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Comparative population genomics in animals uncovers the determinants of genetic diversity

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| 198 | Population structure limits parallel evolution.   | 4  |
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| 158 | Habitat preference predicts genetic diversity and population divergence in Amazonian birds.   |      | 1   |

| 157 | Modern human origins: multiregional evolution of autosomes and East Asia origin of Y and mtDNA.   | 7  |
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| 156 | Size-dependent eco-evolutionary feedbacks in fisheries.   | O  |
| 155 | Influence of historical and human factors on genetic structure and diversity patterns in peripheral populations: implications for the conservation of Moroccan trout. | 4  |
| 154 | Relaxation of purifying selection suggests low effective population size in eusocial Hymenoptera and solitary pollinating bees.                                       | 1  |
| 153 | Predicting amphibian intraspecific diversity with machine learning: Challenges and prospects for integrating traits, geography, and genetic data.                     | 1  |
| 152 | The Multilocus Multispecies Coalescent: A Flexible New Model of Gene Family Evolution.  | 2  |
| 151 | Genetic and species-level biodiversity patterns are linked by demography and ecological opportunity.  | 3  |
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| 144 | Genome-wide features of introns are evolutionary decoupled among themselves and from genome size throughout Eukarya.  | 5  |
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| 142 | Genomic Data from an Endangered Amphibian Reveal Unforeseen Consequences of Fragmentation by Roads.   | 2  |
| 141 | Low genetic variation is associated with low mutation rate in the giant duckweed.   | 1  |
| 140 | Dioecy in plants: an evolutionary dead end? Insights from a population genomics study in the Silene genus.  | 4  |

| 139 | Greater strength of selection and higher proportion of beneficial amino acid changing mutations in humans compared to mice and Drosophila melanogaster.  | 5  |
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| 138 | Error, noise and bias in de novo transcriptome assemblies.   | 2  |
| 137 | A simple model for the evolution of temperature-dependent sex determination explains the temperature sensitivity of embryonic mortality in imperiled reptiles.   | 2  |
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| 113 | Population genomics of C. melanopterususing target gene capture data: demographic inferences and conservation perspectives.  |    |
| 112 | Climate-driven range shifts in fragmented ecosystems.  |    |
| 111 | Lacking conservation genomics in the giant Galpagos tortoise.  | 1  |
| 110 | Genetic equidistance at the nucleotide level.  |    |
| 109 | Comparative genomics of apomictic root-knot nematodes: hybridization, ploidy, and dynamic genome change.   | 1  |
| 108 | Population and conservation genomics of the world's rarest hyena species, the brown hyena (Parahyena brunnea).   |    |
| 107 | Parallel pattern of differentiation at a genomic island shared between clinal and mosaic hybrid zones in a complex of cryptic seahorse lineages.   | 1  |
| 106 | Large-Scale Comparative Analysis of Codon Models Accounting for Protein and Nucleotide Selection.  |    |
| 105 | Codon usage bias in animals: disentangling the effects of natural selection, effective population size and GC-biased gene conversion.  | 2  |
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Effects of demographic stochasticity and life-history strategies on times and probabilities to 103 fixation: an individual-based model. Prevalence of loss-of-function alleles does not correlate with lifetime fecundity and other 102 life-history traits in metazoans. The Response to Past Climate Perturbations Explains Extremely Low Genetic Diversity in the 101 Genome of an Abundant Ice-Age Remnant, the Alpine Marmot. The divergence history of European blue mussel species reconstructed from Approximate Bayesian 100 Computation: the effects of sequencing techniques and sampling strategies. Eco-evolutionary community turnover following environmental change. 99 Recent secondary contacts, background selection and variable recombination rates shape genomic 98 diversity in the model speciesAnolis carolinensis. Combining population genomics and forward simulations to investigate stocking impacts: A case 97 study of Muskellunge (Esox masquinongy) from the St. Lawrence River basin. Population genomics supports clonal reproduction and multiple gains and losses of parasitic 96 abilities in the most devastating nematode plant pest. Social insect colony size is correlated with rates of substitution and DNA repair gene evolution. 95 A Versatile Rapture (RAD-Capture) Platform for Genotyping Marine Turtles. 94 Utilization of tissue ploidy level variation in de novo transcriptome assembly of Pinus sylvestris. 93 1 The determinants of genetic diversity in butterflies Lewontin paradox revisited. 92  $\circ$ Persistence of remnant patches and genetic loss at the distribution periphery in island and 91 1 mainland populations of the quokka. 2019, 67, 38 Contingent Convergence: The ability to detect convergent genomic evolution is dependent on 90 population size and migration. Is adaptation limited by mutation? A timescale-dependent effect of genetic diversity on the 89 3 adaptive substitution rate in animals. 88 Cryptic genetic variation underpins rapid adaptation to ocean acidification. Continent-wide effects of urbanization on bird and mammal genetic diversity. 87 1 Testing the basic tenet of the molecular clock and neutral theory by using ancient proteomes. 86

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| 84             | Vulnerability and life-history traits correlate with the load of deleterious mutations in fish.   | 1 |
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| 83             | Mitochondrial DNA Sequence Diversity in Mammals: a Correlation Between the Effective and Census Population Sizes.   | 1 |
| 82             | A Total-Evidence Dated Phylogeny of Echinoids and the Evolution of Body Size across Adaptive Landscape.   | 2 |
| 81             | Evolutionary transition to XY sex chromosomes associated with Y-linked duplication of a male hormone gene in a terrestrial isopod.                                  |   |
| 80             | High MHC gene copy number maintains diversity despite homozygosity in a Critically Endangered single-island endemic bird, but no evidence of MHC-based mate choice. | O |
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