

Great ape genetic diversity and population history

Nature

499, 471-475

DOI: [10.1038/nature12228](https://doi.org/10.1038/nature12228)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Comparative Species Divergence across Eight Triplets of Spiny Lizards (Sceloporus) Using Genomic Sequence Data. <i>Genome Biology and Evolution</i> , 2013, 5, 2410-2419.	2.5	30
2	Cortical Evolution: Judge the Brain by Its Cover. <i>Neuron</i> , 2013, 80, 633-647.	8.1	444
3	Rates and patterns of great ape retrotransposition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 13457-13462.	7.1	57
4	Dynamics of DNA Methylation in Recent Human and Great Ape Evolution. <i>PLoS Genetics</i> , 2013, 9, e1003763.	3.5	118
5	Improving Genome Assemblies and Annotations for Nonhuman Primates. <i>ILAR Journal</i> , 2013, 54, 144-153.	1.8	23
6	Great Ape Genomics. <i>ILAR Journal</i> , 2013, 54, 82-90.	1.8	16
7	Evolution and diversity of copy number variation in the great ape lineage. <i>Genome Research</i> , 2013, 23, 1373-1382.	5.5	161
8	Great ape skeletal collections: Making the most of scarce and irreplaceable resources in the digital age. <i>American Journal of Physical Anthropology</i> , 2013, 152, 2-32.	2.1	33
9	Extracting population genetics information from a diploid genome sequence. <i>Frontiers in Ecology and Evolution</i> , 0, 2, .	2.2	4
10	Sequence differences at orthologous microsatellites inflate estimates of human-chimpanzee differentiation. <i>BMC Genomics</i> , 2014, 15, 990.	2.8	5
11	Pseudogenization of testis-specific Lfg5 predates human/Neanderthal divergence. <i>Journal of Human Genetics</i> , 2014, 59, 288-291.	2.3	7
12	Genome-Wide Inference of Ancestral Recombination Graphs. <i>PLoS Genetics</i> , 2014, 10, e1004342.	3.5	323
13	Reduced Representation Genome Sequencing Suggests Low Diversity on the Sex Chromosomes of Tonkean Macaque Monkeys. <i>Molecular Biology and Evolution</i> , 2014, 31, 2425-2440.	8.9	16
14	A Homogenizing Process of Selection Has Maintained an "Ultra-Slow" Acetylation & NAT2 Variant in Humans. <i>Human Biology</i> , 2014, 86, 185.	0.2	19
15	Emerging Technologies: Smarter ways to fight wildlife crime. <i>Environmental Development</i> , 2014, 12, 62-72.	4.1	1
16	Unraveling recombination rate evolution using ancestral recombination maps. <i>BioEssays</i> , 2014, 36, 892-900.	2.5	5
17	On the tool use behavior of the bonobo-chimpanzee last common ancestor, and the origins of hominine stone tool use. <i>American Journal of Primatology</i> , 2014, 76, 910-918.	1.7	20
18	Lineage Sorting in Apes. <i>Annual Review of Genetics</i> , 2014, 48, 519-535.	7.6	48

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19	Brief Communication: Quantitative and molecular genetic differentiation in humans and chimpanzees: Implications for the evolutionary processes underlying cranial diversification. <i>American Journal of Physical Anthropology</i> , 2014, 154, 615-620.	2.1	8
20	Khoisan hunter-gatherers have been the largest population throughout most of modern-human demographic history. <i>Nature Communications</i> , 2014, 5, 5692.	12.8	65
21	<scp>ABC</scp> inference of multi-population divergence with admixture from unphased population genomic data. <i>Molecular Ecology</i> , 2014, 23, 4458-4471.	3.9	49
22	Multispecies Coalescent Analysis of the Early Diversification of Neotropical Primates: Phylogenetic Inference under Strong Gene Trees/Species Tree Conflict. <i>Genome Biology and Evolution</i> , 2014, 6, 3105-3114.	2.5	15
23	Bayesian Inference of Shared Recombination Hotspots Between Humans and Chimpanzees. <i>Genetics</i> , 2014, 198, 1621-1628.	2.9	8
24	Generation of SNP datasets for orangutan population genomics using improved reduced-representation sequencing and direct comparisons of SNP calling algorithms. <i>BMC Genomics</i> , 2014, 15, 16.	2.8	72
25	Comparative primate genomics: emerging patterns of genome content and dynamics. <i>Nature Reviews Genetics</i> , 2014, 15, 347-359.	16.3	234
26	The Human Condition—A Molecular Approach. <i>Cell</i> , 2014, 157, 216-226.	28.9	175
27	Resequencing studies of nonmodel organisms using closely related reference genomes: optimal experimental designs and bioinformatics approaches for population genomics. <i>Molecular Ecology</i> , 2014, 23, 1764-1779.	3.9	45
28	DNA-based approaches for evaluating historical demography in terrestrial vertebrates. <i>Biological Journal of the Linnean Society</i> , 2014, 112, 367-386.	1.6	17
29	Stability and phylogenetic correlation in gut microbiota: lessons from ants and apes. <i>Molecular Ecology</i> , 2014, 23, 1268-1283.	3.9	276
30	Why primate models matter. <i>American Journal of Primatology</i> , 2014, 76, 801-827.	1.7	451
31	The complete genome sequence of a Neanderthal from the Altai Mountains. <i>Nature</i> , 2014, 505, 43-49.	27.8	1,830
32	Whole-genome sequencing of the snub-nosed monkey provides insights into folivory and evolutionary history. <i>Nature Genetics</i> , 2014, 46, 1303-1310.	21.4	174
33	Recent divergences and size decreases of eastern gorilla populations. <i>Biology Letters</i> , 2014, 10, 20140811.	2.3	64
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35	Primate evolution of the recombination regulator PRDM9. <i>Nature Communications</i> , 2014, 5, 4370.	12.8	72
36	Genetic and developmental basis for parallel evolution and its significance for hominoid evolution. <i>Evolutionary Anthropology</i> , 2014, 23, 188-200.	3.4	43

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37	Identification of species-specific nuclear insertions of mitochondrial DNA (numts) in gorillas and their potential as population genetic markers. <i>Molecular Phylogenetics and Evolution</i> , 2014, 81, 61-70.	2.7	12
38	Lethal aggression in Pan is better explained by adaptive strategies than human impacts. <i>Nature</i> , 2014, 513, 414-417.	27.8	375
39	Using Pseudogene Database to Identify Lineage-Specific Genes and Pseudogenes in Humans and Chimpanzees. <i>Journal of Heredity</i> , 2014, 105, 436-443.	2.4	4
40	All models are wrong. <i>Molecular Ecology</i> , 2014, 23, 2887-2889.	3.9	7
41	Complete Mitochondrial Genome Sequence of the Eastern Gorilla (<i>Gorilla beringei</i>) and Implications for African Ape Biogeography. <i>Journal of Heredity</i> , 2014, 105, 846-855.	2.4	14
42	How and why should we implement genomics into conservation?. <i>Evolutionary Applications</i> , 2014, 7, 999-1007.	3.1	152
43	Killer Whale Nuclear Genome and mtDNA Reveal Widespread Population Bottleneck during the Last Glacial Maximum. <i>Molecular Biology and Evolution</i> , 2014, 31, 1121-1131.	8.9	61
44	Mouse models of human evolution. <i>Current Opinion in Genetics and Development</i> , 2014, 29, 75-80.	3.3	15
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47	No Positive Selection for G Allele in a p53 Response Element in Europeans. <i>Cell</i> , 2014, 157, 1497-1499.	28.9	2
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49	Further evidence for phenotypic signatures of hybridization in descendant baboon populations. <i>Journal of Human Evolution</i> , 2014, 76, 54-62.	2.6	30
50	Universal Grammar and Biological Variation: An EvoDevo Agenda for Comparative Biolinguistics. <i>Biological Theory</i> , 2014, 9, 122-134.	1.5	30
51	The Genetics of Microdeletion and Microduplication Syndromes: An Update. <i>Annual Review of Genomics and Human Genetics</i> , 2014, 15, 215-244.	6.2	145
52	A fine-scale recombination map of the human-chimpanzee ancestor reveals faster change in humans than in chimpanzees and a strong impact of GC-biased gene conversion. <i>Genome Research</i> , 2014, 24, 467-474.	5.5	37
53	The limiting distribution of the effective population size of the ancestor of humans and chimpanzees. <i>Journal of Theoretical Biology</i> , 2014, 357, 55-61.	1.7	5
54	Evolutionary history inferred from the de novo assembly of a nonmodel organism, the blue-eyed black lemur. <i>Molecular Ecology</i> , 2015, 24, 4392-4405.	3.9	25

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55	Tempo and mode of genomic mutations unveil human evolutionary history. <i>Genes and Genetic Systems</i> , 2015, 90, 123-131.	0.7	0
56	Genetic diversity in humans and non-human primates and its evolutionary consequences. <i>Genes and Genetic Systems</i> , 2015, 90, 133-145.	0.7	27
58	Identification of Diagnostic Mitochondrial DNA Single Nucleotide Polymorphisms Specific to Sumatran Orangutan (<i>Pongo abelii</i>) Populations. <i>HAYATI Journal of Biosciences</i> , 2015, 22, 149-156.	0.4	2
59	Unique human orbital morphology compared with that of apes. <i>Scientific Reports</i> , 2015, 5, 11528.	3.3	9
60	Human rather than ape-like orbital morphology allows much greater lateral visual field expansion with eye abduction. <i>Scientific Reports</i> , 2015, 5, 12437.	3.3	5
62	The geographic distribution of genetic diversity within gorillas. <i>American Journal of Primatology</i> , 2015, 77, 974-985.	1.7	12
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65	Characterization of MHC class II B polymorphism in multiple populations of wild gorillas using non-invasive samples and next-generation sequencing. <i>American Journal of Primatology</i> , 2015, 77, 1193-1206.	1.7	11
66	Engaging Native Americans in Genomics Research. <i>American Anthropologist</i> , 2015, 117, 743-744.	1.4	20
67	Positive selection underlies the species-specific binding of <i>Plasmodium falciparum</i> RH5 to human basigin. <i>Molecular Ecology</i> , 2015, 24, 4711-4722.	3.9	12
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73	Oxytocin receptor gene sequences in owl monkeys and other primates show remarkable interspecific regulatory and protein coding variation. <i>Molecular Phylogenetics and Evolution</i> , 2015, 91, 160-177.	2.7	11
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92	Going the whole orang: Darwin, Wallace and the natural history of orangutans. Studies in History and Philosophy of Science Part C:Studies in History and Philosophy of Biological and Biomedical Sciences, 2015, 51, 53-63.	1.3	11

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95	Whole genome sequencing of an ethnic Pathan (Pakhtun) from the north-west of Pakistan. <i>BMC Genomics</i> , 2015, 16, 172.	2.8	16
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99	Ancestral population genomics using coalescence hidden Markov models and heuristic optimisation algorithms. <i>Computational Biology and Chemistry</i> , 2015, 57, 80-92.	2.3	3
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112	Reconstructing the demographic history of orangâ€utans using Approximate <scp>B</scp>ayesian Computation. <i>Molecular Ecology</i> , 2015, 24, 310-327.	3.9	32
113	Demographic inferences using shortâ€read genomic data in an approximate Bayesian computation framework: in silico evaluation of power, biases and proof of concept in Atlantic walrus. <i>Molecular Ecology</i> , 2015, 24, 328-345.	3.9	54
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122	Genomic analysis of snub-nosed monkeys (<i>Rhinopithecus</i>) identifies genes and processes related to high-altitude adaptation. <i>Nature Genetics</i> , 2016, 48, 947-952.	21.4	109
123	Effects of Linked Selective Sweeps on Demographic Inference and Model Selection. <i>Genetics</i> , 2016, 204, 1207-1223.	2.9	144
124	Bonobo personality traits are heritable and associated with vasopressin receptor gene 1a variation. <i>Scientific Reports</i> , 2016, 6, 38193.	3.3	47
125	The evolutionary history of genes involved in spoken and written language: beyond FOXP2. <i>Scientific Reports</i> , 2016, 6, 22157.	3.3	55
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132	Genomic signatures of sex-biased demography: progress and prospects. <i>Current Opinion in Genetics and Development</i> , 2016, 41, 62-71.	3.3	34
133	Incomplete Lineage Sorting in Mammalian Phylogenomics. <i>Systematic Biology</i> , 2017, 66, syw082.	5.6	88
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137	Evolution and demography of the great apes. <i>Current Opinion in Genetics and Development</i> , 2016, 41, 124-129.	3.3	27
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144	The conservation genetics juggling act: integrating genetics and ecology, science and policy. <i>Evolutionary Applications</i> , 2016, 9, 181-195.	3.1	38
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154	Inter- and intra-varietal structural variation in grapevine genomes. Plant Journal, 2016, 88, 648-661.	5.7	45
155	The population genomics of rhesus macaques (<i>Macaca mulatta</i>) based on whole-genome sequences. Genome Research, 2016, 26, 1651-1662.	5.5	101
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158	The Molecular Basis of Human Brain Evolution. Current Biology, 2016, 26, R1109-R1117.	3.9	47
159	Natural Selection in the Great Apes. Molecular Biology and Evolution, 2016, 33, 3268-3283.	8.9	70
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162	A Comparison Between Bonobos and Chimpanzees: A Review and Update. Evolutionary Anthropology, 2016, 25, 239-252.	3.4	123
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