

# Isolation with Migration Models for More Than Two Populations

Molecular Biology and Evolution

27, 905-920

DOI: [10.1093/molbev/msp296](https://doi.org/10.1093/molbev/msp296)

Citation Report

#	ARTICLE	IF	CITATIONS
1	The population genomics of plant adaptation. <i>New Phytologist</i> , 2010, 188, 313-332.	3.5	105
2	QUANTIFYING THE PLEISTOCENE HISTORY OF THE OAK GALL PARASITOID <i>CECIDOSTIBA FUNGOSA</i> USING TWENTY INTRON LOCI. <i>Evolution; International Journal of Organic Evolution</i> , 2010, 64, 2664-2681.	1.1	26
3	NUCLEAR AND MITOCHONDRIAL SEQUENCE DATA REVEAL AND CONCEAL DIFFERENT DEMOGRAPHIC HISTORIES AND POPULATION GENETIC PROCESSES IN CARIBBEAN REEF FISHES. <i>Evolution; International Journal of Organic Evolution</i> , 2010, 64, 3380-3397.	1.1	65
4	Evolution in caves: Darwin's "wrecks of ancient life" in the molecular era. <i>Molecular Ecology</i> , 2010, 19, 3865-3880.	2.0	174
5	Evidence of recent and continuous speciation in a biodiversity hotspot: a population genetic approach in southern African gladioli ( <i>Gladiolus</i> ; Iridaceae). <i>Molecular Ecology</i> , 2010, 19, 4765-4782.	2.0	36
6	Speciation genetics: Limits and promises. <i>Taxon</i> , 2010, 59, 1404-1412.	0.4	5
7	Morphologically cryptic biological species within the liverwort <i>Frullania asagrayana</i> . <i>American Journal of Botany</i> , 2010, 97, 1707-1718.	0.8	57
8	A test of the sympatric host race formation hypothesis in <i>Neodiprion</i> (Hymenoptera: Diprionidae). <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2010, 277, 3131-3138.	1.2	33
9	It's About Time: Divergence, Demography, and the Evolution of Developmental Modes in Marine Invertebrates. <i>Integrative and Comparative Biology</i> , 2010, 50, 643-661.	0.9	51
10	Species Delimitation Using a Combined Coalescent and Information-Theoretic Approach: An Example from North American <i>Myotis</i> Bats. <i>Systematic Biology</i> , 2010, 59, 400-414.	2.7	167
11	Effective Population Size, Gene Flow, and Species Status in a Narrow Endemic Sunflower, <i>Helianthus neglectus</i> , Compared to Its Widespread Sister Species, <i>H. petiolaris</i> . <i>International Journal of Molecular Sciences</i> , 2010, 11, 492-506.	1.8	18
12	Isolation with Migration Models for More Than Two Populations. <i>Molecular Biology and Evolution</i> , 2010, 27, 905-920.	3.5	796
13	Divergence with Gene Flow: Models and Data. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2010, 41, 215-230.	3.8	326
14	Three roads diverged? Routes to phylogeographic inference. <i>Trends in Ecology and Evolution</i> , 2010, 25, 626-632.	4.2	92
15	Bringing spiders to the multilocus era: novel anonymous nuclear markers for Harpactocrates ground-dwelling spiders (Araneae: Dysderidae) with application to related genera. <i>Journal of Arachnology</i> , 2011, 39, 506-510.	0.3	4
16	Controlling for non-independence in comparative analysis of patterns across populations within species. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2011, 366, 1410-1424.	1.8	124
17	Demographic Processes Underlying Subtle Patterns of Population Structure in the Scalloped Hammerhead Shark, <i>Sphyrna lewini</i> . <i>PLoS ONE</i> , 2011, 6, e21459.	1.1	67
18	Gene Flow and Hybridization between Numerically Imbalanced Populations of Two Duck Species in the Falkland Islands. <i>PLoS ONE</i> , 2011, 6, e23173.	1.1	24

#	ARTICLE	IF	CITATIONS
19	Hybridization and massive mtDNA unidirectional introgression between the closely related Neotropical toads <i>Rhinella marina</i> and <i>R. schneideri</i> inferred from mtDNA and nuclear markers. <i>BMC Evolutionary Biology</i> , 2011, 11, 264.	3.2	70
20	DNA barcoding of African fruit bats (Mammalia, Pteropodidae). The mitochondrial genome does not provide a reliable discrimination between <i>Epomophorus gambianus</i> and <i>Micropteropus pusillus</i> . <i>Comptes Rendus - Biologies</i> , 2011, 334, 544-554.	0.1	55
21	Conservation genetics of evolutionary lineages of the endangered mountain yellow-legged frog, <i>Rana muscosa</i> (Amphibia: Ranidae), in southern California. <i>Biological Conservation</i> , 2011, 144, 2031-2040.	1.9	24
22	Bayesian inference of ancient human demography from individual genome sequences. <i>Nature Genetics</i> , 2011, 43, 1031-1034.	9.4	526
23	Perspectives on Human Population Structure at the Cusp of the Sequencing Era. <i>Annual Review of Genomics and Human Genetics</i> , 2011, 12, 245-274.	2.5	69
24	Species tree inference in a recent radiation of orioles (Genus <i>Icterus</i> ): Multiple markers and methods reveal cytonuclear discordance in the northern oriole group. <i>Molecular Phylogenetics and Evolution</i> , 2011, 61, 460-469.	1.2	27
25	Genotyping HapSTR loci: phase determination from direct sequencing of PCR products. <i>Molecular Ecology Resources</i> , 2011, 11, 1068-1075.	2.2	8
26	Evolution and Population Genetics of Exotic and Re-Emerging Pathogens: Novel Tools and Approaches. <i>Annual Review of Phytopathology</i> , 2011, 49, 249-267.	3.5	98
27	Next-generation sequencing and systematics: What can a billion base pairs of DNA sequence data do for you?. <i>Taxon</i> , 2011, 60, 1552-1566.	0.4	64
28	Estimating Parameters of Speciation Models Based on Refined Summaries of the Joint Site-Frequency Spectrum. <i>PLoS ONE</i> , 2011, 6, e18155.	1.1	16
29	Spatial Geographic Mosaic in an Aquatic Predator-Prey Network. <i>PLoS ONE</i> , 2011, 6, e22472.	1.1	19
30	Multi-Locus Estimates of Population Structure and Migration in a Fence Lizard Hybrid Zone. <i>PLoS ONE</i> , 2011, 6, e25827.	1.1	15
31	Sequential Fragmentation of Pleistocene Forests in an East Africa Biodiversity Hotspot: Chameleons as a Model to Track Forest History. <i>PLoS ONE</i> , 2011, 6, e26606.	1.1	29
32	Gene flow and species cohesion following the spread of <i>Schiedea globosa</i> (Caryophyllaceae) across the Hawaiian Islands. <i>Journal of Evolutionary Biology</i> , 2011, 24, 1-11.	0.8	12
33	Phylogeography of the fiscal shrike ( <i>Lanius collaris</i> ): a novel pattern of genetic structure across the arid zones and savannas of Africa. <i>Journal of Biogeography</i> , 2011, 38, 2210-2222.	1.4	32
34	A tale of two genomes: contrasting patterns of phylogeographic structure in a widely distributed bat. <i>Molecular Ecology</i> , 2011, 20, 357-375.	2.0	66
35	Interpreting the estimated timing of migration events between hybridizing species. <i>Molecular Ecology</i> , 2011, 20, 2353-2366.	2.0	78
36	Making inferences about speciation using sophisticated statistical genetics methods: look before you leap. <i>Molecular Ecology</i> , 2011, 20, 2229-2232.	2.0	17

#	ARTICLE	IF	CITATIONS
37	Increasing evidence of the role of gene flow in animal evolution: hybrid speciation in the yellow-rumped warbler complex. <i>Molecular Ecology</i> , 2011, 20, 2236-2239.	2.0	21
38	Jaatha: a fast composite-likelihood approach to estimate demographic parameters. <i>Molecular Ecology</i> , 2011, 20, 2709-2723.	2.0	35
39	Nuclear and mitochondrial phylogeography of the European firebellied toads <i>Bombina bombina</i> and <i>Bombina variegata</i> supports their independent histories. <i>Molecular Ecology</i> , 2011, 20, 3381-3398.	2.0	68
40	On the nonidentifiability of migration time estimates in isolation with migration models. <i>Molecular Ecology</i> , 2011, 20, 3956-3962.	2.0	47
41	A multi-gene approach reveals a complex evolutionary history in the <i>Cyanistes</i> species group. <i>Molecular Ecology</i> , 2011, 20, 4123-4139.	2.0	37
42	The Rift Valley is a major barrier to dispersal of African clawed frogs ( <i>Xenopus</i> ) in Ethiopia. <i>Molecular Ecology</i> , 2011, 20, 4216-4230.	2.0	38
43	A framework for comparing processes of speciation in the presence of gene flow. <i>Molecular Ecology</i> , 2011, 20, 5123-5140.	2.0	287
44	Direction and extent of organelle DNA introgression between two spruce species in the Qinghai-Tibetan Plateau. <i>New Phytologist</i> , 2011, 192, 1024-1033.	3.5	88
45	MIGRATION RATES, FREQUENCY-DEPENDENT SELECTION AND THE SELF-INCOMPATIBILITY LOCUS IN <i>LEAVENWORTHIA</i> (BRASSICACEAE). <i>Evolution; International Journal of Organic Evolution</i> , 2011, 65, 2357-2369.	1.1	21
46	Cryptic diversity within the endemic prehensile-tailed gecko <i>Urocytyledon inexpectata</i> across the Seychelles Islands: patterns of phylogeographical structure and isolation at the multilocus level. <i>Biological Journal of the Linnean Society</i> , 2011, 104, 177-191.	0.7	21
47	Genetic population structure of grey mackerel <i>Scomberomorus semifasciatus</i> in northern Australia. <i>Journal of Fish Biology</i> , 2011, 79, 633-661.	0.7	25
48	Learning about human population history from ancient and modern genomes. <i>Nature Reviews Genetics</i> , 2011, 12, 603-614.	7.7	172
49	Non-equilibrium allele frequency spectra via spectral methods. <i>Theoretical Population Biology</i> , 2011, 79, 203-219.	0.5	38
50	Comparative phylogeography and connectivity of sibling species of the marine copepod <i>Clausocalanus</i> (Calanoida). <i>Journal of Experimental Marine Biology and Ecology</i> , 2011, 404, 108-115.	0.7	45
51	Interspecific and interploidal gene flow in Central European <i>Arabidopsis</i> (Brassicaceae). <i>BMC Evolutionary Biology</i> , 2011, 11, 346.	3.2	71
52	An observation of the loss of genetic variability in pregnant schizothoracin, <i>Schizothorax prenanti</i> , inhabiting a plateau lake. <i>Biochemical Systematics and Ecology</i> , 2011, 39, 361-370.	0.6	17
53	Recent invasion and low level of divergence between diploid and triploid forms of <i>Carassius auratus</i> complex in Croatia. <i>Genetica</i> , 2011, 139, 789-804.	0.5	37
54	Phylogeography and conservation of the bull shark ( <i>Carcharhinus leucas</i> ) inferred from mitochondrial and microsatellite DNA. <i>Conservation Genetics</i> , 2011, 12, 371-382.	0.8	106

#	ARTICLE	IF	CITATIONS
55	Phylogeography, genetic structure, and gene flow in the endemic freshwater shrimp <i>Palaemonetes suttkusi</i> from Cuatro Ci�negas, Mexico. <i>Conservation Genetics</i> , 2011, 12, 557-567.	0.8	19
56	Genetically effective population sizes of Antarctic seals estimated from nuclear genes. <i>Conservation Genetics</i> , 2011, 12, 1435-1446.	0.8	19
57	Genetic population structure in a commercial marine invertebrate with long-lived lecithotrophic larvae: <i>Cucumaria frondosa</i> (Echinodermata: Holothuroidea). <i>Marine Biology</i> , 2011, 158, 859-870.	0.7	22
58	A Bayesian approach to phylogeographic clustering. <i>Interface Focus</i> , 2011, 1, 909-921.	1.5	23
59	Evaluation of a Bayesian Coalescent Method of Species Delimitation. <i>Systematic Biology</i> , 2011, 60, 747-761.	2.7	242
60	GEOECODYNAMICS AND THE KALAHARI EPEIROGENY: LINKING ITS GENOMIC RECORD, TREE OF LIFE AND PALIMPSEST INTO A UNIFIED NARRATIVE OF LANDSCAPE EVOLUTION. <i>South African Journal of Geology</i> , 2011, 114, 489-514.	0.6	49
61	Joint Inference of Population Assignment and Demographic History. <i>Genetics</i> , 2011, 189, 561-577.	1.2	20
62	The Plant Pathogen <i>Pseudomonas syringae</i> pv. <i>tomato</i> Is Genetically Monomorphic and under Strong Selection to Evade Tomato Immunity. <i>PLoS Pathogens</i> , 2011, 7, e1002130.	2.1	186
63	A New Isolation with Migration Model along Complete Genomes Infers Very Different Divergence Processes among Closely Related Great Ape Species. <i>PLoS Genetics</i> , 2012, 8, e1003125.	1.5	102
64	Maximum Likelihood Implementation of an Isolation-with-Migration Model with Three Species for Testing Speciation with Gene Flow. <i>Molecular Biology and Evolution</i> , 2012, 29, 3131-3142.	3.5	81
65	What can patterns of differentiation across plant genomes tell us about adaptation and speciation?. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 364-373.	1.8	234
66	Pairing dynamics and the origin of species. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 1085-1092.	1.2	33
67	Recombination rate variation and speciation: theoretical predictions and empirical results from rabbits and mice. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 409-421.	1.8	339
68	Complex Population Dynamics and the Coalescent Under Neutrality. <i>Genetics</i> , 2012, 190, 187-201.	1.2	131
69	Phylogenetic and Coalescent Strategies of Species Delimitation in Snubnose Darters (Percidae: <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 18</i> )	2.7	74
70	Testing for "Snowballing" Hybrid Incompatibilities in <i>Solanum</i> : Impact of Ancestral Polymorphism and Divergence Estimates. <i>Molecular Biology and Evolution</i> , 2012, 29, 31-34.	3.5	11
71	Likelihood-Based Inferences under Isolation by Distance: Two-Dimensional Habitats and Confidence Intervals. <i>Molecular Biology and Evolution</i> , 2012, 29, 957-973.	3.5	19
72	Reconstructing the Demographic History of the Human Lineage Using Whole-Genome Sequences from Human and Three Great Apes. <i>Genome Biology and Evolution</i> , 2012, 4, 1133-1145.	1.1	22

#	ARTICLE	IF	CITATIONS
73	Genetic diversity and molecular epidemiology of HIV transmission. <i>Future Virology</i> , 2012, 7, 239-252.	0.9	11
74	Popular misconceptions. <i>Molecular Ecology</i> , 2012, 21, 4155-4156.	2.0	4
75	A likelihood-based comparison of population histories in a parasitoid guild. <i>Molecular Ecology</i> , 2012, 21, 4605-4617.	2.0	19
76	Speciation history of three closely related oak gall wasps, <i>Andricus mukaigawae</i> , <i>A. ashwaphilus</i> , and <i>A. pseudoflos</i> (Hymenoptera: Cynipidae) inferred from nuclear and mitochondrial DNA sequences. <i>Molecular Ecology</i> , 2012, 21, 4681-4694.	2.0	5
77	Testing hypotheses for genealogical discordance in a rainforest lizard. <i>Molecular Ecology</i> , 2012, 21, 5059-5072.	2.0	29
78	Recent Progress in Polymorphism-Based Population Genetic Inference. <i>Journal of Heredity</i> , 2012, 103, 287-296.	1.0	51
79	Rapid phenotypic evolution during incipient speciation in a continental avian radiation. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 1847-1856.	1.2	70
80	Species delimitation and digit number in a North African skink. <i>Ecology and Evolution</i> , 2012, 2, 2962-2973.	0.8	9
81	Spatial and temporal variation in genetic diversity of an endangered freshwater seal. <i>Conservation Genetics</i> , 2012, 13, 1231-1245.	0.8	32
82	Population genetic structure of a widespread coniferous tree, <i>Taxodium distichum</i> [L.] Rich. (Cupressaceae), in the Mississippi River Alluvial Valley and Florida. <i>Tree Genetics and Genomes</i> , 2012, 8, 1135-1147.	0.6	8
83	Genetic divergence and population demography of the Hainan endemic Black-throated Laughingthrush (Aves: Timaliidae, <i>Garrulax chinensis monachus</i> ) and adjacent mainland subspecies. <i>Molecular Phylogenetics and Evolution</i> , 2012, 65, 482-489.	1.2	18
84	Biocomplexity in a demersal exploited fish, white hake ( <i>Urophycis tenuis</i> ): depth-related structure and inadequacy of current management approaches. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2012, 69, 415-429.	0.7	19
85	Coalescent-based species delimitation in an integrative taxonomy. <i>Trends in Ecology and Evolution</i> , 2012, 27, 480-488.	4.2	716
86	Extraordinarily rapid life-history divergence between <i>Cryptasterina</i> sea star species. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 3914-3922.	1.2	45
87	Phylogeography of the Temminck's Stint ( <i>Calidris temminckii</i> ): historical vicariance but little present genetic structure in a regionally endangered Palearctic wader. <i>Diversity and Distributions</i> , 2012, 18, 704-716.	1.9	14
88	Recurrent Introgression of Mitochondrial DNA Among Hares ( <i>Lepus</i> spp.) Revealed by Species-Tree Inference and Coalescent Simulations. <i>Systematic Biology</i> , 2012, 61, 367.	2.7	111
89	Deep Phylogeographic Structure and Environmental Differentiation in the Carnivorous Plant <i>Sarracenia alata</i> . <i>Systematic Biology</i> , 2012, 61, 763-777.	2.7	69
90	Paleopopulation Genetics. <i>Annual Review of Genetics</i> , 2012, 46, 635-649.	3.2	17





#	ARTICLE	IF	CITATIONS
109	POPULATION GENETIC EVIDENCE FOR COMPLEX EVOLUTIONARY HISTORIES OF FOUR HIGH ALTITUDE JUNIPER SPECIES IN THE QINGHAI-TIBETAN PLATEAU. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 831-845.	1.1	70
110	DYNAMICS OF DRIFT, GENE FLOW, AND SELECTION DURING SPECIATION IN <i>SILENE</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 1447-1458.	1.1	26
111	POPULATION GENETICS AND OBJECTIVITY IN SPECIES DIAGNOSIS. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 1413-1429.	1.1	100
112	SPECIES DELIMITATION WITH ABC AND OTHER COALESCENT-BASED METHODS: A TEST OF ACCURACY WITH SIMULATIONS AND AN EMPIRICAL EXAMPLE WITH LIZARDS OF THE <i>LIOLAEMUS DARWINII</i> COMPLEX (SQUAMATA: LIOLAEMIDAE). <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 2834-2849.	1.1	170
113	MULTILOCUS COALESCENCE ANALYSES SUPPORT A mtDNA-BASED PHYLOGEOGRAPHIC HISTORY FOR A WIDESPREAD PALEARCTIC PASSERINE BIRD, <i>SITTA EUROPAEA</i> . <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 2850-2864.	1.1	45
114	Phylogeographic studies of plants in China: Advances in the past and directions in the future. <i>Journal of Systematics and Evolution</i> , 2012, 50, 267-275.	1.6	248
115	The complete mitochondrial genome sequence of the filarial nematode <i>Wuchereria bancrofti</i> from three geographic isolates provides evidence of complex demographic history. <i>Molecular and Biochemical Parasitology</i> , 2012, 183, 32-41.	0.5	52
116	A review of the application of molecular genetics for fisheries management and conservation of sharks and rays. <i>Journal of Fish Biology</i> , 2012, 80, 1789-1843.	0.7	190
117	Genetically separate populations of the ocean-skater <i>Halobates sericeus</i> (Heteroptera: Gerridae) have been maintained since the late Pleistocene. <i>Biological Journal of the Linnean Society</i> , 2012, 105, 797-805.	0.7	8
118	Divergence between passerine populations from the Malvinas - Falkland Islands and their continental counterparts: a comparative phylogeographical study. <i>Biological Journal of the Linnean Society</i> , 2012, 106, 865-879.	0.7	32
119	Inferring the evolutionary history of divergence despite gene flow in a lizard species, <i>Scincella lateralis</i> (Scincidae), composed of cryptic lineages. <i>Biological Journal of the Linnean Society</i> , 2012, 107, 192-209.	0.7	13
120	Genetic structure in a dynamic baboon hybrid zone corroborates behavioural observations in a hybrid population. <i>Molecular Ecology</i> , 2012, 21, 715-731.	2.0	114
121	Speciation in the <i>Rana chensinensis</i> species complex and its relationship to the uplift of the Qinghai-Tibetan Plateau. <i>Molecular Ecology</i> , 2012, 21, 960-973.	2.0	72
122	Divergence and biogeography of the recently evolved Macaronesian red <i>Festuca</i> (Gramineae) species inferred from coalescence-based analyses. <i>Molecular Ecology</i> , 2012, 21, 1702-1726.	2.0	10
123	Extensive sympatry, cryptic diversity and introgression throughout the geographic distribution of two coral species complexes. <i>Molecular Ecology</i> , 2012, 21, 2224-2238.	2.0	139
124	Population genetic structure and long-distance dispersal among seabird populations: Implications for colony persistence. <i>Molecular Ecology</i> , 2012, 21, 2863-2876.	2.0	46
125	Model-based comparisons of phylogeographic scenarios resolve the intraspecific divergence of cactophilic <i>Drosophila mojavensis</i> . <i>Molecular Ecology</i> , 2012, 21, 3293-3307.	2.0	36
126	Effects of vicariant barriers, habitat stability, population isolation and environmental features on species divergence in the south-western Australian coastal reptile community. <i>Molecular Ecology</i> , 2012, 21, 3809-3822.	2.0	34



#	ARTICLE	IF	CITATIONS
127	Molecular population genetics of male and female mitochondrial genomes in subarctic <i>Mytilus trossulus</i> . <i>Marine Biology</i> , 2013, 160, 1709-1721.	0.7	40
128	Influence of late Quaternary climate change on present patterns of genetic variation in valley oak, <i>Quercus lobata</i> Née. <i>Molecular Ecology</i> , 2013, 22, 3598-3612.	2.0	127
129	Ecological speciation in anemone-associated snapping shrimps ( <i>Alpheus armatus</i> ) Tj ETQq0 0.0 rgBT /Overlock 10	2.0	39
130	Identifying the sister species to the rapid capuchino seedeater radiation (Passeriformes: <i>Sporophila</i> ). <i>Auk</i> , 2013, 130, 645-655.	0.7	18
131	High evolutionary potential of marine zooplankton. <i>Ecology and Evolution</i> , 2013, 3, 2765-2781.	0.8	97
132	Model selection as a tool for phylogeographic inference: an example from the willow <i>Salix melanopsis</i> . <i>Molecular Ecology</i> , 2013, 22, 4014-4028.	2.0	58
133	Speciation patterns and processes in the zooplankton of the ancient lakes of Sulawesi island, Indonesia. <i>Ecology and Evolution</i> , 2013, 3, 3083-3094.	0.8	11
134	Inferring the evolutionary histories of divergences in <i>Hylobates</i> and <i>Nomascus</i> gibbons through multilocus sequence data. <i>BMC Evolutionary Biology</i> , 2013, 13, 82.	3.2	31
135	Continental phylogeography of an ecologically and morphologically diverse Neotropical songbird, <i>Zonotrichia capensis</i> . <i>BMC Evolutionary Biology</i> , 2013, 13, 58.	3.2	42
136	A hybrid zone between <i>Bathymodiolus</i> mussel lineages from eastern Pacific hydrothermal vents. <i>BMC Evolutionary Biology</i> , 2013, 13, 21.	3.2	35
137	Phylogeography and diversification history of the day-gecko genus <i>Phelsuma</i> in the Seychelles islands. <i>BMC Evolutionary Biology</i> , 2013, 13, 3.	3.2	22
138	A Continuous Method for Gene Flow. <i>Genetics</i> , 2013, 194, 687-696.	1.2	4
139	Unravelling parasitic nematode natural history using population genetics. <i>Trends in Parasitology</i> , 2013, 29, 438-448.	1.5	30
140	Selection by climatic regime and neutral evolutionary processes in holocentric chromosomes ( <i>Carex</i> ) Systematics, 2013, 15, 118-129.	1.1	21
141	Introgression of Crop Alleles into Wild or Weedy Populations. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2013, 44, 325-345.	3.8	169
142	Ecological genomics of local adaptation. <i>Nature Reviews Genetics</i> , 2013, 14, 807-820.	7.7	1,099
143	Hybridization Reveals the Evolving Genomic Architecture of Speciation. <i>Cell Reports</i> , 2013, 5, 666-677.	2.9	118
144	Continent-wide panmixia of an African fruit bat facilitates transmission of potentially zoonotic viruses. <i>Nature Communications</i> , 2013, 4, 2770.	5.8	105

#	ARTICLE	IF	CITATIONS
145	RECENT ECOLOGICAL SELECTION ON REGULATORY DIVERGENCE IS SHAPING CLINAL VARIATION IN <i>SENECIO</i> ON MOUNT ETNA. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, n/a-n/a.	1.1	16
146	Pliocene intraspecific divergence and Pliocene range expansions within <i>Picea likiangensis</i> (Lijiang spruce), a dominant forest tree of the Qinghai-Tibet Plateau. <i>Molecular Ecology</i> , 2013, 22, 5237-5255.	2.0	112
147	Inferences of evolutionary history of a widely distributed mangrove species, <i>Bruguiera gymnorrhiza</i> , in the Indo-West Pacific region. <i>Ecology and Evolution</i> , 2013, 3, 2251-2261.	0.8	35
148	Phylogeographic analysis of the true lemurs (genus <i>Eulemur</i> ) underlines the role of river catchments for the evolution of micro-endemism in Madagascar. <i>Frontiers in Zoology</i> , 2013, 10, 70.	0.9	31
149	Cytosuclear discordance among Southeast Asian black rats ( <i>Rattus rattus</i> complex). <i>Molecular Ecology</i> , 2013, 22, 1019-1034.	2.0	71
150	Multilocus genetic diversity and historical biogeography of the endemic wall lizard from <i>Lacerta biza</i> and <i>Ferromentera</i> , <i>Pseudacris ptyusensis</i> ( <i>Squamata: Lacertidae</i> ). <i>Molecular Ecology</i> , 2013, 22, 4829-4841.	2.0	23
151	Restricted gene flow within and between rapidly diverging Neotropical plant species. <i>Molecular Ecology</i> , 2013, 22, 4931-4942.	2.0	21
152	Heteropatric speciation in a duck, <i>Anas crecca</i> . <i>Molecular Ecology</i> , 2013, 22, 5922-5935.	2.0	20
153	Simulating gene trees under the multispecies coalescent and time-dependent migration. <i>BMC Evolutionary Biology</i> , 2013, 13, 44.	3.2	55
154	PHYLOGENETIC INFERENCE OF NUPTIAL TRAIT EVOLUTION IN THE CONTEXT OF ASYMMETRICAL INTROGRESSION IN NORTH AMERICAN DARTERS (TELEOSTEI). <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 388-402.	1.1	19
155	Is population structure in the European white stork determined by flyway permeability rather than translocation history?. <i>Ecology and Evolution</i> , 2013, 3, 4881-4895.	0.8	19
156	Is there Genetic Differentiation in the Pyrenean Population of Tengmalm's Owl <i>Aegolius Funereus</i> ?. <i>Ardeola</i> , 2013, 60, 123-132.	0.4	4
157	Methodological challenges to realizing the potential of hybridization research. <i>Journal of Evolutionary Biology</i> , 2013, 26, 259-260.	0.8	11
158	Amazon diversification and cross-Andean dispersal of the widespread Neotropical tree species <i>Jacaranda copaia</i> (Bignoniaceae). <i>Journal of Biogeography</i> , 2013, 40, 707-719.	1.4	25
159	Inferring recent historic abundance from current genetic diversity. <i>Molecular Ecology</i> , 2013, 22, 22-40.	2.0	40
160	Delimiting species in recent radiations with low levels of morphological divergence: A case study in Australian <i>Gehyra</i> geckos. <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 135-143.	1.2	33
161	Recent nonhybrid origin of sunflower ecotypes in a novel habitat. <i>Molecular Ecology</i> , 2013, 22, 799-813.	2.0	47
162	The evolution of north-east Atlantic gadfly petrels using statistical phylogeography. <i>Molecular Ecology</i> , 2013, 22, 495-507.	2.0	19

#	ARTICLE	IF	CITATIONS
163	Stepwise colonization of the Andes by Ruddy Ducks and the evolution of novel $\beta$ -globin variants. <i>Molecular Ecology</i> , 2013, 22, 1231-1249.	2.0	12
164	Culture modifies expectations of kinship and sex-biased dispersal patterns: A case study of patrilineality and patrilocality in tribal yemen. <i>American Journal of Physical Anthropology</i> , 2013, 150, 526-538.	2.1	10
165	Multilocus phylogeography of Australian teals ( <i>Anas</i> spp.): a case study of the relationship between vagility and genetic structure. <i>Journal of Avian Biology</i> , 2013, 44, 169-178.	0.6	12
166	Population genomics based on low coverage sequencing: how low should we go?. <i>Molecular Ecology</i> , 2013, 22, 3028-3035.	2.0	181
167	Use of multiple markers demonstrates a cryptic western refugium and postglacial colonisation routes of Atlantic salmon ( <i>Salmo salar</i> L.) in northwest Europe. <i>Heredity</i> , 2013, 111, 34-43.	1.2	27
168	THE EFFECT OF COLLECTIVE DISPERSAL ON THE GENETIC STRUCTURE OF A SUBDIVIDED POPULATION. <i>Evolution; International Journal of Organic Evolution</i> , 2013, 67, 1649-1659.	1.1	25
169	The evolving male: spinner dolphin ( <i>Stenella longirostris</i> ) ecotypes are divergent at <i>Y</i> chromosome but not mtDNA or autosomal markers. <i>Molecular Ecology</i> , 2013, 22, 2408-2423.	2.0	27
170	<i>Pleistocene</i> climate change and the origin of two desert plant species, <i>Pugionium cornutum</i> and <i>Pugionium Adolabratum</i> ( <i>Boraginaceae</i> ), in northwest China. <i>New Phytologist</i> , 2013, 199, 277-287.	3.5	55
171	Development of genetic diversity, differentiation and structure over 500 years in four ponderosa pine populations. <i>Molecular Ecology</i> , 2013, 22, 2640-2652.	2.0	24
172	Present genetic structure revealed by microsatellites reflects recent history of the Finnish moose ( <i>Alces alces</i> ). <i>European Journal of Wildlife Research</i> , 2013, 59, 613-627.	0.7	9
173	Diversification of plant species in arid Northwest China: Species-level phylogeographical history of <i>Lagochilus Bunge ex Bentham</i> ( <i>Lamiaceae</i> ). <i>Molecular Phylogenetics and Evolution</i> , 2013, 68, 398-409.	1.2	49
174	Recent allopatric divergence and niche evolution in a widespread Palearctic bird, the common rosefinch ( <i>Carpodacus erythrinus</i> ). <i>Molecular Phylogenetics and Evolution</i> , 2013, 66, 103-111.	1.2	17
175	Planktonic larvae do not ensure gene flow in the edible sea urchin <i>Paracentrotus lividus</i> . <i>Marine Ecology - Progress Series</i> , 2013, 480, 155-170.	0.9	33
176	Congruence between distribution modelling and phylogeographical analyses reveals <i>Quaternary</i> survival of a toadflax species ( <i>Linaria elegans</i> ) in oceanic climate areas of a mountain ring range. <i>New Phytologist</i> , 2013, 198, 1274-1289.	3.5	46
177	The Role of Historical Barriers in the Diversification Processes in Open Vegetation Formations during the Miocene/Pliocene Using an Ancient Rodent Lineage as a Model. <i>PLoS ONE</i> , 2013, 8, e61924.	1.1	93
178	A multilocus sequencing approach reveals the cryptic phylogeographical history of <i>Phyllodoce nipponica</i> ...Makino ( <i>Ericaceae</i> ). <i>Biological Journal of the Linnean Society</i> , 2013, 110, 214-226.	0.7	13
179	The genetic structure of crossbills suggests rapid diversification with little niche conservatism. <i>Biological Journal of the Linnean Society</i> , 2013, 109, 908-922.	0.7	11
180	Phylogeography of Silver Pheasant ( <i>Lophura nycthemera</i> L.) across China: aggregate effects of refugia, introgression and riverine barriers. <i>Molecular Ecology</i> , 2013, 22, 3376-3390.	2.0	39

#	ARTICLE	IF	CITATIONS
181	Conservation Genetics. , 2013, , 263-277.		0
182	Multilocus tests of <i>Pleistocene refugia and ancient divergence in a pair of Atlantic forest antbirds (<i>Myrmeciza</i>). Molecular Ecology, 2013, 22, 3996-4013.</i>	2.0	85
183	Integrating phylogenetics, phylogeography and population genetics through genomes and evolutionary theory. Molecular Phylogenetics and Evolution, 2013, 69, 1172-1185.	1.2	63
184	DETECTING RANGE EXPANSIONS FROM GENETIC DATA. Evolution; International Journal of Organic Evolution, 2013, 67, 3274-3289.	1.1	141
185	Identifying Loci Under Selection Against Gene Flow in Isolation-with-Migration Models. Genetics, 2013, 194, 211-233.	1.2	58
186	INTEGRATIVE TESTING OF HOW ENVIRONMENTS FROM THE PAST TO THE PRESENT SHAPE GENETIC STRUCTURE ACROSS LANDSCAPES. Evolution; International Journal of Organic Evolution, 2013, 67, 3386-3402.	1.1	110
187	No evidence for nuclear introgression despite complete mtDNA replacement in the Carpathian newt ( <i>Lissotriton montandoni</i> ). Molecular Ecology, 2013, 22, 1884-1903.	2.0	96
188	Genetic introgression and hybridization in Antillean freshwater turtles ( <i>Trachemys</i> ) revealed by coalescent analyses of mitochondrial and cloned nuclear markers. Molecular Phylogenetics and Evolution, 2013, 67, 176-187.	1.2	50
189	After continents divide: comparative phylogeography of reef fishes from the Red Sea and Indian Ocean. Journal of Biogeography, 2013, 40, 1170-1181.	1.4	110
190	Phylogeography of the shrimp <i>Palaemon floridanus</i> (Crustacea: Caridea: Palaemonidae): a partial test of meta-population genetic structure in the wider Caribbean. Marine Ecology, 2013, 34, 381-393.	0.4	15
191	Did postglacial sea-level changes initiate the evolutionary divergence of a Tasmanian endemic raptor from its mainland relative?. Proceedings of the Royal Society B: Biological Sciences, 2013, 280, 20132448.	1.2	23
192	Robust Demographic Inference from Genomic and SNP Data. PLoS Genetics, 2013, 9, e1003905.	1.5	1,185
193	Genetic Diversity of Black Salamanders ( <i>Aneides flavipunctatus</i> ) across Watersheds in the Klamath Mountains. Diversity, 2013, 5, 657-679.	0.7	7
194	Reproductive isolation between phylogeographic lineages scales with divergence. Proceedings of the Royal Society B: Biological Sciences, 2013, 280, 20132246.	1.2	93
195	Approximate Bayesian computation for modular inference problems with many parameters: the example of migration rates. Molecular Ecology, 2013, 22, 987-1002.	2.0	15
196	Mitochondrial <i>cox</i> sequences of <i>Nilaparvata lugens</i> and <i>Sogatella furcifera</i> (Hemiptera, Delphacidae): low specificity among Asian planthopper populations. Bulletin of Entomological Research, 2013, 103, 382-392.	0.5	32
197	Population genetic evidence for speciation pattern and gene flow between <i>Picea wilsonii</i> , <i>P. morrisonicola</i> and <i>P. neoveitchii</i> . Annals of Botany, 2013, 112, 1829-1844.	1.4	49
198	Range dynamics, rather than convergent selection, explain the mosaic distribution of winged blackbird phenotypes. Ecology and Evolution, 2013, 3, 4910-4924.	0.8	4

#	ARTICLE	IF	CITATIONS
199	Why to account for finite sites in population genetic studies and how to do this with Jaatha 2.0. Ecology and Evolution, 2013, 3, 3647-3662.	0.8	20
200	Inferring Phylogeny and Introgression using RADseq Data: An Example from Flowering Plants ( <i>Pedicularis</i> : Orobanchaceae). Systematic Biology, 2013, 62, 689-706.	2.7	482
201	Interspecific differentiation and gene flow between two desert poplars inferred from six vacuolar Na <sup>+</sup> /H <sup>+</sup> exchanger loci. Journal of Systematics and Evolution, 2013, 51, 652-663.	1.6	2
202	Extensive sampling of polar bears ( <i>Ursus maritimus</i> ) in the Northwest Passage (Canadian Arctic Archipelago) reveals population differentiation across multiple spatial and temporal scales. Ecology and Evolution, 2013, 3, 3152-3165.	0.8	43
203	Tertiary Origin and Pleistocene Diversification of Dragon Blood Tree ( <i>Dracaena</i> ) in Cambodia. PLoS ONE, 2013, 8, e82664.	1.1	13
204	Gene Flow and Hybridization between Numerically Imbalanced Populations of Two Duck Species on the Subantarctic Island of South Georgia. PLoS ONE, 2013, 8, e82664.	1.1	6
205	Two sides of the same coin: extinctions and originations across the Atlantic/Indian Ocean boundary as consequences of the same climate oscillation. Frontiers of Biogeography, 2013, 5, .	0.8	5
206	Phylogeographic Structure in Benthic Marine Invertebrates of the Southeast Pacific Coast of Chile with Differing Dispersal Potential. PLoS ONE, 2014, 9, e88613.	1.1	127
207	Fuzzy Boundaries: Color and Gene Flow Patterns among Parapatric Lineages of the Western Shovel-Nosed Snake and Taxonomic Implication. PLoS ONE, 2014, 9, e97494.	1.1	11
208	Population Genetics of the São Tomé Caecilian ( <i>Gymnophiona</i> : <i>Dermophiidae</i> : <i>Schistometopum</i> ) in the Atlantic. PLoS ONE, 2014, 9, e97494.	1.1	13
209	Postglacial population genetic differentiation potentially facilitated by a flexible migratory strategy in Golden-crowned Kinglets ( <i>Regulus satrapa</i> ). Canadian Journal of Zoology, 2014, 92, 163-172.	0.4	4
210	Models of nucleotide substitution. , 2014, , 1-34.		1
211	Revisiting the vanishing refuge model of diversification. Frontiers in Genetics, 2014, 5, 353.	1.1	37
212	Adaptive divergence with gene flow in incipient speciation of <i>Miscanthus floridulus</i> / <i>M. sinensis</i> complex ( <i>Poaceae</i> ). Plant Journal, 2014, 80, 834-847.	2.8	17
213	Molecular evidence for ancient relicts of arctic-alpine plants in East Asia. New Phytologist, 2014, 203, 980-988.	3.5	11
214	Genomic replacement of native <i>Cobitis lutheri</i> with introduced <i>C. tetralineata</i> through a hybrid swarm following the artificial connection of river systems. Ecology and Evolution, 2014, 4, 1451-1465.	0.8	15
215	Phenotypic and genetic evidence for ecological speciation of <i>Aquilegia japonica</i> and <i>A. oxysepala</i> . New Phytologist, 2014, 204, 1028-1040.	3.5	21
216	Global population structure and demographic history of the grey seal. Molecular Ecology, 2014, 23, 3999-4017.	2.0	32

#	ARTICLE	IF	CITATIONS
217	Testing for shared biogeographic history in the lower continental American freshwater fish assemblage using comparative phylogeography: concerted, independent, or multiple evolutionary responses?. <i>Ecology and Evolution</i> , 2014, 4, 1686-1705.	0.8	15
218	The Woolly Monkey. , 2014, , .		6
219	Likelihood-based inference of population history from low-coverage <i>de novo</i> genome assemblies. <i>Molecular Ecology</i> , 2014, 23, 198-211.	2.0	28
220	Phylogeographical study of the alpine plant <i>Cassiope lycopodioides</i> (Ericaceae) suggests a range connection between the Japanese archipelago and Beringia during the Pleistocene. <i>Biological Journal of the Linnean Society</i> , 2014, 113, 497-509.	0.7	13
221	DIVERSIFICATION AND GENE FLOW IN NASCENT LINEAGES OF ISLAND AND MAINLAND NORTH AMERICAN TREE SQUIRRELS ( <i>TAMIASCIURUS</i> ). <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 1094-1109.	1.1	31
222	An integrated approach to control the introduced forest pathogen <i>Heterobasidion irregulare</i> in Europe. <i>Forestry</i> , 2014, 87, 471-481.	1.2	33
223	Introgressive hybridization and latitudinal admixture clines in North Atlantic eels. <i>BMC Evolutionary Biology</i> , 2014, 14, 61.	3.2	15
224	Populations of a cyprinid fish are self-sustaining despite widespread feminization of males. <i>BMC Biology</i> , 2014, 12, 1.	1.7	199
225	Extensive genetic population structure in the Indo-West Pacific spot-tail shark, <i>Carcharhinus sorrah</i> . <i>Bulletin of Marine Science</i> , 2014, 90, 427-454.	0.4	23
226	Speciation Genomics of Fungal Plant Pathogens. <i>Advances in Botanical Research</i> , 2014, , 397-423.	0.5	2
227	Demographic history and niche conservatism of tropical rainforest trees separated along an altitudinal gradient of a biogeographic barrier. <i>Australian Journal of Botany</i> , 2014, 62, 438.	0.3	10
228	Conservation Genetics and the Implication for Recovery of the Endangered Mitchell's Satyr Butterfly, <i>Neonympha mitchellii mitchellii</i> . <i>Journal of Heredity</i> , 2014, 105, 19-27.	1.0	4
229	Range shift and introgression of the rear and leading populations in two ecologically distinct Rubus species. <i>BMC Evolutionary Biology</i> , 2014, 14, 209.	3.2	25
230	THE INFLUENCE OF SAMPLING DESIGN ON SPECIES TREE INFERENCE: A NEW RELATIONSHIP FOR THE NEW WORLD CHICKADEES (AVES: <i>POECILE</i> ). <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 501-513.	1.1	34
231	Patterns of Evolutionary Divergence and Convergence in the Bushy-Tailed Woodrat ( <i>Neotoma cinerea</i> ) Across Western North America. <i>Journal of Mammalian Evolution</i> , 2014, 21, 243-256.	1.0	1
232	Mitochondrial discordance in genetic structure across the Atlantic/Indian Ocean biogeographical transition zone. <i>Journal of Biogeography</i> , 2014, 41, 392-401.	1.4	25
233	Species taxonomy of birds: Which null hypothesis?. <i>Auk</i> , 2014, 131, 150-161.	0.7	105
234	Genome-scale analysis of demographic history and adaptive selection. <i>Protein and Cell</i> , 2014, 5, 99-112.	4.8	10



#	ARTICLE	IF	CITATIONS
235	Phylogeography of <i>Ramalina menziesii</i> , a widely distributed lichen-forming fungus in western North America. <i>Molecular Ecology</i> , 2014, 23, 2326-2339.	2.0	32
236	A phylogeographic evaluation of the <i>Amolops mantzorum</i> species group: Cryptic species and plateau uplift. <i>Molecular Phylogenetics and Evolution</i> , 2014, 73, 40-52.	1.2	35
237	Mitochondrial genetic diversity and population structure of a vulnerable freshwater fish, rock carp ( <i>Procypris rabaudi</i> ) in upper Yangtze River drainage. <i>Biochemical Systematics and Ecology</i> , 2014, 55, 1-9.	0.6	15
238	The contribution of Anatolia to European phylogeography: the centre of origin of the meadow grasshopper, <i>Chorthippus parallelus</i> . <i>Journal of Biogeography</i> , 2014, 41, 1793-1805.	1.4	43
239	The Influence of Gene Flow on Species Tree Estimation: A Simulation Study. <i>Systematic Biology</i> , 2014, 63, 17-30.	2.7	308
240	Recent divergences and size decreases of eastern gorilla populations. <i>Biology Letters</i> , 2014, 10, 20140811.	1.0	64
241	Testing hypotheses of mitochondrial gene tree paralogy: unravelling mitochondrial capture of the Streak-breasted Scimitar Babbler ( <i>Pomatorhinus ruficollis</i> ) by the Taiwan Scimitar Babbler ( <i>Pomatorhinus musicus</i> ). <i>Molecular Ecology</i> , 2014, 23, 5855-5867.	2.0	12
242	The Lengths of Admixture Tracts. <i>Genetics</i> , 2014, 197, 953-967.	1.2	121
243	Can novel genetic analyses help to identify low-dispersal marine invasive species?. <i>Ecology and Evolution</i> , 2014, 4, 2848-2866.	0.8	19
244	Historical and recent processes shaping the geographic range of a rocky intertidal gastropod: phylogeography, ecology, and habitat availability. <i>Ecology and Evolution</i> , 2014, 4, 3244-3255.	0.8	26
245	Genetic variation among western populations of the Horned Lark ( <i>Eremophila alpestris</i> ) indicates recent colonization of the Channel Islands off southern California, mainland-bound dispersal, and postglacial range shifts. <i>Auk</i> , 2014, 131, 162-174.	0.7	18
246	Comparing Phylogeographic Hypotheses by Simulating DNA Sequences under a Spatially Explicit Model of Coalescence. <i>Molecular Biology and Evolution</i> , 2014, 31, 3359-3372.	3.5	14
247	Hybridization and mitochondrial genome introgression between <i>Rana chensinensis</i> and <i>R. kukunoris</i> . <i>Molecular Ecology</i> , 2014, 23, 5575-5588.	2.0	17
248	Influence of gene flow on divergence dating – implications for the speciation history of <i>Takydromus</i> grass lizards. <i>Molecular Ecology</i> , 2014, 23, 4770-4784.	2.0	17
249	Climatic adaptation and ecological divergence between two closely related pine species in Southeast China. <i>Molecular Ecology</i> , 2014, 23, 3504-3522.	2.0	48
250	Contrasting Population Histories of the Deep-Sea Demersal Fish, <i>Lycodes matsubarai</i> , in the Sea of Japan and the Sea of Okhotsk. <i>Zoological Science</i> , 2014, 31, 375.	0.3	18
251	Interglacial genetic diversification of <i>Moussonia deppeana</i> (Gesneriaceae), a hummingbird-pollinated, cloud forest shrub in northern Mesoamerica. <i>Molecular Ecology</i> , 2014, 23, 4119-4136.	2.0	25
252	Phylogeographical Analysis of a Cold-Temperate Freshwater Fish, the Amur Sleeper ( <i>Perccottus</i> )	1.0	16



#	ARTICLE	IF	CITATIONS
253	Unique mitochondrial <scp>DNA</scp> lineages in Irish stickleback populations: cryptic refugium or rapid recolonization?. <i>Ecology and Evolution</i> , 2014, 4, 2488-2504.	0.8	15
254	Sequential adaptive introgression of the mitochondrial genome in <i><scp>D</scp>rosophila yakuba</i> and <i><scp>D</scp>rosophila santomea</i>. <i>Molecular Ecology</i> , 2014, 23, 1124-1136.	2.0	66
255	Reanalysis suggests that genomic islands of speciation are due to reduced diversity, not reduced gene flow. <i>Molecular Ecology</i> , 2014, 23, 3133-3157.	2.0	937
256	Climate refugia: joint inference from fossil records, species distribution models and phylogeography. <i>New Phytologist</i> , 2014, 204, 37-54.	3.5	361
257	Dispersal potential and population genetic structure in the marine intertidal of the eastern North Pacific. <i>Ecological Monographs</i> , 2014, 84, 435-456.	2.4	59
258	Clinal colour variation within a panmictic population of tree squirrels, <i>Tamiasciurus douglasii</i> (Rodentia: Sciuridae), across an ecological gradient. <i>Biological Journal of the Linnean Society</i> , 2014, 113, 536-546.	0.7	3
259	The hidden history of the snowshoe hare, <i><scp>L</scp>epus americanus</i>: extensive mitochondrial <scp>DNA</scp> introgression inferred from multilocus genetic variation. <i>Molecular Ecology</i> , 2014, 23, 4617-4630.	2.0	40
260	Ecological divergence combined with ancient allopatry in lizard populations from a small volcanic island. <i>Molecular Ecology</i> , 2014, 23, 4799-4812.	2.0	8
261	Glacial history of the European marine mussels <i>Mytilus</i> , inferred from distribution of mitochondrial DNA lineages. <i>Heredity</i> , 2014, 113, 250-258.	1.2	27
262	Cytosuclear discordance and historical demography of two brown frogs, <i>Rana tagoi</i> and <i>R. sakuraii</i> (Amphibia: Ranidae). <i>Molecular Phylogenetics and Evolution</i> , 2014, 79, 231-239.	1.2	13
263	Maximum-Likelihood Inference of Population Size Contractions from Microsatellite Data. <i>Molecular Biology and Evolution</i> , 2014, 31, 2805-2823.	3.5	67
264	Diversification of the Alpine Chipmunk, <i>Tamias alpinus</i> , an alpine endemic of the Sierra Nevada, California. <i>BMC Evolutionary Biology</i> , 2014, 14, 34.	3.2	24
265	Multilocus coalescent analyses reveal the demographic history and speciation patterns of mouse lemur sister species. <i>BMC Evolutionary Biology</i> , 2014, 14, 57.	3.2	22
266	Variation in palaeo-shorelines explains contemporary population genetic patterns of rocky shore species. <i>Biology Letters</i> , 2014, 10, 20140330.	1.0	39
267	Bears in a Forest of Gene Trees: Phylogenetic Inference Is Complicated by Incomplete Lineage Sorting and Gene Flow. <i>Molecular Biology and Evolution</i> , 2014, 31, 2004-2017.	3.5	148
268	Genetic variation in horizontally transmitted fungal endophytes of pine needles reveals population structure in cryptic species. <i>American Journal of Botany</i> , 2014, 101, 1362-1374.	0.8	34
269	Utility of island populations in re-introduction programmes – relationships between <scp>A</scp>rabian gazelles (<i><scp>G</scp>azella arabica</i>) from the <scp>F</scp>arasan <scp>A</scp>rchipelago and endangered mainland populations. <i>Molecular Ecology</i> , 2014, 23, 1910-1922.	2.0	8
270	Australia's arid-adapted butcherbirds experienced range expansions during Pleistocene glacial maxima. <i>Nature Communications</i> , 2014, 5, 3994.	5.8	65

#	ARTICLE	IF	CITATIONS
271	One species or two? Multilocus analysis of nucleotide variation of <i>Melastoma penicillatum</i> and <i>Melastoma sanguineum</i> (Melastomataceae) in Hainan, China. <i>Biochemical Systematics and Ecology</i> , 2014, 55, 275-282.	0.6	7
272	The Irish potato famine pathogen <i>Phytophthora infestans</i> originated in central Mexico rather than the Andes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8791-8796.	3.3	186
273	Demographic history of a common pioneer tree, <i>Zanthoxylum ailanthoides</i> , reconstructed using isolation-with-migration model. <i>Tree Genetics and Genomes</i> , 2014, 10, 1213-1222.	0.6	4
274	Integrating phylogeography and morphometrics to assess conservation merits and inform conservation strategies for an endangered subspecies of a common bird species. <i>Biological Conservation</i> , 2014, 174, 136-146.	1.9	17
275	Phylogeography of <i>Hipposideros armiger</i> (Chiroptera: Hipposideridae) in the Oriental Region: the contribution of multiple Pleistocene glacial refugia and intrinsic factors to contemporary population genetic structure. <i>Journal of Biogeography</i> , 2014, 41, 317-327.	1.4	37
276	Models of Selection, Isolation, and Gene Flow in Speciation. <i>Biological Bulletin</i> , 2014, 227, 133-145.	0.7	2
277	Comparative transcriptomics allows for rapid development of population-level nuclear markers in <i>Hesperoperla pacifica</i> (Plecoptera:Perlidae). <i>Freshwater Science</i> , 2014, 33, 364-373.	0.9	7
278	After the gold rush: population structure of spiny lobsters in Hawaii following a fishery closure and the implications for contemporary spatial management. <i>Bulletin of Marine Science</i> , 2014, 90, 331-357.	0.4	9
279	On the occurrence of false positives in tests of migration under an isolation-with-migration model. <i>Molecular Ecology</i> , 2015, 24, 5078-5083.	2.0	38
280	Testing Taxon Tenacity of Tortoises: evidence for a geographical selection gradient at a secondary contact zone. <i>Ecology and Evolution</i> , 2015, 5, 2095-2114.	0.8	18
281	Gene flow between <i>Drosophila yakuba</i> and <i>Drosophila santomea</i> in subunit V of cytochrome c oxidase: A potential case of cytonuclear cointegration. <i>Evolution; International Journal of Organic Evolution</i> , 2015, 69, 1973-1986.	1.1	45
284	Assortative mating between two sympatric closely-related specialists: inferred from molecular phylogenetic analysis and behavioral data. <i>Scientific Reports</i> , 2014, 4, 5436.	1.6	21
285	The BPP program for species tree estimation and species delimitation. <i>Environmental Epigenetics</i> , 2015, 61, 854-865.	0.9	568
286	Out-of-the tropics or trans-tropical dispersal? The origins of the disjunct distribution of the gooseneck barnacle <i>Pollicipes elegans</i> . <i>Frontiers in Zoology</i> , 2015, 12, 39.	0.9	10
287	Hybrid "superswarm"™ leads to rapid divergence and establishment of populations during a biological invasion. <i>Molecular Ecology</i> , 2015, 24, 5394-5411.	2.0	29
288	Phenotypic differentiation in love song traits among sibling species of the <i>Lutzomyia longipalpis</i> complex in Brazil. <i>Parasites and Vectors</i> , 2015, 8, 290.	1.0	22
289	Distinguishing noise from signal in patterns of genomic divergence in a highly polymorphic avian radiation. <i>Molecular Ecology</i> , 2015, 24, 4238-4251.	2.0	72
290	Population structure within an alpine archipelago: strong signature of past climate change in the New Zealand rock wren ( <i>Xenicus gilviventris</i> ). <i>Molecular Ecology</i> , 2015, 24, 4778-4794.	2.0	34

#	ARTICLE	IF	CITATIONS
291	Speciation with gene flow in whiptail lizards from a Neotropical xeric biome. <i>Molecular Ecology</i> , 2015, 24, 5957-5975.	2.0	44
293	Speciation processes in putative island endemic sister bat species: false impressions from mitochondrial <i>&lt;sc&gt;DNA&lt;/sc&gt;</i> and microsatellite data. <i>Molecular Ecology</i> , 2015, 24, 5910-5926.	2.0	11
294	Mito-nuclear discordance with evidence of shared ancestral polymorphism and selection in cactophilic species of <i>&lt;i&gt;Drosophila&lt;/i&gt;</i> . <i>Biological Journal of the Linnean Society</i> , 2015, 116, 197-210.	0.7	17
295	Understanding the mechanisms of antitropical divergence in the seabird <i>&lt;sc&gt;W&lt;/sc&gt;hite-faced <i>&lt;sc&gt;S&lt;/sc&gt;torm-petrel (&lt;sc&gt;P&lt;/sc&gt;rococellariiformes: <i>&lt;i&gt;P&lt;/i&gt;elagodroma marina&lt;/i&gt;</i>) using a multilocus approach. <i>Molecular Ecology</i>, 2015, 24, 3122-3137.</i></i>	2.0	15
296	Narrow endemics in European mountains: high genetic diversity within the monospecific genus <i>&lt;i&gt;Pseudomisopates&lt;/i&gt;</i> (Plantaginaceae) despite isolation since the late Pleistocene. <i>Journal of Biogeography</i> , 2015, 42, 1455-1468.	1.4	53
297	Migration and isolation during the turbulent Ponto-Caspian Pleistocene create high diversity in the crustacean <i>&lt;i&gt;Paramysis lacustris&lt;/i&gt;</i> . <i>Molecular Ecology</i> , 2015, 24, 4537-4555.	2.0	13
298	Phylogeographic inference using Bayesian model comparison across a fragmented chorus frog species complex. <i>Molecular Ecology</i> , 2015, 24, 4739-4758.	2.0	22
299	Influence of the larval phase on connectivity: strong differences in the genetic structure of brooders and broadcasters in the <i>&lt;i&gt;Ophioderma longicauda&lt;/i&gt;</i> species complex. <i>Molecular Ecology</i> , 2015, 24, 6080-6094.	2.0	26
300	Persistent inter- and intraspecific gene exchange within a parallel radiation of caterpillar hunter beetles ( <i>&lt;i&gt;C&lt;/i&gt;alosoma&lt;/i&gt; sp.) from the <i>&lt;sc&gt;Galápagos&lt;/sc&gt;</i>. <i>Molecular Ecology</i>, 2015, 24, 3107-3121.</i>	2.0	21
301	Evolutionary Migration of the Disjunct Salt Cress <i>Eutrema salsugineum</i> (= <i>Thellungiella salsuginea</i> ), <i>Tj ETQq1 1 0.784314 rgBT / Overl</i>	1.1	17
302	Mitochondrial Analysis of the Most Basal Canid Reveals Deep Divergence between Eastern and Western North American Gray Foxes ( <i>Urocyon</i> spp.) and Ancient Roots in Pleistocene California. <i>PLoS ONE</i> , 2015, 10, e0136329.	1.1	13
303	Coalescent Modelling Suggests Recent Secondary-Contact of Cryptic Penguin Species. <i>PLoS ONE</i> , 2015, 10, e0144966.	1.1	33
304	Evolutionary origin and demographic history of an ancient conifer ( <i>Juniperus microsperma</i> ) in the Qinghai-Tibetan Plateau. <i>Scientific Reports</i> , 2015, 5, 10216.	1.6	15
305	Phylogeny and Differentiation of Wide-Ranging Ryukyu Kajika Frog <i>&lt;i&gt;Buergeria japonica&lt;/i&gt;</i> (Amphibia): <i>Tj ETQq1 1 0.784314 rgBT / Overl</i> Formation. <i>Zoological Science</i> , 2015, 32, 240-247.	0.3	31
306	The Inference of Gene Trees with Species Trees. <i>Systematic Biology</i> , 2015, 64, e42-e62.	2.7	226
307	Postglacial range shift and demographic expansion of the marine intertidal snail <i>Batillaria attramentaria</i> . <i>Ecology and Evolution</i> , 2015, 5, 419-435.	0.8	18
308	Multilocus species trees and species delimitation in a temporal context: application to the water shrews of the genus <i>Neomys</i> . <i>BMC Evolutionary Biology</i> , 2015, 15, 209.	3.2	21
309	The phylogeny of pikas ( <i>Ochotona</i> ) inferred from a multilocus coalescent approach. <i>Molecular Phylogenetics and Evolution</i> , 2015, 84, 240-244.	1.2	28

#	ARTICLE	IF	CITATIONS
310	Comparative multilocus phylogeography of two Palaeartic spruce bark beetles: influence of contrasting ecological strategies on genetic variation. <i>Molecular Ecology</i> , 2015, 24, 1292-1310.	2.0	34
311	Statistical Inference on Genetic Data Reveals the Complex Demographic History of Human Populations in Central Asia. <i>Molecular Biology and Evolution</i> , 2015, 32, 1411-1424.	3.5	27
312	Molecular Systematics of the Least Darter (Percidae: <i>Etheostoma microperca</i> ): Historical Biogeography and Conservation Implications. <i>Copeia</i> , 2015, 103, 87-98.	1.4	9
313	Origin and speciation of <i>Picea schrenkiana</i> and <i>Picea smithiana</i> in the Center Asian Highlands and Himalayas. <i>Plant Molecular Biology Reporter</i> , 2015, 33, 661-672.	1.0	13
314	Genetic data from the red alga <i>Palmaria palmata</i> reveal a mid-Pleistocene deep genetic split in the North Atlantic. <i>Journal of Biogeography</i> , 2015, 42, 902-913.	1.4	23
315	Strong population structure of <i>Schizopygopsis chengi</i> and the origin of <i>S. chengi</i> <i>baoxingensis</i> revealed by mtDNA and microsatellite markers. <i>Genetica</i> , 2015, 143, 73-84.	0.5	11
316	Geographical barriers and climate influence demographic history in narrowleaf cottonwoods. <i>Heredity</i> , 2015, 114, 387-396.	1.2	27
317	Differential introgression and effective size of marker type influence phylogenetic inference of a recently divergent avian group (Phasianidae: <i>Tympanuchus</i> ). <i>Molecular Phylogenetics and Evolution</i> , 2015, 84, 1-13.	1.2	18
318	A coalescent-based method for population tree inference with haplotypes. <i>Bioinformatics</i> , 2015, 31, 691-698.	1.8	9
319	A flexible theoretical representation for the temporal dynamics of structured populations as paths on polytope complexes. <i>Journal of Mathematical Biology</i> , 2015, 71, 735-766.	0.8	1
320	Ancient divergence and recent population expansion in a leaf frog endemic to the southern Brazilian Atlantic forest. <i>Organisms Diversity and Evolution</i> , 2015, 15, 695-710.	0.7	17
321	Inter and intra island introgression in a wolf spider radiation from the Galpagos, and its implications for parallel evolution. <i>Molecular Phylogenetics and Evolution</i> , 2015, 84, 73-84.	1.2	9
322	Phylogeography of <i>Haplocarpha rueppelii</i> (Asteraceae) suggests a potential geographic barrier for plant dispersal and gene flow in East Africa. <i>Science Bulletin</i> , 2015, 60, 1184-1192.	4.3	8
323	Effect of oceanic straits on gene flow in the recently endangered little brown bat ( <i>Myotis</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 TFF <i>Journal of Zoology</i> , 2015, 93, 427-437.	0.4	7
324	Contrasting signals of genetic diversity and historical demography between two recently diverged marine and estuarine fish species. <i>Marine Ecology - Progress Series</i> , 2015, 526, 157-167.	0.9	8
325	The phylogeographic history of the threatened <i>Diana fritillary</i> , <i>Speyeria diana</i> (Lepidoptera:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 TFF	0.8	9
326	Concordant genetic structure in two species of woodpecker distributed across the primary West African biogeographic barriers. <i>Molecular Phylogenetics and Evolution</i> , 2015, 88, 64-74.	1.2	30
327	Climate as a driver of tropical insular diversity: comparative phylogeography of two ecologically distinctive frogs in Puerto Rico. <i>Ecography</i> , 2015, 38, 769-781.	2.1	10

#	ARTICLE	IF	CITATIONS
328	Genome-Enabled Analysis of Plant-Pathogen Migration. Annual Review of Phytopathology, 2015, 53, 121-135.	3.5	30
329	Estimating the temporal and spatial extent of gene flow among sympatric lizard populations (genus <i>Tj ETQq1</i> ). <i>Journal of Biogeography</i> , 2015, 42, 1078-1091.	2.0	16
330	Secondary contact seeds phenotypic novelty in cichlid fishes. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20142272.	1.2	41
331	Genetic admixture supports an ancient hybrid origin of the endangered Hawaiian duck. Journal of Evolutionary Biology, 2015, 28, 1005-1015.	0.8	31
332	Complex history of isolation and gene flow in hoary, Olympic, and endangered Vancouver Island marmots. Journal of Mammalogy, 2015, 96, 810-826.	0.6	16
333	The complex phylogeography of the Indo-Malayan <i>Allophoixus</i> bulbuls with the description of a putative new ring species complex. Molecular Ecology, 2015, 24, 5460-5474.	2.0	25
335	Comparative phylogeography of five bumblebees: impact of range fragmentation, range size and diet specialization. Biological Journal of the Linnean Society, 2015, 116, 926-939.	0.7	20
336	Divergence and population traits in evolution of the genus <i>Pisum</i> L. as reconstructed using genes of two histone H1 subtypes showing different phylogenetic resolution. Gene, 2015, 556, 235-244.	1.0	26
337	A parameter to quantify the degree of genetic mixing among individuals in hybrid populations. Heredity, 2015, 114, 249-254.	1.2	7
338	Combined next-generation sequencing and morphology reveal fine-scale speciation in Crocodile Skinks (Squamata: Scincidae: <i>Tribolonotus</i> ). Molecular Ecology, 2015, 24, 466-483.	2.0	15
339	A primer on the phylogeography of <i>Lagothrix lagotricha</i> (sensu Fooden) in northern South America. Molecular Phylogenetics and Evolution, 2015, 82, 511-517.	1.2	34
340	Cryptic diversity and biogeographical patterns within the black salamander ( <i>Aneides</i> ). <i>Journal of Biogeography</i> , 2015, 42, 1078-1091.	1.4	22
341	Weeds, as ancillary hosts, pose disproportionate risk for virulent pathogen transfer to crops. BMC Evolutionary Biology, 2016, 16, 101.	3.2	18
342	Patterns of gene flow and selection across multiple species of <i>Acrocephalus</i> warblers: footprints of parallel selection on the Z chromosome. BMC Evolutionary Biology, 2016, 16, 130.	3.2	7
343	Multi-locus sequence data illuminate demographic drivers of Pleistocene speciation in semi-arid southern Australian birds ( <i>Cinclosoma</i> spp.). BMC Evolutionary Biology, 2016, 16, 226.	3.2	13
344	Population Genetic Structure, Abundance, and Health Status of Two Dominant Benthic Species in the Saba Bank National Park, Caribbean Netherlands: <i>Montastraea cavernosa</i> and <i>Xestospongia muta</i> . PLoS ONE, 2016, 11, e0155969.	1.1	14
345	Population Structure of the Rockpool Blenny <i>Entomacrodus vomerinus</i> Shows Source-Sink Dynamics among Ecoregions in the Tropical Southwestern Atlantic. PLoS ONE, 2016, 11, e0157472.	1.1	18
346	Ancient Geographical Barriers Drive Differentiation among <i>Sonneratia caseolaris</i> Populations and Recent Divergence from <i>S. lanceolata</i> . Frontiers in Plant Science, 2016, 7, 1618.	1.7	18

#	ARTICLE	IF	CITATIONS
347	Genetic Structure and Evolutionary History of Three Alpine Sclerophyllous Oaks in East Himalaya-Hengduan Mountains and Adjacent Regions. <i>Frontiers in Plant Science</i> , 2016, 7, 1688.	1.7	32
348	Ecological divergence of two closely related <i>Roscoea</i> species associated with late Quaternary climate change. <i>Journal of Biogeography</i> , 2016, 43, 1990-2001.	1.4	48
349	The evolutionary history of <i>Biston suppressaria</i> ( <i>Guenée</i> ) ( <i>Lepidoptera: Geometridae</i> ) related to complex topography and geological history. <i>Systematic Entomology</i> , 2016, 41, 732-743.	1.7	10
350	Genetic distinction between contiguous urban and rural multimammate mice in Tanzania despite gene flow. <i>Journal of Evolutionary Biology</i> , 2016, 29, 1952-1967.	0.8	14
351	Contrasting support for alternative models of genomic variation based on microhabitat preference: species-specific effects of climate change in alpine sedges. <i>Molecular Ecology</i> , 2016, 25, 3974-3986.	2.0	55
352	The large effect in plants: increased species divergence and reduced gene flow on the <i>Silene</i> X-chromosome. <i>Molecular Ecology</i> , 2016, 25, 2609-2619.	2.0	34
353	Population differentiation in the context of Holocene climate change for a migratory marine species, the southern elephant seal. <i>Journal of Evolutionary Biology</i> , 2016, 29, 1667-1679.	0.8	19
354	Heterogeneous genome divergence, differential introgression, and the origin and structure of hybrid zones. <i>Molecular Ecology</i> , 2016, 25, 2454-2466.	2.0	183
355	Complex longitudinal diversification across South China and Vietnam in Stejneger's pit viper, <i>Viridovipera stejnegeri</i> (Schmidt, 1925) (Reptilia: Serpentes: Viperidae). <i>Molecular Ecology</i> , 2016, 25, 2920-2936.	2.0	18
356	Evolutionary melting pots: a biodiversity hotspot shaped by ring diversifications around the Black Sea in the Eastern tree frog ( <i>Hyla orientalis</i> ). <i>Molecular Ecology</i> , 2016, 25, 4285-4300.	2.0	53
357	Genetic isolation between coastal and fishery-impacted, offshore bottlenose dolphin ( <i>Tursiops</i> ) <i>Tursiops truncatus</i> <i>offshore</i> . <i>Molecular Ecology</i> , 2016, 25, 3974-3986.	2.0	36
358	Phylogeography of a semi-aquatic bug, <i>Microvelia horvathi</i> (Hemiptera: Veliidae): an evaluation of historical, geographical and ecological factors. <i>Scientific Reports</i> , 2016, 6, 21932.	1.6	25
359	Pronounced genetic differentiation and recent secondary contact in the mangrove tree <i>Lumnitzera racemosa</i> revealed by population genomic analyses. <i>Scientific Reports</i> , 2016, 6, 29486.	1.6	21
360	A new species of shrew ( <i>Soricomorpha: Crocidura</i> ) from Java, Indonesia: possible character displacement despite interspecific gene flow. <i>Journal of Mammalogy</i> , 2016, , gyw183.	0.6	6
361	Species Delimitation with Gene Flow. <i>Systematic Biology</i> , 2017, 66, syw117.	2.7	118
362	Range-wide fragmentation in a threatened fish associated with post-European settlement modification in the Murray-Darling Basin, Australia. <i>Conservation Genetics</i> , 2016, 17, 1377-1391.	0.8	29
363	Determining the extent and direction of introgression between three spruce species based on molecular markers from three genomes with different rates of gene flow. <i>Plant Systematics and Evolution</i> , 2016, 302, 691-701.	0.3	6
364	Incongruent range dynamics between co-occurring Asian temperate tree species facilitated by life history traits. <i>Ecology and Evolution</i> , 2016, 6, 2346-2358.	0.8	10



#	ARTICLE	IF	CITATIONS
365	Are we overestimating the niche? Removing marginal localities helps ecological niche models detect environmental barriers. <i>Ecology and Evolution</i> , 2016, 6, 1267-1279.	0.8	21
366	Conservation genetics of the endangered San Francisco Bay endemic salt marsh harvest mouse ( <i>Reithrodontomys raviventris</i> ). <i>Conservation Genetics</i> , 2016, 17, 1055-1066.	0.8	15
367	The dual role of Andean topography in primary divergence: functional and neutral variation among populations of the hummingbird, <i>Metallura tyrianthina</i> . <i>BMC Evolutionary Biology</i> , 2016, 16, 22.	3.2	31
368	Coalescent inferences in conservation genetics: should the exception become the rule?. <i>Biology Letters</i> , 2016, 12, 20160211.	1.0	15
369	Speciation history and species-delimitation within the Seychelles Bronze geckos, <i>Ailuronyx</i> spp.: molecular and morphological evidence. <i>Biological Journal of the Linnean Society</i> , 2016, , .	0.7	2
370	Maximum Likelihood Implementation of an Isolation-with-Migration Model for Three Species. <i>Systematic Biology</i> , 2017, 66, syw063.	2.7	45
371	Getting a grip at the edge: recolonization and introgression in eastern Pacific <i>Porites</i> corals. <i>Journal of Biogeography</i> , 2016, 43, 2147-2159.	1.4	21
372	Recent speciation and elevated Z chromosome differentiation between sexually monochromatic and dichromatic species of Australian teals. <i>Journal of Avian Biology</i> , 2016, 47, 92-102.	0.6	24
373	Posterior predictive checks of coalescent models: P2C2M, an R package. <i>Molecular Ecology Resources</i> , 2016, 16, 193-205.	2.2	21
374	Comparative Phylogeography of Two Bird Species, <i>Tachyphonus phoenicius</i> (Thraupidae) and <i>Polytmus theresiae</i> (Trochilidae), Specialized in Amazonian White-sand Vegetation. <i>Biotropica</i> , 2016, 48, 110-120.	0.8	32
375	Ecological speciation in sympatric palms: 1. Gene expression, selection and pleiotropy. <i>Journal of Evolutionary Biology</i> , 2016, 29, 1472-1487.	0.8	29
376	Genetic structure among remnant populations of a migratory passerine, the Northern Wheatear <i>Oenanthe oenanthe</i> . <i>Ibis</i> , 2016, 158, 857-867.	1.0	9
377	Phylogeography and population structure of two <i>Brachistosternus</i> species (Scorpiones: Bothriuridae) from the Chilean coastal desert - the perils of coastal living. <i>Biological Journal of the Linnean Society</i> , 2016, , .	0.7	5
378	Local endemism and within-island diversification of shrews illustrate the importance of speciation in building Sundaland mammal diversity. <i>Molecular Ecology</i> , 2016, 25, 5158-5173.	2.0	36
379	Distribution of coalescent histories under the coalescent model with gene flow. <i>Molecular Phylogenetics and Evolution</i> , 2016, 105, 177-192.	1.2	11
380	Genetic diversity and evolutionary history of the <i>Schizothorax</i> species complex in the Lancang River (upper Mekong). <i>Ecology and Evolution</i> , 2016, 6, 6023-6036.	0.8	16
381	Genetic structure in two <i>Phascolosoma</i> species in the Pacific Ocean. <i>Marine Biology Research</i> , 2016, 12, 739-747.	0.3	4
382	Phylogeographic model selection leads to insight into the evolutionary history of four-eyed frogs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8010-8017.	3.3	43



#	ARTICLE	IF	CITATIONS
383	Rapid postglacial diversification and long-term stasis within the songbird genus <i>Junco</i> : phylogeographic and phylogenomic evidence. <i>Molecular Ecology</i> , 2016, 25, 6175-6195.	2.0	47
384	Pleistocene sea level fluctuation and host plant habitat requirement influenced the historical phylogeography of the invasive species <i>Amphiareus obscuriceps</i> (Hemiptera: Anthocoridae) in its native range. <i>BMC Evolutionary Biology</i> , 2016, 16, 174.	3.2	24
385	Speciation with Gene Flow in North American <i>Myotis</i> Bats. <i>Systematic Biology</i> , 2017, 66, syw100.	2.7	50
386	The influence of locus number and information content on species delimitation: an empirical test case in an endangered Mexican salamander. <i>Molecular Ecology</i> , 2016, 25, 5959-5974.	2.0	30
387	Colonization and diversification of the <i>Euphorbia</i> species (sect. <i>Aphyllis</i> subsect. <i>Macaronesicae</i> ) on the Canary Islands. <i>Scientific Reports</i> , 2016, 6, 34454.	1.6	13
388	Contrasting global genetic patterns in two biologically similar, widespread and invasive <i>Ciona</i> species (Tunicata, Ascidiacea). <i>Scientific Reports</i> , 2016, 6, 24875.	1.6	66
389	Are microsatellite fragment lengths useful for population-level studies? The case of <i>Polygala lewtonii</i> (Polygalaceae). <i>Applications in Plant Sciences</i> , 2016, 4, 1500115.	0.8	13
390	Population subdivision of hydrothermal vent polychaete <i>Alvinella pompejana</i> across equatorial and Easter Microplate boundaries. <i>BMC Evolutionary Biology</i> , 2016, 16, 235.	3.2	17
391	Conservation of genetic uniqueness of populations may increase extinction likelihood of endangered species: the case of Australian mammals. <i>Frontiers in Zoology</i> , 2016, 13, 31.	0.9	103
392	Voyage of discovery? A comment on Koch et al. "A voyage to Terra Australis: human-mediated dispersal of cats". <i>BMC Evolutionary Biology</i> , 2016, 16, 270.	3.2	0
393	A zoogeographical boundary between the Palearctic and Sino-Japanese realms documented by consistent north/south phylogeographical divergences in three woodland birds in eastern China. <i>Journal of Biogeography</i> , 2016, 43, 2099-2112.	1.4	12
394	Connectivity in the cold: the comparative population genetics of vent-endemic fauna in the Scotia Sea, Southern Ocean. <i>Molecular Ecology</i> , 2016, 25, 1073-1088.	2.0	23
395	Lineage isolation in the face of active gene flow in the coastal plant wild radish is reinforced by differentiated vernalisation responses. <i>BMC Evolutionary Biology</i> , 2016, 16, 84.	3.2	11
396	Simulating and Summarizing Sources of Gene Tree Incongruence. <i>Genome Biology and Evolution</i> , 2016, 8, 1299-1315.	1.1	12
397	The Genomic Signature of Population Reconnection Following Isolation: From Theory to HIV. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 107-120.	0.8	17
398	Genetic discontinuities in a dominant mangrove <i>Rhizophora apiculata</i> (Rhizophoraceae) in the Indo-Malesian region. <i>Journal of Biogeography</i> , 2016, 43, 1856-1868.	1.4	28
399	Hybridization during altitudinal range shifts: nuclear introgression leads to extensive cyto-nuclear discordance in the fire salamander. <i>Molecular Ecology</i> , 2016, 25, 1551-1565.	2.0	38
400	Genetic diversity and structure of remnant <i>Magnolia stellata</i> populations affected by anthropogenic pressures and a conservation strategy for maintaining their current genetic diversity. <i>Conservation Genetics</i> , 2016, 17, 715-725.	0.8	10

#	ARTICLE	IF	CITATIONS
401	Quaternary History of an Endemic Passerine Bird on Corsica Island: Glacial Refugium and Impact of Recent Forest Regression. <i>Quaternary Research</i> , 2016, 85, 271-278.	1.0	5
402	Mechanisms of global diversification in the marine species Madeiran Storm-petrel <i>Oceanodroma castro</i> and Monteiro's Storm-petrel <i>O. monteiroi</i> : Insights from a multi-locus approach. <i>Molecular Phylogenetics and Evolution</i> , 2016, 98, 314-323.	1.2	8
403	Phylogeographic and population genetic structure of bighorn sheep ( <i>Ovis canadensis</i> ) in North American deserts. <i>Journal of Mammalogy</i> , 2016, 97, 823-838.	0.6	39
404	Survival in Glacial Refugia Versus Postglacial Dispersal in the North Atlantic: The Cases of Red Seaweeds. , 2016, , 309-330.		10
405	Historical population size of the threatened New Zealand sea lion <i>Phocarcos hookeri</i> . <i>Journal of Mammalogy</i> , 2016, 97, 436-443.	0.6	7
406	Phylogeographic surveys and apomictic genetic connectivity in the North Atlantic red seaweed <i>Mastocarpus stellatus</i> . <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 463-472.	1.2	8
407	Importance of demographic history for phylogeographic inference on the arctic alpine plant <i>Phyllodoce caerulea</i> in East Asia. <i>Heredity</i> , 2016, 116, 232-238.	1.2	6
408	Barn owls ( <i>Tyto alba</i> ) in western North America: phylogeographic structure, connectivity, and genetic diversity. <i>Conservation Genetics</i> , 2016, 17, 357-367.	0.8	9
409	Past lake shore dynamics explain present pattern of unidirectional introgression across a habitat barrier. <i>Hydrobiologia</i> , 2017, 791, 69-82.	1.0	15
410	Phylogeny and phylogeography of <i>Altolamprologus</i> : ancient introgression and recent divergence in a rock-dwelling Lake Tanganyika cichlid genus. <i>Hydrobiologia</i> , 2017, 791, 35-50.	1.0	24
411	The problem of estimating recent genetic connectivity in a changing world. <i>Conservation Biology</i> , 2017, 31, 126-135.	2.4	48
412	Morphological and molecular evolution and their consequences for conservation and taxonomy in the Le Conte's thrasher <i>Toxostoma lecontei</i> . <i>Journal of Avian Biology</i> , 2017, 48, 941-954.	0.6	11
413	Phylogeography of the sergeants <i>Abudefduf sexfasciatus</i> and <i>A. vaigiensis</i> reveals complex introgression patterns between two widespread and sympatric Indo-West Pacific reef fishes. <i>Molecular Ecology</i> , 2017, 26, 2527-2542.	2.0	17
414	Strong isolation by distance argues for separate population management of endangered blue duck ( <i>Hymenolaimus malacorhynchos</i> ). <i>Conservation Genetics</i> , 2017, 18, 327-341.	0.8	14
415	Geographic extent of introgression in <i>Sebastes mentella</i> and its effect on genetic population structure. <i>Evolutionary Applications</i> , 2017, 10, 77-90.	1.5	26
416	Effects of Pleistocene sea-level fluctuations on mangrove population dynamics: a lesson from <i>Sonneratia alba</i> . <i>BMC Evolutionary Biology</i> , 2017, 17, 22.	3.2	38
417	Inference of Gene Flow in the Process of Speciation: An Efficient Maximum-Likelihood Method for the Isolation-with-Initial-Migration Model. <i>Genetics</i> , 2017, 205, 1597-1618.	1.2	24
418	PHRAPL: Phylogeographic Inference Using Approximate Likelihoods. <i>Systematic Biology</i> , 2017, 66, 1045-1053.	2.7	59

#	ARTICLE	IF	CITATIONS
419	Bayesian Analysis of Evolutionary Divergence with Genomic Data under Diverse Demographic Models. <i>Molecular Biology and Evolution</i> , 2017, 34, 1517-1528.	3.5	14
420	Fuzzy species limits in Mediterranean gorgonians (Cnidaria, Octocorallia): inferences on speciation processes. <i>Zoologica Scripta</i> , 2017, 46, 767-778.	0.7	12
421	Integrative inference of population history in the Ibero-Maghrebian endemic <i>Pleurodeles waltl</i> (Salamandridae). <i>Molecular Phylogenetics and Evolution</i> , 2017, 112, 122-137.	1.2	38
422	Life history predicts past and present population connectivity in two sympatric sea stars. <i>Ecology and Evolution</i> , 2017, 7, 3916-3930.	0.8	17
423	Allopatric divergence and secondary contact without genetic admixture for <i>Arichanna perimelaina</i> (Lepidoptera: Geometridae), an alpine moth endemic to the Himalayas. <i>Systematic Entomology</i> , 2017, 42, 703-713.	1.7	4
424	Phylogeography and diversification of an Amazonian understory hummingbird: paraphyly and evidence for widespread cryptic speciation in the Pliocene. <i>Ibis</i> , 2017, 159, 778-791.	1.0	10
425	Phylogeography and geno-phenotypic discordance in a widespread Australian bird, the Variegated Fairy-wren, <i>Malurus lamberti</i> (Aves: Maluridae). <i>Biological Journal of the Linnean Society</i> , 2017, 121, 655-669.	0.7	13
426	Distinct patterns of natural selection in <i>NaH antiporter</i> genes in <i>Populus euphratica</i> and <i>Populus pruinosa</i> . <i>Ecology and Evolution</i> , 2017, 7, 82-91.	0.8	6
427	Perpendicular axes of differentiation generated by mitochondrial introgression. <i>Molecular Ecology</i> , 2017, 26, 3241-3255.	2.0	28
428	Shifting barriers and phenotypic diversification by hybridisation. <i>Ecology Letters</i> , 2017, 20, 651-662.	3.0	24
429	Parallel adaptive responses to abiotic but not biotic conditions after cryptic speciation in European peat moss <i>Sphagnum magellanicum</i> Brid.. <i>Perspectives in Plant Ecology, Evolution and Systematics</i> , 2017, 26, 14-27.	1.1	12
430	Mediterranean lineage endemism, cold-adapted palaeodemographic dynamics and recent changes in population size in two solitary bees of the genus <i>Anthophora</i> . <i>Conservation Genetics</i> , 2017, 18, 521-538.	0.8	10
431	IMGui—A Desktop GUI Application for Isolation with Migration Analyses. <i>Molecular Biology and Evolution</i> , 2017, 34, 500-504.	3.5	2
432	Origins of the Greenland shark ( <i>Somniosus microcephalus</i> ): Impacts of ice isolation and introgression. <i>Ecology and Evolution</i> , 2017, 7, 8113-8125.	0.8	14
433	Genetic variation and population structure of a threatened timber tree <i>Dalbergia cochinchinensis</i> in Cambodia. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	10
434	Allopatric divergence, demographic history, and conservation implications of an endangered conifer <i>Cupressus chengiana</i> in the eastern Qinghai-Tibet Plateau. <i>Tree Genetics and Genomes</i> , 2017, 13, 1.	0.6	9
435	Late Pleistocene origin of the entire circumarctic range of the arctic-alpine plant <i>Kalmia procumbens</i> . <i>Molecular Ecology</i> , 2017, 26, 5773-5783.	2.0	17
436	Invertebrate population genetics across Earth's largest habitat: The deep-sea floor. <i>Molecular Ecology</i> , 2017, 26, 4872-4896.	2.0	87

#	ARTICLE	IF	CITATIONS
437	The Time of Origin and Genetic Diversity of Three Isolated Kokanee Populations in Southwest Alaska. Transactions of the American Fisheries Society, 2017, 146, 1212-1222.	0.6	0
438	Objective choice of phylogeographic models. Molecular Phylogenetics and Evolution, 2017, 116, 136-140.	1.2	13
439	Estimating synchronous demographic changes across populations using <i>hABC</i> and its application for a herpetological community from northeastern Brazil. Molecular Ecology, 2017, 26, 4756-4771.	2.0	79
440	After 100 years: hydroelectric dam-induced life-history divergence and population genetic changes in sockeye salmon ( <i>Oncorhynchus nerka</i> ). Conservation Genetics, 2017, 18, 1449-1462.	0.8	11
441	Effective Dispersal of Caribbean Reef Fish is Smaller than Current Spacing Among Marine Protected Areas. Scientific Reports, 2017, 7, 4689.	1.6	15
442	Genetic differentiation of the <i>Schizothorax</i> species complex (Cyprinidae) in the Nujiang River (upper) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5	1.6	7
443	Wing Morphometry and Genetic Variability Between <i>Culex coronator</i> and <i>Culex usquatus</i> (Diptera:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 901-908.	0.9	7
444	Geographical features are the predominant driver of molecular diversification in widely distributed North American whipsnakes. Molecular Ecology, 2017, 26, 5729-5751.	2.0	19
445	Multilocus DNA barcoding – Species Identification with Multilocus Data. Scientific Reports, 2017, 7, 16601.	1.6	33
446	Reassessment of a possible case of intraspecific gene flow across Australia's Great Dividing Range in the variegated fairy wren, <i>Malurus lamberti</i> (Aves: Maluridae), and its systematic consequences. Biological Journal of the Linnean Society, 2017, 122, 210-223.	0.7	9
447	Cryptic <i>Sebastes norvegicus</i> species in Greenland waters revealed by microsatellites. ICES Journal of Marine Science, 2017, 74, 2148-2158.	1.2	10
448	Human-mediated secondary contact of two tortoise lineages results in sex-biased introgression. Scientific Reports, 2017, 7, 4019.	1.6	10
449	AFLP markers contribute to species delimitation and evolutionary understanding of the recent genus <i>Petunia</i> (Solanaceae). Botanical Journal of the Linnean Society, 2017, 183, 413-428.	0.8	4
450	The Structured Coalescent and Its Approximations. Molecular Biology and Evolution, 2017, 34, 2970-2981.	3.5	98
451	Importance of incomplete lineage sorting and introgression in the origin of shared genetic variation between two closely related pines with overlapping distributions. Heredity, 2017, 118, 211-220.	1.2	73
452	Understanding and monitoring the consequences of human impacts on intraspecific variation. Evolutionary Applications, 2017, 10, 121-139.	1.5	145
453	Phylogeographical insight into the Aleutian flora inferred from the historical range shifts of the alpine shrub <i>Therorhodium camtschaticum</i> (Pall.) Small (Ericaceae). Journal of Biogeography, 2017, 44, 283-293.	1.4	10
454	There is more to the picture than meets the eye: adaptation for crypsis blurs phylogeographical structure in a lizard. Journal of Biogeography, 2017, 44, 397-408.	1.4	16

#	ARTICLE	IF	CITATIONS
455	Hybrids and horizontal transfer: introgression allows adaptive allele discovery. <i>Journal of Experimental Botany</i> , 2017, 68, 5453-5470.	2.4	24
456	PhyloParser: A Hybrid Algorithm for Extracting Phylogenies from Dendrograms. , 2017, , .		2
457	Avian introgression in the genomic era. <i>Avian Research</i> , 2017, 8, .	0.5	58
458	Importance of Beringia for the divergence of two northern Pacific alpine plants, <i>Phyllodoce aleutica</i> and <i>Phyllodoce glanduliflora</i> (Ericaceae). <i>Biological Journal of the Linnean Society</i> , 2017, 122, 249-257.	0.7	2
459	Genetic Evidence for the Introduction of <i>Rhagoletis pomonella</i> (Diptera: Tephritidae) into the Northwestern United States. <i>Journal of Economic Entomology</i> , 2017, 110, 2599-2608.	0.8	9
460	Baltic Sea genetic biodiversity: Current knowledge relating to conservation management. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2017, 27, 1069-1090.	0.9	29
461	Phylogeographic structure, cryptic speciation and demographic history of the sharpbelly (Hemiculter) <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf</i> 17, 216.	3.2	45
462	Mechanisms of peripheral phylogeographic divergence in the indo-Pacific: lessons from the spiny lobster <i>Panulirus homarus</i> . <i>BMC Evolutionary Biology</i> , 2017, 17, 195.	3.2	17
463	What happened in the South American Gran Chaco? Diversification of the endemic frog genus <i>Lepidobatrachus</i> Budgett, 1899 (Anura: Ceratophryidae). <i>Molecular Phylogenetics and Evolution</i> , 2018, 123, 123-136.	1.2	13
464	The Biogeography of Deep Time Phylogenetic Reticulation. <i>Systematic Biology</i> , 2018, 67, 743-755.	2.7	61
465	Post-glacial East Asian origin of the alpine shrub <i>Phyllodoce aleutica</i> (Ericaceae) in Beringia. <i>Journal of Biogeography</i> , 2018, 45, 1261-1274.	1.4	13
466	Pervasive migration across rainforest and sandy coastal plain <i>Aechmea nudicaulis</i> (Bromeliaceae) populations despite contrasting environmental conditions. <i>Molecular Ecology</i> , 2018, 27, 1261-1272.	2.0	8
467	Relative contributions of neutral and non-neutral processes to clinal variation in calyx lobe length in the series <i>Sakawanum</i> (Asarum: Aristolochiaceae). <i>Annals of Botany</i> , 2018, 121, 37-46.	1.4	4
468	Combining allele frequency and tree-based approaches improves phylogeographic inference from natural history collections. <i>Molecular Ecology</i> , 2018, 27, 1012-1024.	2.0	9
469	Biogeography and diversification of <i>Rhegmatorhina</i> (Aves: Thamnophilidae): Implications for the evolution of Amazonian landscapes during the Quaternary. <i>Journal of Biogeography</i> , 2018, 45, 917-928.	1.4	40
470	Bayesian Inference of Species Networks from Multilocus Sequence Data. <i>Molecular Biology and Evolution</i> , 2018, 35, 504-517.	3.5	158
471	Genetic connectivity from the Arctic to the Antarctic: <i>Sclerolimum contortum</i> and <i>Nicomache lokii</i> (Annelida) are both widespread in reducing environments. <i>Scientific Reports</i> , 2018, 8, 4810.	1.6	33
472	Evidence for late Pleistocene origin of <i>Astyanax mexicanus</i> cavefish. <i>BMC Evolutionary Biology</i> , 2018, 18, 43.	3.2	117

#	ARTICLE	IF	CITATIONS
473	Rapid sexual and genomic isolation in sympatric <i>Drosophila</i> without reproductive character displacement. <i>Ecology and Evolution</i> , 2018, 8, 2852-2867.	0.8	5
474	Strong population structure but no equilibrium yet: Genetic connectivity and phylogeography in the kelp <i>Saccharina latissima</i> (Laminariales, Phaeophyta). <i>Ecology and Evolution</i> , 2018, 8, 4265-4277.	0.8	17
475	Pliocene–Pleistocene ecological niche evolution shapes the phylogeography of a Mediterranean plant group. <i>Molecular Ecology</i> , 2018, 27, 1696-1713.	2.0	25
476	Phylogenomic evidence for a recent and rapid radiation of lizards in the Patagonian <i>Liolaemus fitzingerii</i> species group. <i>Molecular Phylogenetics and Evolution</i> , 2018, 125, 243-254.	1.2	25
477	The Effect of Gene Flow on Coalescent-based Species-Tree Inference. <i>Systematic Biology</i> , 2018, 67, 770-785.	2.7	83
478	Detecting hybridization by likelihood calculation of gene tree extra lineages given explicit models. <i>Methods in Ecology and Evolution</i> , 2018, 9, 121-133.	2.2	8
479	Genetic divergence between colonies of Flesh-footed Shearwater <i>Ardenna carneipes</i> exhibiting different foraging strategies. <i>Conservation Genetics</i> , 2018, 19, 27-41.	0.8	11
480	Poor genetic differentiation but clear cytoform divergence among cryptic species in <i>Simulium damnosum</i> complex (scpd: Simuliidae). <i>Systematic Entomology</i> , 2018, 43, 123-135.	1.7	3
481	Significant genetic differentiation of <i>Gobiopterus lacustris</i> , a newly recorded transparent goby in China. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2018, 29, 785-791.	0.7	8
482	Coalescent-Based Analyses of Genomic Sequence Data Provide a Robust Resolution of Phylogenetic Relationships among Major Groups of Gibbons. <i>Molecular Biology and Evolution</i> , 2018, 35, 159-179.	3.5	69
483	Resolving taxonomic turbulence and uncovering cryptic diversity in the musk turtles ( <i>Sternotherus</i> ) using robust demographic modeling. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 1-15.	1.2	23
484	Phylogeography of southern brown and golden bandicoots: implications for the taxonomy and distribution of endangered subspecies and species. <i>Australian Journal of Zoology</i> , 2018, 66, 379.	0.6	12
485	Asymmetric hybridization in <i>Cordulegaster</i> (Odonata: Cordulegastridae): Secondary postglacial contact and the possible role of mechanical constraints. <i>Ecology and Evolution</i> , 2018, 8, 9657-9671.	0.8	18
486	Evolutionary insights from comparative transcriptome and transcriptome-wide coalescence analyses in <i>Tetrastigma hemsleyanum</i> . <i>BMC Plant Biology</i> , 2018, 18, 208.	1.6	11
487	Effects of Geological and Environmental Events on the Diversity and Genetic Divergence of Four Closely Related Pines: <i>Pinus koraiensis</i> , <i>P. armandii</i> , <i>P. griffithii</i> , and <i>P. pumila</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1264.	1.7	8
488	Use of rapidly evolving molecular markers to distinguish species and clarify range uncertainties in the spearfishes (Istiophoridae, Tetrapturus). <i>Bulletin of Marine Science</i> , 2018, 94, 1355-1378.	0.4	2
489	Evidence for Introgression Among Three Species of the <i>Anastrepha fraterculus</i> Group, a Radiating Species Complex of Fruit Flies. <i>Frontiers in Genetics</i> , 2018, 9, 359.	1.1	15
490	Evolutionary melting pots and reproductive isolation: A ring-shaped diversification of an odorous frog ( <i>Odorrana margaratea</i> ) around the Sichuan Basin. <i>Molecular Ecology</i> , 2018, 27, 4888-4900.	2.0	17



#	ARTICLE	IF	CITATIONS
491	Genetic evidence indicates ecological divergence rather than geographic barriers structure Florida fox squirrels. <i>Journal of Mammalogy</i> , 2018, , .	0.6	1
492	Genetic structure of the grey side-gilled sea slug ( <i>Pleurobranchaea maculata</i> ) in coastal waters of New Zealand. <i>PLoS ONE</i> , 2018, 13, e0202197.	1.1	7
493	Genetic analysis of European red foxes reveals multiple distinct peripheral populations and central continental admixture. <i>Quaternary Science Reviews</i> , 2018, 197, 257-266.	1.4	11
494	Distinguishing Between Convergent Evolution and Violation of the Molecular Clock for Three Taxa. <i>Systematic Biology</i> , 2018, 67, 905-915.	2.7	3
495	Repeated Selection of Alternatively Adapted Haplotypes Creates Sweeping Genomic Remodeling in Stickleback. <i>Genetics</i> , 2018, 209, 921-939.	1.2	64
496	Divergence Estimation in the Presence of Incomplete Lineage Sorting and Migration. <i>Systematic Biology</i> , 2019, 68, 19-31.	2.7	26
497	Interspecific Divergence of Two <i>Sinallaria</i> (Brassicaceae) Species in Eastern China. <i>Frontiers in Plant Science</i> , 2018, 9, 77.	1.7	3
498	Assessing population structure in the face of isolation by distance: Are we neglecting the problem?. <i>Diversity and Distributions</i> , 2018, 24, 1883-1889.	1.9	93
499	Phylogeography of the Japanese ratsnake, <i>Elaphe climacophora</i> (Serpentes: Colubridae): impacts of Pleistocene climatic oscillations and sea-level fluctuations on geographical range. <i>Biological Journal of the Linnean Society</i> , 2018, 124, 174-187.	0.7	3
500	Phylogeny Estimation by Integration over Isolation with Migration Models. <i>Molecular Biology and Evolution</i> , 2018, 35, 2805-2818.	3.5	89
501	Demographic and genetic approaches to study dispersal in wild animal populations: A methodological review. <i>Molecular Ecology</i> , 2018, 27, 3976-4010.	2.0	113
502	Neutral and functionally important genes shed light on phylogeography and the history of high-altitude colonization in a widespread New World duck. <i>Ecology and Evolution</i> , 2018, 8, 6515-6528.	0.8	3
503	Demographic expansion and genetic load of the halophyte model plant <i>Eutrema salsugineum</i> . <i>Molecular Ecology</i> , 2018, 27, 2943-2955.	2.0	11
505	Mitochondrial Divergence between Western and Eastern Great Bustards: Implications for Conservation and Species Status. <i>Journal of Heredity</i> , 2018, 109, 641-652.	1.0	5
506	The Spectre of Too Many Species. <i>Systematic Biology</i> , 2019, 68, 168-181.	2.7	189
507	Old divergence and restricted gene flow between torrent duck ( <i>Merganetta armata</i> ) subspecies in the Central and Southern Andes. <i>Ecology and Evolution</i> , 2019, 9, 9961-9976.	0.8	1
508	Distinctiveness, speciation and demographic history of the rare endemic conifer <i>Juniperus erectopatens</i> in the eastern Qinghai-Tibet Plateau. <i>Conservation Genetics</i> , 2019, 20, 1289-1301.	0.8	8
509	Deep south-north genetic divergence in Godlewski's bunting ( <i>Emberiza godlewskii</i> ) related to uplift of the Qinghai-Tibet Plateau and habitat preferences. <i>BMC Evolutionary Biology</i> , 2019, 19, 161.	3.2	22



#	ARTICLE	IF	CITATIONS
510	Ancestral Population Genomics. <i>Methods in Molecular Biology</i> , 2019, 1910, 555-589.	0.4	2
511	Population analysis reveals genetic structure of an invasive agricultural thrips pest related to invasion of greenhouses and suitable climatic space. <i>Evolutionary Applications</i> , 2019, 12, 1868-1880.	1.5	21
512	Population Structure of <i>Colletotrichum tanacetii</i> in Australian <i>Pyrethrum</i> Reveals High Evolutionary Potential. <i>Phytopathology</i> , 2019, 109, 1779-1792.	1.1	5
513	Amplicon sequencing of 42 nuclear loci supports directional gene flow between South Pacific populations of a hydrothermal vent limpet. <i>Ecology and Evolution</i> , 2019, 9, 6568-6580.	0.8	8
514	Genetic, phenotypic and ecological differentiation suggests incipient speciation in two <i>Charadrius</i> plovers along the Chinese coast. <i>BMC Evolutionary Biology</i> , 2019, 19, 135.	3.2	30
515	Geographic and Ecological Dimensions of Host Plant-Associated Genetic Differentiation and Speciation in the <i>Rhagoletis cingulata</i> (Diptera: Tephritidae) Sibling Species Group. <i>Insects</i> , 2019, 10, 275.	1.0	12
516	Evolutionary networks from RAD seq loci point to hybrid origins of <i>Medicago carstiensis</i> and <i>Medicago cretacea</i> . <i>American Journal of Botany</i> , 2019, 106, 1219-1228.	0.8	3
517	Silicon-based light absorbers with unique polarization-adjusting effects. <i>Journal Physics D: Applied Physics</i> , 2019, 52, 505109.	1.3	7
518	Host hybridization as a potential mechanism of lateral symbiont transfer in deep-sea vesicomyid clams. <i>Molecular Ecology</i> , 2019, 28, 4697-4708.	2.0	14
519	Comparison of Markov Chain Monte Carlo Software for the Evolutionary Analysis of Y-Chromosomal Microsatellite Data. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 1082-1090.	1.9	1
520	An integrative taxonomic and phylogenetic approach reveals a complex of cryptic species in the "peppermint" shrimp <i>Lysmata wurdemanni sensu stricto</i> . <i>Zoological Journal of the Linnean Society</i> , 2019, 185, 1018-1038.	1.0	7
522	Rapid plant speciation associated with the last glacial period: reproductive isolation and genetic drift in sedges. <i>Botanical Journal of the Linnean Society</i> , 2019, 190, 303-314.	0.8	7
523	New Insight into the Evolution of Symbiotic Genes in Black Locust-Associated Rhizobia. <i>Genome Biology and Evolution</i> , 2019, 11, 1736-1750.	1.1	9
524	Historical demography of the Caribbean spiny lobster <i>Panulirus argus</i> (Latreille, 1804) (Decapoda: Tj ETQq1 1 0.784314 rgBT /Overlook <i>Journal of Crustacean Biology</i> , 2019, 39, 378-385.	0.3	8
525	Multispecies hybridization in birds. <i>Avian Research</i> , 2019, 10, .	0.5	27
526	Historical climate changes and hybridization shaped the evolution of Atlantic Forest spinetails (Aves: Tj ETQq1 1 0.784314 rgBT /Overlook <i>Journal of Crustacean Biology</i> , 2019, 39, 378-385.	1.2	42
527	The evolutionary history of the Cape hare ( <i>Lepus capensis sensu lato</i> ): insights for systematics and biogeography. <i>Heredity</i> , 2019, 123, 634-646.	1.2	12
528	Phylogeography of the Neotropical epiphytic orchid, <i>Brassavola nodosa</i> : evidence for a secondary contact zone in northwestern Costa Rica. <i>Heredity</i> , 2019, 123, 662-674.	1.2	4

#	ARTICLE	IF	CITATIONS
529	Advances in Computational Methods for Phylogenetic Networks in the Presence of Hybridization. <i>Computational Biology</i> , 2019, , 317-360.	0.1	55
530	Pleistocene-dated biogeographic barriers drove divergence within the Australo-Papuan region in a sex-specific manner: an example in a widespread Australian songbird. <i>Heredity</i> , 2019, 123, 608-621.	1.2	13
531	More grist for the mill? Species delimitation in the genomic era and its implications for conservation. <i>Conservation Genetics</i> , 2019, 20, 101-113.	0.8	73
533	Dark offshoot: Phylogenomic data sheds light on the evolutionary history of a new species of cave brittle star. <i>Molecular Phylogenetics and Evolution</i> , 2019, 136, 151-163.	1.2	4
534	Historical Population Size Change and Differentiation of Relict Populations of the Endangered Giant Kangaroo Rat. <i>Journal of Heredity</i> , 2019, 110, 548-558.	1.0	9
535	Complex population evolutionary history of four cold-tolerant <i>Notopterygium</i> herb species in the Qinghai-Tibetan Plateau and adjacent areas. <i>Heredity</i> , 2019, 123, 242-263.	1.2	14
536	Phase-type distributions in population genetics. <i>Theoretical Population Biology</i> , 2019, 127, 16-32.	0.5	33
537	Delineating management units for Pacific cod ( <i>Gadus macrocephalus</i> ) in the Sea of Japan. <i>Estuarine, Coastal and Shelf Science</i> , 2019, 229, 106401.	0.9	7
538	Multilocus phylogeography of the brown-spotted pitviper <i>Protobothrops mucrosquamatus</i> (Reptilia: Tj ETQq0 0 0 rgBT /Overlock 10 Tf and Evolution, 2019, 133, 82-91.	1.2	19
539	Low genetic differentiation between two morphologically and ecologically distinct giant-leaved Mexican oaks. <i>Plant Systematics and Evolution</i> , 2019, 305, 89-101.	0.3	16
540	Implications of introgression for wildlife translocations: the case of North American martens. <i>Conservation Genetics</i> , 2019, 20, 153-166.	0.8	16
541	Human Population History Over the Last Two Million Years. , 2019, , 195-236.		0
542	Extending phylogeography to account for lineage fusion. <i>Journal of Biogeography</i> , 2019, 46, 268-278.	1.4	23
543	The Unreasonable Effectiveness of Convolutional Neural Networks in Population Genetic Inference. <i>Molecular Biology and Evolution</i> , 2019, 36, 220-238.	3.5	151
544	Evolutionary and demographic correlates of Pleistocene coastline changes in the Sicilian wall lizard <i>Podarcis wagleriana</i> . <i>Journal of Biogeography</i> , 2019, 46, 224-237.	1.4	18
545	Inferring introgression using RADseq and <i>D<sub>FOIL</sub></i> : Power and pitfalls revealed in a case study of spiny lizards ( <i>Sceloporus</i> ). <i>Molecular Ecology Resources</i> , 2019, 19, 818-837.	2.2	23
546	Phenotypic and life-history diversification in Amazonian frogs despite past introgressions. <i>Molecular Phylogenetics and Evolution</i> , 2019, 130, 169-180.	1.2	9
547	Divergence and hybridization in the desert plant <i>Reaumuria soongarica</i> . <i>Journal of Systematics and Evolution</i> , 2020, 58, 159-173.	1.6	5

#	ARTICLE	IF	CITATIONS
548	Navigating the southern seas with small fins: Genetic connectivity of seahorses ( <i>Hippocampus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 74	1.4	6
549	Secondary contact after allopatric divergence explains avian speciation and high species diversity in the Himalayan-Hengduan Mountains. <i>Molecular Phylogenetics and Evolution</i> , 2020, 143, 106671.	1.2	14
550	The roles of vicariance and dispersal in the differentiation of two species of the <i>Rhinella marina</i> species complex. <i>Molecular Phylogenetics and Evolution</i> , 2020, 145, 106723.	1.2	12
551	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
552	Founder effects and species introductions: A host versus parasite perspective. <i>Evolutionary Applications</i> , 2020, 13, 559-574.	1.5	13
553	Phylogeography, speciation and demographic history: Contrasting evidence from mitochondrial and nuclear markers of the <i>Odorrana graminea</i> sensu lato (Anura, Ranidae) in China. <i>Molecular Phylogenetics and Evolution</i> , 2020, 144, 106701.	1.2	14
554	Evolutionary history of a relict conifer, <i>Pseudotaxus chienii</i> (Taxaceae), in south-east China during the late Neogene: old lineage, young populations. <i>Annals of Botany</i> , 2020, 125, 105-117.	1.4	27
555	The ghost of connections past: A role for mainland vicariance in the isolation of an insular population of the red-billed chough ( <i>Aves: Corvidae</i> ). <i>Journal of Biogeography</i> , 2020, 47, 2567-2583.	1.4	4
557	Insights from Population Genomics to Enhance and Sustain Biological Control of Insect Pests. <i>Insects</i> , 2020, 11, 462.	1.0	19
558	Regional drivers of diversification in the late Quaternary in a widely distributed generalist species, the common pheasant <i>Phasianus colchicus</i> . <i>Journal of Biogeography</i> , 2020, 47, 2714-2727.	1.4	10
559	The roles of vicariance and isolation by distance in shaping biotic diversification across an ancient archipelago: evidence from a Seychelles caecilian amphibian. <i>BMC Evolutionary Biology</i> , 2020, 20, 110.	3.2	3
560	Phylogeographic structure and population connectivity of a small benthic fish ( <i>Tripterygion</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 74	1.4	7
561	Evolutionary history of endangered and relict tree species <i>Dipteronia sinensis</i> in response to geological and climatic events in the Qinling Mountains and adjacent areas. <i>Ecology and Evolution</i> , 2020, 10, 14052-14066.	0.8	6
562	Phylogenetic tree building in the genomic age. <i>Nature Reviews Genetics</i> , 2020, 21, 428-444.	7.7	226
563	Large-Scale Hybridisation as an Extinction Threat to the Suweon Treefrog ( <i>Hylidae: Dryophytes</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 74	1.0	8
564	Phylogeny of <i>Pseudocercospora griseola</i> from Puerto Rico, Central America and Tanzania confirms the existence of an Afro-Andean clade. <i>European Journal of Plant Pathology</i> , 2020, 157, 533-547.	0.8	6
565	Deep phylogeographic structure may indicate cryptic species within the Sparid genus <i>Spondyliosoma</i> . <i>Journal of Fish Biology</i> , 2020, 96, 1434-1443.	0.7	3
566	Limited Genetic Connectivity Among <i>Sargassum horneri</i> (Phaeophyceae) Populations in the Chinese Marginal Seas Despite Their high Dispersal Capacity. <i>Journal of Phycology</i> , 2020, 56, 994-1005.	1.0	15

#	ARTICLE	IF	CITATIONS
567	New insights about species delimitation in red snappers ( <i>Lutjanus purpureus</i> and <i>L. campechanus</i> ) using multilocus data. <i>Molecular Phylogenetics and Evolution</i> , 2020, 147, 106780.	1.2	10
568	Morphological and molecular evidence supports the first occurrence of two fishes, <i>Siganus sutor</i> (Valenciennes, 1835) and <i>Seriolina nigrofasciata</i> (Rä¼ppell, 1829) (Actinopterygii: Perciformes), from marine waters of Odisha coast, Bay of Bengal, India. <i>Acta Oceanologica Sinica</i> , 2020, 39, 26-35.	0.4	1
569	A Simulation Study to Examine the Information Content in Phylogenomic Data Sets under the Multispecies Coalescent Model. <i>Molecular Biology and Evolution</i> , 2020, 37, 3211-3224.	3.5	20
570	Genetic variation in morphologically divergent mainland and island populations of Soemmerring's gazelles ( <i>Nanger soemmerringii</i> ). <i>Mammal Research</i> , 2020, 65, 403-412.	0.6	2
571	Phylogeographic history of flat periwinkles, <i>Littorina fabalis</i> and <i>L. obtusata</i> . <i>BMC Evolutionary Biology</i> , 2020, 20, 23.	3.2	16
572	Phylogeographic analyses of a migratory freshwater fish ( <i>Megalobrama terminalis</i> ) reveal a shallow genetic structure and pronounced effects of sea-level changes. <i>Gene</i> , 2020, 737, 144478.	1.0	19
573	Genetic analysis provides insights into species distribution and population structure in East Atlantic horse mackerel ( <i>Trachurus trachurus</i> and <i>T. capensis</i> ). <i>Journal of Fish Biology</i> , 2020, 96, 795-805.	0.7	8
574	Complex mosaic of sexual dichromatism and monochromatism in Pacific robins results from both gains and losses of elaborate coloration. <i>Journal of Avian Biology</i> , 2020, 51, .	0.6	6
575	Evolutionary history of two cryptic species of northern African jerboas. <i>BMC Evolutionary Biology</i> , 2020, 20, 26.	3.2	16
576	Genome-wide SNPs resolve spatiotemporal patterns of connectivity within striped marlin ( <i>Kajikia</i> ) Tj ETQq1 1 0.784314 rgBT /Overl 13, 677-698.	1.5	23
577	The Impact of Cross-Species Gene Flow on Species Tree Estimation. <i>Systematic Biology</i> , 2020, 69, 830-847.	2.7	37
578	Phylogeography of the Volcano Rabbit ( <i>Romerolagus diazi</i> ): the Evolutionary History of a Mountain Specialist Molded by the Climatic-Volcanism Interaction in the Central Mexican Highlands. <i>Journal of Mammalian Evolution</i> , 2020, 27, 745-757.	1.0	9
579	Speciation and gene flow in two sympatric small mammals from Madagascar, <i>Microgale fotsifotsy</i> and <i>M. Asoricoides</i> (Mammalia: Tenrecidae). <i>Molecular Ecology</i> , 2020, 29, 1717-1729.	2.0	2
580	Defining Species When There is Gene Flow. <i>Systematic Biology</i> , 2021, 70, 108-119.	2.7	29
581	Phylogeographical history of the Olive Woodpecker <i>Dendropicos griseocephalus</i> , a species widely distributed across Africa. <i>Ibis</i> , 2021, 163, 417-428.	1.0	2
582	Dsuite's Fast D-statistics and related admixture evidence from VCF files. <i>Molecular Ecology Resources</i> , 2021, 21, 584-595.	2.2	356
583	Multiple species delimitation approaches applied to the avian lark genus <i>Alaudala</i> . <i>Molecular Phylogenetics and Evolution</i> , 2021, 154, 106994.	1.2	14
584	Conservation Genetics of New World Crocodylians. , 2021, , .		4

#	ARTICLE	IF	CITATIONS
585	Phylogeography of a widespread Palearctic forest bird species: The White-backed Woodpecker (Aves.) <i>Tj ETQq0.0.0 rgBT /0</i> <i>Overlock 1</i>	0.7	0
586	Molecular systematics and phylogeography of a widespread Neotropical avian lineage: evidence for cryptic speciation with protracted gene flow throughout the Late Quaternary. <i>Biological Journal of the Linnean Society</i> , 2021, 132, 431-450.	0.7	5
587	Isolation by environment and recurrent gene flow shaped the evolutionary history of a continentally distributed Neotropical treefrog. <i>Journal of Biogeography</i> , 2021, 48, 760-772.	1.4	18
588	Resolving spatial complexities of hybridization in the context of the gray zone of speciation in North American ratsnakes ( <i>Pantherophis obsoletus</i> complex). <i>Evolution; International Journal of Organic Evolution</i> , 2021, 75, 260-277.	1.1	32
589	Coalescent Models. , 2021, , 3-30.		0
590	Conservation priorities in an endangered estuarine seahorse are informed by demographic history. <i>Scientific Reports</i> , 2021, 11, 4205.	1.6	1
592	Evaluating the genetic diversity in two tropical leguminous trees, <i>Dalbergia cochinchinensis</i> and <i>D. nigrescens</i> , in lowland forests in Cambodia and Thailand using MIG-seq. <i>Genes and Genetic Systems</i> , 2021, 96, 41-53.	0.2	1
593	Genome-wide DNA and phenotypic information supports recent colonization of South American grasslands by <i>Correndera Pipit</i> (Aves, Motacillidae). <i>Zoologica Scripta</i> , 2021, 50, 397-410.	0.7	1
594	Spatio-temporal variation in environmental features predicts the distribution and abundance of <i>Ixodes scapularis</i> . <i>International Journal for Parasitology</i> , 2021, 51, 311-320.	1.3	17
595	A multi-locus approach to discern conservation units and adaptive potential of Pacific Black Ducks across Australia and surrounding islands. <i>Emu</i> , 2021, 121, 124-135.	0.2	3
596	Phylogeography and diversification of the Dead Sea Sparrow ( <i>Passer moabiticus</i> ) in Iran: insights from a multilocus approach. <i>Ibis</i> , 2021, 163, 1355-1368.	1.0	0
597	Genome-scale data resolves the timing of divergence in Joshua trees. <i>American Journal of Botany</i> , 2021, 108, 647-663.	0.8	9
598	Ring distribution patterns—diversification or speciation? Comparative phylogeography of two small mammals in the mountains surrounding the Sichuan Basin. <i>Molecular Ecology</i> , 2021, 30, 2641-2658.	2.0	11
599	Hierarchical genetic structure in an evolving species complex: Insights from genome wide ddRAD data in <i>Sebastes mentella</i> . <i>PLoS ONE</i> , 2021, 16, e0251976.	1.1	5
600	Evidence for two types of <i>Aquilegia ecalcarata</i> and its implications for adaptation to new environments. <i>Plant Diversity</i> , 2021, 44, 153-162.	1.8	1
601	Different population size change and migration histories created genetic diversity of three oaks in Tokai region, central Japan. <i>Journal of Plant Research</i> , 2021, 134, 933-946.	1.2	5
602	Evolutionary history of <i>Hemerocallis</i> in Japan inferred from chloroplast and nuclear phylogenies and levels of interspecific gene flow. <i>Molecular Phylogenetics and Evolution</i> , 2021, 164, 107264.	1.2	14
603	Contrasting Phylogeographic Patterns Among Northern and Southern Hemisphere Fin Whale Populations With New Data From the Southern Pacific. <i>Frontiers in Marine Science</i> , 2021, 8, .	1.2	9

#	ARTICLE	IF	CITATIONS
604	Multispecies coalescent and its applications to infer species phylogenies and cross-species gene flow. National Science Review, 2021, 8, nwab127.	4.6	36
605	Fossil-calibrated time tree of Podarcis wall lizards provides limited support for biogeographic calibration models. Molecular Phylogenetics and Evolution, 2021, 161, 107169.	1.2	15
606	Estimating hybridization as a consequence of climatic fluctuations: A case study of two geometridae species. Molecular Phylogenetics and Evolution, 2021, 161, 107168.	1.2	2
607	Inference of gene flow in the process of speciation: Efficient maximum-likelihood implementation of a generalised isolation-with-migration model. Theoretical Population Biology, 2021, 140, 1-15.	0.5	3
608	Dynamic genetic diversity and population structure of Coreius guichenoti. ZooKeys, 2021, 1055, 135-148.	0.5	2
609	A brief history and popularity of methods and tools used to estimate microevolutionary forces. Ecology and Evolution, 2021, 11, 13723-13743.	0.8	1
610	Contemporary Philosophy and Methods for Studying Speciation and Delimiting Species. Ichthyology and Herpetology, 2021, 109, .	0.3	23
611	Phylogeography of the Rough Greensnake, <i>Opheodrys aestivus</i> (Squamata: Colubridae), Using Multilocus Sanger Sequence and Genomic ddRADseq Data. Journal of Herpetology, 2021, 55, .	0.2	0
612	Prevalence and Adaptive Impact of Introgression. Annual Review of Genetics, 2021, 55, 265-283.	3.2	99
613	The Phylogeographic Shortfall in Hexapods: A Lot of Leg Work Remaining. Insect Systematics and Diversity, 2021, 5, .	0.7	6
615	Coat Color is not an Indicator of Subspecies Identity in Colombian Woolly Monkeys. , 2014, , 17-31.		2
619	Primate census and survey techniques. , 2013, , 10-26.		21
620	Darting, anesthesia, and handling. , 2013, , 27-39.		8
621	Health assessment and epidemiology. , 2013, , 40-57.		5
622	Behavior within groups. , 2013, , 58-78.		2
623	Habitat assessment and species niche modeling. , 2013, , 79-102.		8
624	Characterization of primate environments through assessment of plant phenology. , 2013, , 103-127.		11
625	Methods in ethnoprimateology: exploring the human–non-human primate interface. , 2013, , 128-150.		73

#	ARTICLE	IF	CITATIONS
626	Social and spatial relationships between primate groups. , 2013, , 151-176.		13
627	Experiments in primatology: from the lab to the field and back again. , 2013, , 177-194.		8
628	Diet and nutrition. , 2013, , 195-212.		3
629	Physiology and energetics. , 2013, , 213-223.		1
630	Primate behavioral endocrinology. , 2013, , 224-237.		3
631	Captive breeding and ex situ conservation. , 2013, , 294-322.		1
632	Primates in trade. , 2013, , 323-345.		46
633	The Multispecies Coalescent Model Outperforms Concatenation Across Diverse Phylogenomic Data Sets. <i>Systematic Biology</i> , 2020, 69, 795-812.	2.7	47
649	The Evolutionary History of the <i>Arabidopsis arenosa</i> Complex: Diverse Tetraploids Mask the Western Carpathian Center of Species and Genetic Diversity. <i>PLoS ONE</i> , 2012, 7, e42691.	1.1	56
650	lociNGS: A Lightweight Alternative for Assessing Suitability of Next-Generation Loci for Evolutionary Analysis. <i>PLoS ONE</i> , 2012, 7, e46847.	1.1	6
651	Evolutionary History of the Plant Pathogenic Bacterium <i>Xanthomonas axonopodis</i> . <i>PLoS ONE</i> , 2013, 8, e58474.	1.1	71
652	Distinguishing between Incomplete Lineage Sorting and Genomic Introgressions: Complete Fixation of Allopecific Mitochondrial DNA in a Sexually Reproducing Fish (Cobitids; Teleostei), despite Clonal Reproduction of Hybrids. <i>PLoS ONE</i> , 2014, 9, e80641.	1.1	54
653	Strong Phylogeographic Structure in a Millipede Indicates Pleistocene Vicariance between Populations on Banded Iron Formations in Semi-Arid Australia. <i>PLoS ONE</i> , 2014, 9, e93038.	1.1	10
654	Evolutionary History of the Live-Bearing Endemic <i>Allotoca diazi</i> Species Complex (Actinopterygii). <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i> e0124138.	1.1	15
655	gPGA: GPU Accelerated Population Genetics Analyses. <i>PLoS ONE</i> , 2015, 10, e0135028.	1.1	5
656	Phylogeography of <i>Partamona rustica</i> (Hymenoptera, Apidae), an Endemic Stingless Bee from the Neotropical Dry Forest Diagonal. <i>PLoS ONE</i> , 2016, 11, e0164441.	1.1	22
657	Genetic Diversity and Structure Analysis of <i>Percocypris pingi</i> (Cypriniformes: Cyprinidae): Implications for Conservation and Hatchery Release in the Yalong River. <i>PLoS ONE</i> , 2016, 11, e0166769.	1.1	14
658	Cryptic genetic diversity in the mottled rabbitfish <i>Siganus fuscescens</i> with mitochondrial introgression at a contact zone in the South China Sea. <i>PLoS ONE</i> , 2018, 13, e0193220.	1.1	11



#	ARTICLE	IF	CITATIONS
660	Wetlands, Evolution, and Conservation of the Pine Barrens Treefrog ( <i>Hyla andersonii</i> ). <i>Journal of Herpetology</i> , 2020, 54, 206.	0.2	2
661	Intraspecific Divergence Associated with a Biogeographic Barrier and Climatic Models Show Future Threats and Long-Term Decline of a Rainforest Conifer. <i>The Open Conservation Biology Journal</i> , 2013, 7, 1-10.	1.0	6
662	Isolation by distance and low connectivity in the peppery furrow shell <i>Scrobicularia plana</i> (Bivalvia). <i>Marine Ecology - Progress Series</i> , 2012, 462, 111-124.	0.9	11
663	Dispersal barriers and stochastic reproductive success do not explain small-scale genetic structure in a broadcast spawning marine mussel. <i>Marine Ecology - Progress Series</i> , 2013, 482, 133-140.	0.9	3
664	Passive dispersal against an ocean current. <i>Marine Ecology - Progress Series</i> , 2015, 539, 153-163.	0.9	17
665	Chaotic genetic patchiness without sweepstakes reproduction in the shore crab <i>Hemigrapsus oregonensis</i> . <i>Marine Ecology - Progress Series</i> , 2016, 548, 139-152.	0.9	11
666	Mitochondrial DNA sequence data reveal the origins of postglacial marine macroalgal flora in the Northwest Atlantic. <i>Marine Ecology - Progress Series</i> , 2018, 589, 45-58.	0.9	23
667	Reproductive isolation and morphological divergence between cryptic lineages of the copepod <i>Acartia tonsa</i> in Chesapeake Bay. <i>Marine Ecology - Progress Series</i> , 2018, 597, 99-113.	0.9	17
668	Population genetics and biophysical modeling inform metapopulation connectivity of the Caribbean king crab <i>Maguimithrax spinosissimus</i> . <i>Marine Ecology - Progress Series</i> , 2019, 610, 83-97.	0.9	16
669	Mind the gaps: investigating the cause of the current range disjunction in the Cape Platanna, <i>Xenopus gilli</i> (Anura: Pipidae). <i>PeerJ</i> , 2013, 1, e166.	0.9	13
670	Reconstructing the demographic history of divergence between European river and brook lampreys using approximate Bayesian computations. <i>PeerJ</i> , 2016, 4, e1910.	0.9	25
671	A potential third Manta Ray species near the Yucatán Peninsula? Evidence for a recently diverged and novel genetic <i>Manta</i> group from the Gulf of Mexico. <i>PeerJ</i> , 2016, 4, e2586.	0.9	32
672	Rape and the prevalence of hybrids in broadly sympatric species: a case study using albatrosses. <i>PeerJ</i> , 2014, 2, e409.	0.9	8
673	Embracing heterogeneity: coalescing the Tree of Life and the future of phylogenomics. <i>PeerJ</i> , 2019, 7, e6399.	0.9	111
674	Genetic approaches to the conservation of migratory bats: a study of the eastern red bat ( <i>Lasiurus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.9	13
675	Genetic differentiation and gene flow of the Amazonian catfish <i>Pseudoplatystoma punctifer</i> across the Madeira River rapids prior to the construction of hydroelectric dams. <i>Hydrobiologia</i> , 2022, 849, 29-46.	1.0	2
676	Rapid evolution of post-zygotic reproductive isolation is widespread in Arctic plant lineages. <i>Annals of Botany</i> , 2022, 129, 171-184.	1.4	9
677	Hybridization and genetic introgression in birds. <i>Japanese Journal of Ornithology</i> , 2012, 61, 238-255.	0.0	0

#	ARTICLE	IF	CITATIONS
679	Population Genetics in the Genomic Era. , 0, , .		0
680	Population genetics, molecular phylogenetics, and phylogeography. , 2013, , 238-256.		0
681	Demography, life histories, and population dynamics. , 2013, , 257-277.		0
682	Determining conservation status and contributing to in situ conservation action. , 2013, , 278-293.		3
683	Conclusion: the future of studying primates in a changing world. , 2013, , 346-350.		1
684	Introduction: why a new methods book on primate ecology and conservation?. , 2013, , 1-9.		0
685	Phylogeny reconstruction: overview. , 2014, , 70-101.		0
686	Comparison of phylogenetic methods and tests on trees. , 2014, , 153-181.		0
687	Molecular clock and estimation of species divergence times. , 2014, , 361-389.		0
688	Models of amino acid and codon substitution. , 2014, , 35-69.		0
689	Maximum likelihood methods. , 2014, , 102-152.		0
690	Bayesian theory. , 2014, , 182-213.		0
691	Simulating molecular evolution. , 2014, , 418-441.		2
692	Neutral and adaptive protein evolution. , 2014, , 390-417.		0
694	Bayesian phylogenetics. , 2014, , 263-307.		0
695	Coalescent theory and species trees. , 2014, , 308-360.		0
696	Bayesian computation (MCMC). , 2014, , 214-262.		0
708	Coalescent history of nuclear introgression between gadwall and falcated duck fails to explain among-locus heterogeneity in genetic diversity. International International Journal of Avian & Wildlife Biology, 2018, 3, .	0.2	0

#	ARTICLE	IF	CITATIONS
715	Recent advances in Bayesian inference of isolation-with-migration models. <i>Genomics and Informatics</i> , 2019, 17, e37.	0.4	4
718	Navigating the temporal continuum of effective population size. <i>Methods in Ecology and Evolution</i> , 2022, 13, 22-41.	2.2	34
720	Hybridization and Speciation Among New-World Crocodylian Species. , 2021, , 171-183.		4
723	Ecological Divergence and the History of Gene Flow in the Nearctic Milkshakes ( <i>Lampropeltis</i> ) Tj ETQq1 1 0.784314 rgBT /Over	2.7	11
724	Towards an improved understanding of molecular evolution: the relative roles of selection, drift, and everything in between. , 0, 1, .		6
725	Subtle East-West Phylogeographic Break of <i>Asteropyrum</i> (Ranunculaceae) in Subtropical China and Adjacent Areas. <i>Diversity</i> , 2021, 13, 627.	0.7	2
726	Diversification and secondary contact in the magpie-jays ( <i>Calocitta</i> ) throughout the pacific lowlands of Mesoamerica. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2021, 59, 2371-2386.	0.6	5
729	More opportunities more species: Pleistocene differentiation and northward expansion of an evergreen broad-leaved tree species <i>Machilus thunbergii</i> (Lauraceae) in Southeast China. <i>BMC Plant Biology</i> , 2022, 22, 35.	1.6	4
730	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
731	Little Sharks in a Big World: Mitochondrial DNA Reveals Small-scale Population Structure in the California Horn Shark ( <i>Heterodontus francisci</i> ). <i>Journal of Heredity</i> , 2022, 113, 298-310.	1.0	3
732	Population divergence time estimation using individual lineage label switching. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	4
733	Candidate-species delimitation in <i>Desmognathus</i> salamanders reveals gene flow across lineage boundaries, confounding phylogenetic estimation and clarifying hybrid zones. <i>Ecology and Evolution</i> , 2022, 12, e8574.	0.8	18
734	Taxonomic reappraisal for toothfish ( <i>Dissostichus</i> : <i>Notothenioidea</i> ) across the Antarctic Polar Front using genomic and morphological studies. <i>Journal of Fish Biology</i> , 2022, 100, 1158-1170.	0.7	10
735	Divergence time estimation using ddRAD data and an isolation-with-migration model applied to water vole populations of <i>Arvicola</i> . <i>Scientific Reports</i> , 2022, 12, 4065.	1.6	9
736	A simulation study to examine the impact of recombination on phylogenomic inferences under the multispecies coalescent model. <i>Molecular Ecology</i> , 2022, 31, 2814-2829.	2.0	20
737	Evolutionary footprints of a cold relic in a rapidly warming world. <i>ELife</i> , 2021, 10, .	2.8	5
738	Global genetic diversity status and trends: towards a suite of Essential Biodiversity Variables (EBVs) for genetic composition. <i>Biological Reviews</i> , 2022, 97, 1511-1538.	4.7	73
754	Biogeography and diversification of bare-eyes, an endemic Amazonian clade. <i>Journal of Biogeography</i> , 2022, 49, 1110-1123.	1.4	3

#	ARTICLE	IF	CITATIONS
755	Epidemiological inference from pathogen genomes: A review of phylodynamic models and applications. <i>Virus Evolution</i> , 2022, 8, .	2.2	9
756	Admixture of evolutionary rates across a butterfly hybrid zone. <i>ELife</i> , 0, 11, .	2.8	8
757	Impact of Ghost Introgression on Coalescent-Based Species Tree Inference and Estimation of Divergence Time. <i>Systematic Biology</i> , 2023, 72, 35-49.	2.7	7
758	Habitat connectivity, gene flow, and population genetic structure in a Neotropical understory insectivore, the Rufous-and-white Wren. <i>Auk</i> , 0, , .	0.7	1
762	Diversity patterns and speciation processes in a two-island system with continuous migration. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 2260-2271.	1.1	5
764	Inference of Gene Flow between Species under Misspecified Models. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	10
765	Allopatric Lineage Divergence of the East Asian Endemic Herb <i>Conandron ramondioides</i> Inferred from Low-Copy Nuclear and Plastid Markers. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14932.	1.8	0
766	Conservation Genetics. , 2024, , 506-522.		0
767	Isolation by distance in populations with power-law dispersal. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	0.8	2
768	Contrasting patterns of population structure of Bulwer's petrel ( <i>Bulweria bulwerii</i> ) between oceans revealed by statistical phylogeography. <i>Scientific Reports</i> , 2023, 13, .	1.6	0
769	Genomic architecture underlying morphological and physiological adaptation to high elevation in a songbird. <i>Molecular Ecology</i> , 0, , .	2.0	0