

# Genomic evidence for the Pleistocene and recent popul

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Functional Impact and Evolution of a Novel Human Polymorphic Inversion That Disrupts a Gene and Creates a Fusion Transcript. <i>PLoS Genetics</i> , 2015, 11, e1005495.	1.5	22
2	“Ghost population” hints at long-lost migration to the Americas. <i>Nature</i> , 2015, , .	13.7	0
3	Does Mitochondrial Haplogroup X Indicate Ancient Trans-Atlantic Migration to the Americas? A Critical Re-Evaluation. <i>PaleoAmerica</i> , 2015, 1, 297-304.	0.4	49
4	Two contemporaneous mitogenomes from terminal Pleistocene burials in eastern Beringia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13833-13838.	3.3	56
6	The Early Human Occupation of the Bonneville Basin. <i>Developments in Earth Surface Processes</i> , 2016, , 504-525.	2.8	8
7	Multispecies Outcomes of Sympatric Speciation after Admixture with the Source Population in Two Radiations of Nicaraguan Crater Lake Cichlids. <i>PLoS Genetics</i> , 2016, 12, e1006157.	1.5	97
8	Better together: Thinking anthropologically about genetics. <i>American Journal of Physical Anthropology</i> , 2016, 160, 557-560.	2.1	5
9	Evolutionary Patterns and Processes: Lessons from Ancient DNA. <i>Systematic Biology</i> , 2017, 66, syw059.	2.7	73
10	Genetic Affiliation of Pre-Hispanic and Contemporary Mayas through Maternal Lineage. <i>Human Biology</i> , 2016, 88, 136.	0.4	13
11	Fire history on the California Channel Islands spanning human arrival in the Americas. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150167.	1.8	19
12	Population biobanks: Organizational models and prospects of application in gene geography and personalized medicine. <i>Russian Journal of Genetics</i> , 2016, 52, 1227-1243.	0.2	26
13	Pre-Clovis occupation 14,550 years ago at the Page-Ladson site, Florida, and the peopling of the Americas. <i>Science Advances</i> , 2016, 2, e1600375.	4.7	171
14	Archaic adaptive introgression in <i>TBX15/WARS2</i> . <i>Molecular Biology and Evolution</i> , 2017, 34, msw283.	3.5	101
15	Post-invasion demography of prehistoric humans in South America. <i>Nature</i> , 2016, 532, 232-235.	13.7	167
16	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. <i>Nature Genetics</i> , 2016, 48, 593-599.	9.4	273
17	Genomic signatures of sex-biased demography: progress and prospects. <i>Current Opinion in Genetics and Development</i> , 2016, 41, 62-71.	1.5	34
18	Native American foods: History, culture, and influence on modern diets. <i>Journal of Ethnic Foods</i> , 2016, 3, 171-177.	0.8	36
19	Native American Genomics and Population Histories. <i>Annual Review of Anthropology</i> , 2016, 45, 319-340.	0.4	49

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20	A genomic view of the peopling of the Americas. <i>Current Opinion in Genetics and Development</i> , 2016, 41, 27-35.	1.5	103
21	Postglacial viability and colonization in North America's ice-free corridor. <i>Nature</i> , 2016, 537, 45-49.	13.7	363
22	Ancestral Origins and Genetic History of Tibetan Highlanders. <i>American Journal of Human Genetics</i> , 2016, 99, 580-594.	2.6	208
23	Toward high-resolution population genomics using archaeological samples. <i>DNA Research</i> , 2016, 23, 295-310.	1.5	25
24	Possible similarities between the folk medicine historically used by First Nations and American Indians in North America and the ethnoveterinary knowledge currently used in British Columbia, Canada. <i>Journal of Ethnopharmacology</i> , 2016, 192, 53-66.	2.0	16
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26	Bison phylogeography constrains dispersal and viability of the Ice Free Corridor in western Canada. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8057-8063.	3.3	140
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30	Detecting hybridization using ancient DNA. <i>Molecular Ecology</i> , 2016, 25, 2398-2412.	2.0	37
31	Deep Roots for Aboriginal Australian Y Chromosomes. <i>Current Biology</i> , 2016, 26, 809-813.	1.8	54
32	Ancient DNA and the rewriting of human history: be sparing with Occam's razor. <i>Genome Biology</i> , 2016, 17, 1.	3.8	1,335
33	Enfermedad de Paget: aproximación a sus orígenes históricos. <i>Reumatología Clínica</i> , 2017, 13, 66-72.	0.2	15
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35	The peopling of the Americas and the origin of the Beringian occupation model. <i>American Journal of Physical Anthropology</i> , 2017, 162, 403-408.	2.1	34
36	First analysis of ancient mtDNA genetic diversity in Northern coast of Argentinean Patagonia. <i>Journal of Archaeological Science: Reports</i> , 2017, 12, 91-98.	0.2	9
37	Paget's Disease of Bone: Approach to Its Historical Origins. <i>Reumatología Clínica (English Edition)</i> , 2017, 13, 66-72.	0.2	4

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38	Genome-wide Analysis in Brazilians Reveals Highly Differentiated Native American Genome Regions. <i>Molecular Biology and Evolution</i> , 2017, 34, msw249.	3.5	21
39	Archaeogenomic evidence reveals prehistoric matrilineal dynasty. <i>Nature Communications</i> , 2017, 8, 14115.	5.8	210
40	Did Monkeys Make the Pre-Clovis Pebble Tools of Northeastern Brazil?. <i>PaleoAmerica</i> , 2017, 3, 6-12.	0.4	44
41	Evolutionary population history of early Paleoamerican cranial morphology. <i>Science Advances</i> , 2017, 3, e1602289.	4.7	50
42	Genome-wide data from two early Neolithic East Asian individuals dating to 7700 years ago. <i>Science Advances</i> , 2017, 3, e1601877.	4.7	100
43	Clustering of 770,000 genomes reveals post-colonial population structure of North America. <i>Nature Communications</i> , 2017, 8, 14238.	5.8	99
44	A paleogenetic perspective on the early population history of the high altitude Andes. <i>Quaternary International</i> , 2017, 461, 25-33.	0.7	12
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49	Genetic studies of the peopling of the Americas: What insights do diachronic mitochondrial genome datasets provide?. <i>Quaternary International</i> , 2017, 444, 26-35.	0.7	29
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51	Resolving relationships between several Neolithic and Mesolithic populations in Northern Eurasia using geometric morphometrics. <i>American Journal of Physical Anthropology</i> , 2017, 164, 163-183.	2.1	2
52	News Feature: Is theory about peopling of the Americas a bridge too far?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 5554-5557.	3.3	5
53	THE EARLIEST SHELL FISHHOOKS FROM THE AMERICAS REVEAL FISHING TECHNOLOGY OF PLEISTOCENE MARITIME FORAGERS. <i>American Antiquity</i> , 2017, 82, 498-516.	0.6	17
54	Fueguian crania and the circum-Pacific rim variation. <i>American Journal of Physical Anthropology</i> , 2017, 163, 295-316.	2.1	5
55	Ancient individuals from the North American Northwest Coast reveal 10,000 years of regional genetic continuity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4093-4098.	3.3	100

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57	Detecting past male-mediated expansions using the Y chromosome. <i>Human Genetics</i> , 2017, 136, 547-557.	1.8	23
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63	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , 2017, 358, 659-662.	6.0	263
64	40,000-Year-Old Individual from Asia Provides Insight into Early Population Structure in Eurasia. <i>Current Biology</i> , 2017, 27, 3202-3208.e9.	1.8	191
65	Genetic Discontinuity between the Maritime Archaic and Beothuk Populations in Newfoundland, Canada. <i>Current Biology</i> , 2017, 27, 3149-3156.e11.	1.8	17
66	Demographic history and biologically relevant genetic variation of Native Mexicans inferred from whole-genome sequencing. <i>Nature Communications</i> , 2017, 8, 1005.	5.8	44
67	Genetics: Ancient DNA Clarifies Population Histories of the Northeastern Margin of North America. <i>Current Biology</i> , 2017, 27, R1116-R1118.	1.8	0
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75	The Anzick genome proves Clovis is first, after all. <i>Quaternary International</i> , 2017, 444, 4-9.	0.7	13
76	Exact Calculation of the Joint Allele Frequency Spectrum for Isolation with Migration Models. <i>Genetics</i> , 2017, 207, 241-253.	1.2	22
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79	Admixture and Ancestry Inference from Ancient and Modern Samples through Measures of Population Genetic Drift. <i>Human Biology</i> , 2017, 89, 21.	0.4	30
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84	Between Lake Baikal and the Baltic Sea: genomic history of the gateway to Europe. <i>BMC Genetics</i> , 2017, 18, 110.	2.7	34
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87	Forensic parameters and admixture in Mestizos from five geographic regions of Mexico based on 20 autosomal STRs (Powerplex 21 system). <i>International Journal of Legal Medicine</i> , 2018, 132, 1293-1296.	1.2	17
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90	Environmental selection during the last ice age on the mother-to-infant transmission of vitamin D and fatty acids through breast milk. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4426-E4432.	3.3	70
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103	Patterns of Genetic Coding Variation in a Native American Population before and after European Contact. <i>American Journal of Human Genetics</i> , 2018, 102, 806-815.	2.6	33
104	Origins and spread of fluted-point technology in the Canadian Ice-Free Corridor and eastern Beringia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4116-4121.	3.3	65
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106	The peopling of eastern Beringia and its archaeological complexities. <i>Quaternary International</i> , 2018, 466, 284-298.	0.7	34
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109	Ancient maternal lineages in hunter-gatherer groups of Argentinean Patagonia. Settlement, population continuity and divergence. <i>Journal of Archaeological Science: Reports</i> , 2018, 18, 689-695.	0.2	6
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123	Reconstructing the Deep Population History of Central and South America. <i>Cell</i> , 2018, 175, 1185-1197.e22.	13.5	259
124	Principles of Archaeogenetics and the Current Trends of Ancient Genome Studies. <i>Korean Journal of Physical Anthropology</i> , 2018, 31, 105.	0.2	0
125	Population Genetic Diversity and Phylogenetic Characteristics for High-Altitude Adaptive Kham Tibetan Revealed by DNATyper™ 19 Amplification System. <i>Frontiers in Genetics</i> , 2018, 9, 630.	1.1	17
126	<i>FADS1</i> and the Timing of Human Adaptation to Agriculture. <i>Molecular Biology and Evolution</i> , 2018, 35, 2957-2970.	3.5	113
127	Quantifying and reducing spurious alignments for the analysis of ultra-short ancient DNA sequences. <i>BMC Biology</i> , 2018, 16, 121.	1.7	41
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133	Complex virome in feces from Amerindian children in isolated Amazonian villages. <i>Nature Communications</i> , 2018, 9, 4270.	5.8	51
134	Nutritional features of indigenous people of Siberia and North America: Are we relatives?. <i>Journal of Ethnic Foods</i> , 2018, 5, 155-160.	0.8	4
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137	Ancient human parallel lineages within North America contributed to a coastal expansion. <i>Science</i> , 2018, 360, 1024-1027.	6.0	138
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150	Great Salt Lake microbiology: a historical perspective. <i>International Microbiology</i> , 2018, 21, 79-95.	1.1	47
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153	Inference of complex population histories using whole-genome sequences from multiple populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17115-17120.	3.3	52
155	More on Clovis Learning: Individual-level Processes Aggregate to Form Population-level Patterns. <i>PaleoAmerica</i> , 2019, 5, 157-168.	0.4	10
156	Ancestral Population Genomics. <i>Methods in Molecular Biology</i> , 2019, 1910, 555-589.	0.4	2
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159	The Current Genomic Landscape of Western South America: Andes, Amazonia, and Pacific Coast. <i>Molecular Biology and Evolution</i> , 2019, 36, 2698-2713.	3.5	59
160	Reconstructed lost Native American populations from Eastern Brazil are shaped by differential J <sup>A</sup> /Tupi ancestry. <i>Genome Biology and Evolution</i> , 2019, 11, 2593-2604.	1.1	8
161	A Serra da Capivara e os primeiros povoamentos sul-americanos: uma revisÃo bibliogrÃfica. <i>Boletim do Museu Paraense Emilio Goeldi: Ciencias Humanas</i> , 2019, 14, 367-398.	0.0	16
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166	Palaeo-Eskimo genetic ancestry and the peopling of Chukotka and North America. <i>Nature</i> , 2019, 570, 236-240.	13.7	118
167	The population history of northeastern Siberia since the Pleistocene. <i>Nature</i> , 2019, 570, 182-188.	13.7	259
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