ecology and Evolution</i> , 2020, 4, 979-986.	3.4	21
217	Polyploidy breaks speciation barriers in Australian burrowing frogs <i>Neobatrachus</i> . <i>PLoS Genetics</i> , 2020, 16, e1008769.	1.5	40
218	A mitochondrial genetic divergence proxy predicts the reproductive compatibility of mammalian hybrids. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2020, 287, 20200690.	1.2	14

#	ARTICLE	IF	CITATIONS
219	Nuclear phylogenomic analyses of asterids conflict with plastome trees and support novel relationships among major lineages. <i>American Journal of Botany</i> , 2020, 107, 790-805.	0.8	75
220	Evolution of the Insecticide Target Rdl in African Anopheles Is Driven by Interspecific and Interkaryotypic Introgression. <i>Molecular Biology and Evolution</i> , 2020, 37, 2900-2917.	3.5	31
221	Reticulate evolution as a management challenge: Patterns of admixture with phylogenetic distance in endemic fishes of western North America. <i>Evolutionary Applications</i> , 2020, 13, 1400-1419.	1.5	13
222	Maximum Likelihood Estimation of Species Trees from Gene Trees in the Presence of Ancestral Population Structure. <i>Genome Biology and Evolution</i> , 2020, 12, 3977-3995.	1.1	5
223	Assessing biological factors affecting postspeciation introgression. <i>Evolution Letters</i> , 2020, 4, 137-154.	1.6	49
224	Toward the Definition of Efficacy and Safety Criteria for Advancing Gene Drive-Modified Mosquitoes to Field Testing. <i>Vector-Borne and Zoonotic Diseases</i> , 2020, 20, 237-251.	0.6	60
225	Triad hybridization via a conduit species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 7888-7896.	3.3	23
226	Linked-read sequencing identifies abundant microinversions and introgression in the arboviral vector <i>Aedes aegypti</i> . <i>BMC Biology</i> , 2020, 18, 26.	1.7	16
227	Introgressive hybridization between two non-native apple snails in China: widespread hybridization and homogenization in egg morphology. <i>Pest Management Science</i> , 2020, 76, 4231-4239.	1.7	10
228	Evolutionary History of the <i>Marchantia polymorpha</i> Complex. <i>Frontiers in Plant Science</i> , 2020, 11, 829.	1.7	15
229	Assessing connectivity despite high diversity in island populations of a malaria mosquito. <i>Evolutionary Applications</i> , 2020, 13, 417-431.	1.5	11
230	Evidence for widespread selection in shaping the genomic landscape during speciation of <i>Populus</i> . <i>Molecular Ecology</i> , 2020, 29, 1120-1136.	2.0	31
231	Speciation in North American <i>Junonia</i> from a genomic perspective. <i>Systematic Entomology</i> , 2020, 45, 803-837.	1.7	11
232	Genes and speciation: is it time to abandon the biological species concept?. <i>National Science Review</i> , 2020, 7, 1387-1397.	4.6	34
233	The Impact of Cross-Species Gene Flow on Species Tree Estimation. <i>Systematic Biology</i> , 2020, 69, 830-847.	2.7	37
234	Three-dimensional Organization of Polytene Chromosomes in Somatic and Germline Tissues of Malaria Mosquitoes. <i>Cells</i> , 2020, 9, 339.	1.8	11
235	Adaptive Introgression across Semipermeable Species Boundaries between Local <i>Helicoverpa zea</i> and Invasive <i>Helicoverpa armigera</i> Moths. <i>Molecular Biology and Evolution</i> , 2020, 37, 2568-2583.	3.5	64
236	High-density genetic variation maps reveal the correlation between asymmetric interspecific introgressions and improvement of agronomic traits in Upland and Pima cotton varieties developed in Xinjiang, China. <i>Plant Journal</i> , 2020, 103, 677-689.	2.8	22

#	ARTICLE	IF	CITATIONS
237	The Gene and Gene Expression (GAGE) Species Concept: An Universal Approach for All Eukaryotic Organisms. <i>Systematic Biology</i> , 2020, 69, 1033-1038.	2.7	13
238	Integrated likelihood for phylogenomics under a no-common-mechanism model. <i>BMC Genomics</i> , 2020, 21, 219.	1.2	0
239	Defining Species When There is Gene Flow. <i>Systematic Biology</i> , 2021, 70, 108-119.	2.7	29
240	Disentangling Sources of Gene Tree Discordance in Phylogenomic Data Sets: Testing Ancient Hybridizations in <i>Amaranthaceae</i> s.l. <i>Systematic Biology</i> , 2021, 70, 219-235.	2.7	112
241	Dsuite â€•Fast <i>D</i>â€•statistics and related admixture evidence from VCF files. <i>Molecular Ecology Resources</i> , 2021, 21, 584-595.	2.2	356
242	A population genomic unveiling of a new cryptic mosquito taxon within the malariaâ€•transmitting <i>Anopheles gambiae</i> complex. <i>Molecular Ecology</i> , 2021, 30, 775-790.	2.0	16
243	The Legacy of Recurrent Introgression during the Radiation of Hares. <i>Systematic Biology</i> , 2021, 70, 593-607.	2.7	47
244	Phylogenomics and the Genetic Architecture of the Placental Mammal Radiation. <i>Annual Review of Animal Biosciences</i> , 2021, 9, 29-53.	3.6	32
245	Beyond taxonomy: species complexes in New World phlebotomine sand flies. <i>Medical and Veterinary Entomology</i> , 2021, 35, 267-283.	0.7	20
247	A Polynomial-Time Algorithm for Minimizing the Deep Coalescence Cost for Level-1 Species Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 2642-2653.	1.9	5
248	A Minimally Morphologically Destructive Approach for DNA Retrieval and Whole-Genome Shotgun Sequencing of Pinned Historic Dipteran Vector Species. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	12
249	Ancient and recent introgression shape the evolutionary history of pollinator adaptation and speciation in a model monkeyflower radiation (<i>Mimulus</i> section <i>Erythranthe</i>). <i>PLoS Genetics</i> , 2021, 17, e1009095.	1.5	56
251	Profile of Nora J. Besansky. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, e2101734118.	3.3	0
252	Total Ortholog Median Matrix as an alternative unsupervised approach for phylogenomics based on evolutionary distance between protein coding genes. <i>Scientific Reports</i> , 2021, 11, 3791.	1.6	2
254	The genomic revolution and species delimitation in birds (and other organisms): Why phenotypes should not be overlooked. <i>Auk</i> , 2021, 138, .	0.7	23
255	The Genomic Architecture and Evolutionary Fates of Supergenes. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	63
256	Most Genomic Loci Misrepresent the Phylogeny of an Avian Radiation Because of Ancient Gene Flow. <i>Systematic Biology</i> , 2021, 70, 961-975.	2.7	45
257	Extensive Genome-Wide Phylogenetic Discordance Is Due to Incomplete Lineage Sorting and Not Ongoing Introgression in a Rapidly Radiated Bryophyte Genus. <i>Molecular Biology and Evolution</i> , 2021, 38, 2750-2766.	3.5	54

#	ARTICLE	IF	CITATIONS
258	Systematic identification of plausible pathways to potential harm via problem formulation for investigational releases of a population suppression gene drive to control the human malaria vector <i>Anopheles gambiae</i> in West Africa. <i>Malaria Journal</i> , 2021, 20, 170.	0.8	26
259	Ultra-conserved sequences in the genomes of highly diverse <i>Anopheles</i> mosquitoes, with implications for malaria vector control. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	3
260	Chromosome-level genome assemblies of the malaria vectors <i>Anopheles coluzzii</i> and <i>Anopheles arabiensis</i> . <i>GigaScience</i> , 2021, 10, .	3.3	12
262	Geography is more important than life history in the recent diversification of the tiger salamander complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	13
264	Novel genotyping approaches to easily detect genomic admixture between the major Afrotropical malaria vector species, <i>Anopheles coluzzii</i> and <i>An. gambiae</i> . <i>Molecular Ecology Resources</i> , 2021, 21, 1504-1516.	2.2	7
265	Synteny-Based Genome Assembly for 16 Species of <i>Heliconius</i> Butterflies, and an Assessment of Structural Variation across the Genus. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	15
266	Advances and opportunities in malaria population genomics. <i>Nature Reviews Genetics</i> , 2021, 22, 502-517.	7.7	61
267	Rampant Genome-Wide Admixture across the <i>Heliconius</i> Radiation. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	31
269	Identification of the sex chromosome system in a sand fly species, <i>Lutzomyia longipalpis</i> s.l. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	0
271	Unravelling population structure heterogeneity within the genome of the malaria vector <i>Anopheles gambiae</i> . <i>BMC Genomics</i> , 2021, 22, 422.	1.2	1
272	Whole-genome microsynteny-based phylogeny of angiosperms. <i>Nature Communications</i> , 2021, 12, 3498.	5.8	53
273	Asymmetric Phenotypes of Sterile Hybrid Males From Reciprocal Crosses Between Species of the <i>Anopheles gambiae</i> Complex. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	1.1	3
274	A targeted amplicon sequencing panel to simultaneously identify mosquito species and <i>Plasmodium</i> presence across the entire <i>Anopheles</i> genus. <i>Molecular Ecology Resources</i> , 2022, 22, 28-44.	2.2	18
276	Deep Ancestral Introgression Shapes Evolutionary History of Dragonflies and Damselflies. <i>Systematic Biology</i> , 2022, 71, 526-546.	2.7	32
277	Multispecies coalescent and its applications to infer species phylogenies and cross-species gene flow. <i>National Science Review</i> , 2021, 8, nwab127.	4.6	36
278	Genome-Wide Evidence for Complex Hybridization and Demographic History in a Group of <i>Cycas</i> From China. <i>Frontiers in Genetics</i> , 2021, 12, 717200.	1.1	10
279	Phylogenomic assessment of the role of hybridization and introgression in trait evolution. <i>PLoS Genetics</i> , 2021, 17, e1009701.	1.5	8
280	Ancient divergence of Indian and Tibetan wolves revealed by recombination-aware phylogenomics. <i>Molecular Ecology</i> , 2021, 30, 6687-6700.	2.0	26

#	ARTICLE	IF	CITATIONS
281	Phylogenomics reveals ancient and contemporary gene flow contributing to the evolutionary history of sea ducks (Tribe Mergini). <i>Molecular Phylogenetics and Evolution</i> , 2021, 161, 107164.	1.2	9
282	Evolutionary impacts of introgressive hybridization in a rapidly evolving group of jumping spiders (F. Tj ETQq1 1 0.784314 rgBT /Overlo	1.2	2
283	Ecological plasticity to ions concentration determines genetic response and dominance of <i>Anopheles coluzzii</i> larvae in urban coastal habitats of Central Africa. <i>Scientific Reports</i> , 2021, 11, 15781.	1.6	7
284	Intraspecific Transcriptome Variation and Sex-Biased Expression in <i>Anopheles arabiensis</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	3
285	On the inference of complex phylogenetic networks by Markov Chain Monte-Carlo. <i>PLoS Computational Biology</i> , 2021, 17, e1008380.	1.5	12
286	Persistence and expansion of cryptic endangered red wolf genomic ancestry along the American Gulf coast. <i>Molecular Ecology</i> , 2022, 31, 5440-5454.	2.0	7
287	Phylogenomic approach reveals strong signatures of introgression in the rapid diversification of neotropical true fruit flies (<i>Anastrepha</i> : Tephritidae). <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107200.	1.2	8
288	Prevalence and Adaptive Impact of Introgression. <i>Annual Review of Genetics</i> , 2021, 55, 265-283.	3.2	99
289	How mitonuclear discordance and geographic variation have confounded species boundaries in a widely studied snake. <i>Molecular Phylogenetics and Evolution</i> , 2021, 162, 107194.	1.2	21
291	Improving mosquito control strategies with population genomics. <i>Trends in Parasitology</i> , 2021, 37, 907-921.	1.5	11
292	Introgression is widespread in the radiation of carnivorous <i>Nepenthes</i> pitcher plants. <i>Molecular Phylogenetics and Evolution</i> , 2021, 163, 107214.	1.2	8
293	Autosomal, sex-linked and mitochondrial loci resolve evolutionary relationships among wrens in the genus <i>Campylorhynchus</i> . <i>Molecular Phylogenetics and Evolution</i> , 2021, 163, 107242.	1.2	5
294	Resistance to pirimiphos-methyl in West African <i>Anopheles</i> is spreading via duplication and introgression of the <i>Ace1</i> locus. <i>PLoS Genetics</i> , 2021, 17, e1009253.	1.5	33
295	Inferring Local Genealogies on Closely Related Genomes. <i>Lecture Notes in Computer Science</i> , 2017, 10562, 213-231.	1.0	1
296	Radiation with reticulation marks the origin of a major malaria vector. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31583-31590.	3.3	29
336	Mitochondrial genomes of <i>Anopheles arabiensis</i> , <i>An. gambiae</i> and <i>An. coluzzii</i> show no clear species division. <i>F1000Research</i> , 2018, 7, 347.	0.8	12
337	Mitochondrial genomes of <i>Anopheles arabiensis</i> , <i>An. gambiae</i> and <i>An. coluzzii</i> show no clear species division. <i>F1000Research</i> , 2018, 7, 347.	0.8	9
338	Evolutionary Novelty in a Butterfly Wing Pattern through Enhancer Shuffling. <i>PLoS Biology</i> , 2016, 14, e1002353.	2.6	136

#	ARTICLE	IF	CITATIONS
339	Phylogenomics Reveals Three Sources of Adaptive Variation during a Rapid Radiation. PLoS Biology, 2016, 14, e1002379.	2.6	364
340	What Is Speciation?. PLoS Genetics, 2016, 12, e1005860.	1.5	115
341	Bayesian Inference of Reticulate Phylogenies under the Multispecies Network Coalescent. PLoS Genetics, 2016, 12, e1006006.	1.5	100
342	Adaptive introgression from distant Caribbean islands contributed to the diversification of a microendemic adaptive radiation of trophic specialist pupfishes. PLoS Genetics, 2017, 13, e1006919.	1.5	81
343	Fine scale mapping of genomic introgressions within the Drosophila yakuba clade. PLoS Genetics, 2017, 13, e1006971.	1.5	90
344	malERA: An updated research agenda for basic science and enabling technologies in malaria elimination and eradication. PLoS Medicine, 2017, 14, e1002451.	3.9	29
345	Genetic Structure of a Local Population of the Anopheles gambiae Complex in Burkina Faso. PLoS ONE, 2016, 11, e0145308.	1.1	8
346	Characterisation of Species and Diversity of Anopheles gambiae Keele Colony. PLoS ONE, 2016, 11, e0168999.	1.1	18
347	An Evolution-Based Screen for Genetic Differentiation between Anopheles Sister Taxa Enriches for Detection of Functional Immune Factors. PLoS Pathogens, 2015, 11, e1005306.	2.1	37
349	Evolution of gene expression levels in the male reproductive organs of <i>Anopheles</i> mosquitoes. Life Science Alliance, 2019, 2, e201800191.	1.3	10
350	Chapitre 10. Les anophèles (Diptera: Culicidae: Anophelinae). , 2017, , 181-241.		1
351	The Impact of Periodic Distribution Campaigns of Long-Lasting Insecticidal-Treated Bed Nets on Malaria Vector Dynamics and Human Exposure in Dielmo, Senegal. American Journal of Tropical Medicine and Hygiene, 2018, 98, 1343-1352.	0.6	20
352	Evidence for suppression of immunity as a driver for genomic introgressions and host range expansion in races of Albugo candida, a generalist parasite. ELife, 2015, 4, .	2.8	71
353	Determining the probability of hemiplasy in the presence of incomplete lineage sorting and introgression. ELife, 2020, 9, .	2.8	25
354	Selective sorting of ancestral introgression in maize and teosinte along an elevational cline. PLoS Genetics, 2021, 17, e1009810.	1.5	50
367	Detecting Introgression in Anopheles Mosquito Genomes Using a Reconciliation-Based Approach. Lecture Notes in Computer Science, 2018, , 163-178.	1.0	0
371	8. Mosquito-borne diseases in the livestock industry. Ecology and Control of Vector-Borne Diseases, 2018, , 195-219.	0.3	3
385	Monotypy Justified: Genitalia and DNA Move Ephyriades eugramma (Mabille) to New Genus Neomorphuncus Burns (Lepidoptera: Hesperidae: Pyrginae). Proceedings of the Entomological Society of Washington, 2019, 121, 557.	0.0	0

#	ARTICLE	IF	CITATIONS
388	The expanding <i>Anopheles gambiae</i> species complex. <i>Pathogens and Global Health</i> , 2020, 114, 1-1.	1.0	6
392	Transposable Elements in <i>Anopheles</i> Species: Refining Annotation Strategies Towards Population Genomics Analyses. <i>Population Genomics</i> , 2020, , 1.	0.2	1
393	Engineered Gene Drives and their Value in the Control of Vector-Borne Diseases, Weeds, Pests, and Invasive Species. <i>Topics in Biodiversity and Conservation</i> , 2020, , 401-419.	0.3	0
394	The effects of introgression across thousands of quantitative traits revealed by gene expression in wild tomatoes. <i>PLoS Genetics</i> , 2021, 17, e1009892.	1.5	9
398	Detecting inversions with PCA in the presence of population structure. <i>PLoS ONE</i> , 2020, 15, e0240429.	1.1	8
399	Assessment of the ecologically dependent post-zygotic isolation between <i>Anopheles coluzzii</i> and <i>Anopheles gambiae</i> . <i>PLoS ONE</i> , 2020, 15, e0240625.	1.1	1
402	Widespread introgression across a phylogeny of 155 <i>Drosophila</i> genomes. <i>Current Biology</i> , 2022, 32, 111-123.e5.	1.8	132
404	Ancient hybridization patterns between bighorn and thinhorn sheep. <i>Molecular Ecology</i> , 2021, 30, 6273-6288.	2.0	4
405	Extensive Interspecific Gene Flow Shaped Complex Evolutionary History and Underestimated Species Diversity in Rapidly Radiated Dolphins. <i>Journal of Mammalian Evolution</i> , 2022, 29, 353-367.	1.0	6
406	Automated Detection and Localization of Genome Inversions using Principal Component Analysis. , 2021, , .		0
407	Fine-grained habitat-associated genetic connectivity in an admixed population of mussels in the small isolated Kerguelen Islands. , 0, 1, .		1
408	Phylogenomic approaches to detecting and characterizing introgression. <i>Genetics</i> , 2022, 220, .	1.2	79
414	Spontaneous mutation rate estimates for the principal malaria vectors <i>Anopheles coluzzii</i> and <i>Anopheles stephensi</i> . <i>Scientific Reports</i> , 2022, 12, 226.	1.6	3
416	Species delimitation and mitonuclear discordance within a species complex of biting midges. <i>Scientific Reports</i> , 2022, 12, 1730.	1.6	14
417	Full-Likelihood Genomic Analysis Clarifies a Complex History of Species Divergence and Introgression: The Example of the <i>erato-sara</i> Group of <i>Heliconius</i> Butterflies. <i>Systematic Biology</i> , 2022, 71, 1159-1177.	2.7	16
418	Ghost Lineages Highly Influence the Interpretation of Introgression Tests. <i>Systematic Biology</i> , 2022, 71, 1147-1158.	2.7	49
419	Does the Pachytene Checkpoint, a Feature of Meiosis, Filter Out Mistakes in Double-Strand DNA Break Repair and as a side-Effect Strongly Promote Adaptive Speciation?. <i>Integrative Organismal Biology</i> , 2022, 4, .	0.9	1
420	Modelling spatiotemporal trends in the frequency of genetic mutations conferring insecticide target-site resistance in African mosquito malaria vector species. <i>BMC Biology</i> , 2022, 20, 46.	1.7	8

#	ARTICLE	IF	CITATIONS
423	Phylogeny of <i>Drosophila saltans</i> group (Diptera: Drosophilidae) based on morphological and molecular evidence. PLoS ONE, 2022, 17, e0266710.	1.1	2
424	Layered evolution of gene expression in <i>superfast</i> muscles for courtship. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2119671119.	3.3	11
425	Transposable element variants and their potential adaptive impact in urban populations of the malaria vector <i>Anopheles coluzzii</i> . Genome Research, 2022, 32, 189-202.	2.4	5
426	Limited Introgression between Rock-Wallabies with Extensive Chromosomal Rearrangements. Molecular Biology and Evolution, 2022, 39, .	3.5	17
427	Plastome structure, phylogenomics and evolution of plastid genes in <i>Swertia</i> (Gentianaceae) in the Qing-Tibetan Plateau. BMC Plant Biology, 2022, 22, 195.	1.6	11
428	Incomplete lineage sorting and phenotypic evolution in marsupials. Cell, 2022, 185, 1646-1660.e18.	13.5	43
435	Divergence With Gene Flow and Contrasting Population Size Blur the Species Boundary in <i>Cycas</i> Sect. <i>Asiorientales</i> , as Inferred From Morphology and RAD-Seq Data. Frontiers in Plant Science, 2022, 13, .	1.7	5
436	Approaches to the Detection of Hybridization Events and Genetic Introgression upon Phylogenetic Incongruence. Biology Bulletin Reviews, 2022, 12, 240-253.	0.3	1
437	Retrogene Duplication and Expression Patterns Shaped by the Evolution of Sex Chromosomes in Malaria Mosquitoes. Genes, 2022, 13, 968.	1.0	7
438	Systematic Review on Diversity and Distribution of <i>Anopheles</i> Species in Gabon: A Fresh Look at the Potential Malaria Vectors and Perspectives. Pathogens, 2022, 11, 668.	1.2	3
440	Impact of Ghost Introgression on Coalescent-Based Species Tree Inference and Estimation of Divergence Time. Systematic Biology, 2023, 72, 35-49.	2.7	7
441	Gene drive in species complexes: defining target organisms. Trends in Biotechnology, 2022, , .	4.9	8
442	A need for standardized reporting of introgression: Insights from studies across eukaryotes. Evolution Letters, 2022, 6, 344-357.	1.6	14
444	Radiation and hybridization underpin the spread of the fire ant social supergene. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	10
447	Ghost lineages can invalidate or even reverse findings regarding gene flow. PLoS Biology, 2022, 20, e3001776.	2.6	24
451	High-resolution species assignment of <i>Anopheles</i> mosquitoes using k-mer distances on targeted sequences. ELife, 0, 11, .	2.8	1
453	Temporal and biting dynamics of the chromosomal inversion 2La in the malaria vectors <i>Anopheles gambiae</i> and <i>Anopheles coluzzii</i> in Bangui, Central African Republic. Frontiers in Ecology and Evolution, 0, 10, .	1.1	0
456	Phylogenomics, plastome structure and species identification in <i>Mahonia</i> (Berberidaceae). BMC Genomics, 2022, 23, .	1.2	3

#	ARTICLE	IF	CITATIONS
457	Recurrent co-domestication of PIF/Harbinger transposable element proteins in insects. <i>Mobile DNA</i> , 2022, 13, .	1.3	2
458	Divergence and introgression among the <i>virilis</i> group of <i>Drosophila</i> . <i>Evolution Letters</i> , 2022, 6, 537-551.	1.6	4
459	Population genomics reveal distinct and diverging populations of <i>An. minimus</i> in Cambodia. <i>Communications Biology</i> , 2022, 5, .	2.0	1
460	Allopatric origin, secondary contact and subsequent isolation of sympatric rockfishes (Sebastidae): <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i> 37-50.	0.7	1
466	Re-evaluating Homoploid Reticulate Evolution in <i>Helianthus</i> Sunflowers. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	9
467	The Ant Genus <i>Cardiocondyla</i> (Hymenoptera: Formicidae): The Species Groups with Oriental and Australasian Origin. <i>Diversity</i> , 2023, 15, 25.	0.7	3
468	Rapid identification of mosquito species and age by mass spectrometric analysis. <i>BMC Biology</i> , 2023, 21, .	1.7	1
469	Phylogenomics reveal extensive phylogenetic discordance due to incomplete lineage sorting following the rapid radiation of alpine butterflies (Papilionidae: <i>Parnassius</i>). <i>Systematic Entomology</i> , 2023, 48, 585-599.	1.7	2
470	What are species and how are they formed?. <i>National Science Review</i> , 2022, 9, .	4.6	2
471	Recombination Variation Shapes Phylogeny and Introgression in Wild Diploid Strawberries. <i>Molecular Biology and Evolution</i> , 2023, 40, .	3.5	6
472	Standing genetic variation and chromosome differences drove rapid ecotype formation in a major malaria mosquito. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	1
473	Phylogenetic Analysis of Allotetraploid Species Using Polarized Genomic Sequences. <i>Systematic Biology</i> , 0, , .	2.7	1
474	The first genome sequence of <i>Anopheles squamous</i> from Macha, Zambia. <i>F1000Research</i> , 0, 12, 330.	0.8	0
476	Phylogenomics revealed migration routes and adaptive radiation timing of Holarctic malaria mosquito species of the <i>Maculipennis</i> Group. <i>BMC Biology</i> , 2023, 21, .	1.7	0
477	Climate and Environmental Changes and Their Potential Effects on the Dynamics of Chagas Disease: Hybridization in <i>Rhodniini</i> (Hemiptera, Triatominae). <i>Insects</i> , 2023, 14, 378.	1.0	2
492	Physical Mapping of Two Nested Fixed Inversions in the X Chromosome of the Malaria Mosquito <i>Anopheles messeae</i> . <i>Lecture Notes in Computer Science</i> , 2023, , 84-99.	1.0	0
496	Population Differentiation with Introgression. , 2023, , 89-116.		0