Tracking the origins of Yakutian horses and the genetic subarctic environments

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Citation Report

CITATION	DEDODT

#	Article	IF	CITATIONS
1	Whole-Genome Sequencing of Native Sheep Provides Insights into Rapid Adaptations to Extreme Environments. Molecular Biology and Evolution, 2016, 33, 2576-2592.	8.9	271
2	meta <scp>BIT</scp> , an integrative and automated metagenomic pipeline for analysing microbial profiles from highâ€throughput sequencing shotgun data. Molecular Ecology Resources, 2016, 16, 1415-1427.	4.8	35
3	Evolutionary Patterns and Processes: Lessons from Ancient DNA. Systematic Biology, 2017, 66, syw059.	5.6	73
4	Genome sequence, population history, and pelage genetics of the endangered African wild dog (Lycaon) Tj ETQq1	1 0.7843 2.8	14.rgBT /0
5	Spotted phenotypes in horses lost attractiveness in the Middle Ages. Scientific Reports, 2016, 6, 38548.	3.3	31
6	The Evolutionary Origin and Genetic Makeup of Domestic Horses. Genetics, 2016, 204, 423-434.	2.9	61
7	Fast, Accurate and Automatic Ancient Nucleosome and Methylation Maps with epiPALEOMIX. Molecular Biology and Evolution, 2016, 33, 3284-3298.	8.9	53
8	Genome Sequence of a 5,310-Year-Old Maize Cob Provides Insights into the Early Stages of Maize Domestication. Current Biology, 2016, 26, 3195-3201.	3.9	130
9	Ancient genomic changes associated with domestication of the horse. Science, 2017, 356, 442-445.	12.6	185
10	A new model for ancient DNA decay based on paleogenomic meta-analysis. Nucleic Acids Research, 2017, 45, 6310-6320.	14.5	168
12	Genome-Guided Phylo-Transcriptomic Methods and the Nuclear Phylogenetic Tree of the Paniceae Grasses. Scientific Reports, 2017, 7, 13528.	3.3	27
13	Harnessing ancient genomes to study the history of human adaptation. Nature Reviews Genetics, 2017, 18, 659-674.	16.3	165
14	Humans and Animals in Northern Regions. Annual Review of Anthropology, 2017, 46, 133-149.	1.5	23
15	Y Chromosome Uncovers the Recent Oriental Origin of Modern Stallions. Current Biology, 2017, 27, 2029-2035.e5.	3.9	75
16	Taming the Past: Ancient DNA and the Study of Animal Domestication. Annual Review of Animal Biosciences, 2017, 5, 329-351.	7.4	120
17	Experimental conditions improving inâ€solution target enrichment for ancient <scp>DNA</scp> . Molecular Ecology Resources, 2017, 17, 508-522.	4.8	67
18	A compendium and functional characterization of mammalian genes involved in adaptation to Arctic or Antarctic environments. BMC Genetics, 2017, 18, 111.	2.7	37
19	Genome-Wide microRNA Binding Site Variation between Extinct Wild Aurochs and Modern Cattle Identifies Candidate microRNA-Regulated Domestication Genes. Frontiers in Genetics, 2017, 8, 3.	2.3	24

#	ARTICLE	IF	CITATIONS
20	Developing a 670k genotyping array to tag ~2M SNPs across 24 horse breeds. BMC Genomics, 2017, 18, 565.	2.8	116
21	Ancient genomes revisit the ancestry of domestic and Przewalski's horses. Science, 2018, 360, 111-114.	12.6	241
22	Decline of genetic diversity in ancient domestic stallions in Europe. Science Advances, 2018, 4, eaap9691.	10.3	29
23	Paleogenomics: Genome-Scale Analysis of Ancient DNA and Population and Evolutionary Genomic Inferences. Population Genomics, 2018, , 323-360.	0.5	4
24	Asian horses deepen the MSY phylogeny. Animal Genetics, 2018, 49, 90-93.	1.7	32
25	Ancient Epigenomics. Population Genomics, 2018, , 75-111.	0.5	11
26	A study of a frozen mummy of a wild horse from the Holocene of Yakutia, East Siberia, Russia. Mammal Research, 2018, 63, 307-314.	1.3	16
27	Improved reference genome for the domestic horse increases assembly contiguity and composition. Communications Biology, 2018, 1, 197.	4.4	148
28	Paleogenomics of Animal Domestication. Population Genomics, 2018, , 225-272.	0.5	14
29	Genetic diversity and origin of the feral horses in Theodore Roosevelt National Park. PLoS ONE, 2018, 13, e0200795.	2.5	6
30	Technical Advances and Challenges in Genome-Scale Analysis of Ancient DNA. Population Genomics, 2018, , 3-29.	0.5	2
31	Contrasting Patterns of Genomic Diversity Reveal Accelerated Genetic Drift but Reduced Directional Selection on X-Chromosome in Wild and Domestic Sheep Species. Genome Biology and Evolution, 2018, 10, 1282-1297.	2.5	23
32	An Ancient DNA Perspective on Horse Evolution. Population Genomics, 2018, , 325-351.	0.5	6
33	High-throughput sequencing of the mitochondrial genomes from archived fish scales: an example of the endangered putative species flock of Sevan trout Salmo ischchan. Hydrobiologia, 2018, 822, 217-228.	2.0	14
34	Genetic characterization of free-ranging Asiatic wild ass in Central Asia as a basis for future conservation strategies. Conservation Genetics, 2018, 19, 1169-1184.	1.5	6
35	Late Quaternary horses in Eurasia in the face of climate and vegetation change. Science Advances, 2018, 4, eaar5589.	10.3	32
36	Horse Y chromosome assembly displays unique evolutionary features and putative stallion fertility genes. Nature Communications, 2018, 9, 2945.	12.8	56
37	Population Genomics of Ungulates. Population Genomics, 2018, , 185-209.	0.5	4

CITATION REPORT

		CITATION REPORT	
#	Article	IF	CITATIONS
38	Population Genetic Analysis of the Estonian Native Horse Suggests Diverse and Distinct Genetics, Ancient Origin and Contribution from Unique Patrilines. Genes, 2019, 10, 629.	2.4	12
39	Ten years of the horse reference genome: insights into equine biology, domestication and population dynamics in the postâ€genome era. Animal Genetics, 2019, 50, 569-597.	1.7	43
41	Is Determinism Dead?. , 2019, , 23-49.		0
42	Incorporating New Methods I: The Stable Isotope Revolution. , 2019, , 50-74.		0
43	Incorporating New Methods III: Answering Palaeoeconomic Questions with Molecular Genetics. , 2019, , 99-122.		0
44	Integrated Case Study I: Early Farming in Central Europe. , 2019, , 137-162.		0
48	Integrated Case Study II: Horse Domestication and the Origins of Pastoralism in Central Asia. , 2019, , 163-194.		0
49	Incorporating New Methods II: Residue Chemistry. , 2019, , 75-98.		0
50	Incorporating New Methods IV: Phytoliths and Starch Grains in the Tropics and Beyond. , 2019, , 123-136.		0
51	Origin and Evolution of Deleterious Mutations in Horses. Genes, 2019, 10, 649.	2.4	31
52	Linking a mutation to survival in wild mice. Science, 2019, 363, 499-504.	12.6	126
53	Joint Estimates of Heterozygosity and Runs of Homozygosity for Modern and Ancient Samples. Genetics, 2019, 212, 587-614.	2.9	61
54	The horse Y chromosome as an informative marker for tracing sire lines. Scientific Reports, 2019, 9, 6095.	3.3	39
55	Tracking Five Millennia of Horse Management with Extensive Ancient Genome Time Series. Cell, 2019, 177, 1419-1435.e31.	28.9	195
57	Authentication and Assessment of Contamination in Ancient DNA. Methods in Molecular Biology, 2019, 1963, 163-194.	0.9	23
58	Whole blood transcriptome analysis reveals footprints of cattle adaptation to subâ€arctic conditions. Animal Genetics, 2019, 50, 217-227.	1.7	9
59	The Promise of Paleogenomics Beyond Our Own Species. Trends in Genetics, 2019, 35, 319-329.	6.7	55
60	Diet of autochthonous populations in Yakutia using isotopic, ethnographic, historical and archaeological data. Journal of Archaeological Science: Reports, 2019, 28, 102022.	0.5	1

CITATION REPORT

#	Article	IF	CITATIONS
61	Functional Annotation of Animal Genomes (FAANG): Current Achievements and Roadmap. Annual Review of Animal Biosciences, 2019, 7, 65-88.	7.4	172
62	Whole-Genome Sequencing of Three Native Cattle Breeds Originating From the Northernmost Cattle Farming Regions. Frontiers in Genetics, 2018, 9, 728.	2.3	57
63	Ancient Genomes Reveal Unexpected Horse Domestication and Management Dynamics. BioEssays, 2020, 42, e1900164.	2.5	31
64	Genetics and Signaling Pathways of Laminitis. Veterinary Clinics of North America Equine Practice, 2020, 36, 379-394.	0.7	2
65	Determination of season-of-death and age-at-death by cementum increment analysis of horses Equus ferus (Boddaert, 1785) from cultural layer IVa at Upper Paleolithic site Kostenki 14 (Markina Gora) (Voronezh region, Russia). Quaternary International, 2020, 557, 110-120.	1.5	9
66	Genome diversity of Chinese indigenous chicken and the selective signatures in Chinese gamecock chicken. Scientific Reports, 2020, 10, 14532.	3.3	39
67	The Evolutionary and Historical Foundation of the Modern Horse: Lessons from Ancient Genomics. Annual Review of Genetics, 2020, 54, 563-581.	7.6	17
68	Using paleo-archives to safeguard biodiversity under climate change. Science, 2020, 369, .	12.6	98
69	Horse males became over-represented in archaeological assemblages during the Bronze Age. Journal of Archaeological Science: Reports, 2020, 31, 102364.	0.5	7
71	Population genetics of wild <i>Macaca fascicularis</i> with lowâ€coverage shotgun sequencing of museum specimens. American Journal of Physical Anthropology, 2020, 173, 21-33.	2.1	11
72	Fatty Acid Content and Composition of the Yakutian Horses and Their Main Food Source: Living in Extreme Winter Conditions. Biomolecules, 2020, 10, 315.	4.0	9
74	Pleistocene Arctic megafaunal ecological engineering as a natural climate solution?. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190122.	4.0	40
75	The complete mitochondrial genome of the extinct Pleistocene horse (Equus cf. lenensis) from Kotelny Island (New Siberian Islands, Russia) and its phylogenetic assessment. Mitochondrial DNA Part B: Resources, 2020, 5, 243-245.	0.4	3
76	Ancient Genomes Reveal the Evolutionary History and Origin of Cashmere-Producing Goats in China. Molecular Biology and Evolution, 2020, 37, 2099-2109.	8.9	29
77	Genomics and the Evolutionary History of Equids. Annual Review of Animal Biosciences, 2021, 9, 81-101.	7.4	22
78	Genome-wide scan for selective footprints and genes related to cold tolerance in Chantecler chickens. Zoological Research, 2021, 42, 710-720.	2.1	15
80	Traces of Late Bronze and Early Iron Age Mongolian Horse Mitochondrial Lineages in Modern Populations. Genes, 2021, 12, 412.	2.4	7
81	Demographic History, Adaptation, and NRAP Convergent Evolution at Amino Acid Residue 100 in the World Northernmost Cattle from Siberia. Molecular Biology and Evolution, 2021, 38, 3093-3110.	8.9	27

ARTICLE

IF CITATIONS

84 Morphometric and genetic analyses of diversity of the Lena horse (Equus lenensis Russanov, 1968;) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5

85	Genomics of Adaptations in Ungulates. Animals, 2021, 11, 1617.	2.3	3
86	Ancient horse genomes reveal the timing and extent of dispersals across the Bering Land Bridge. Molecular Ecology, 2021, 30, 6144-6161.	3.9	30
87	Insights into cold tolerance in sable (Martes zibellina) from the adaptive evolution of lipid metabolism. Mammalian Biology, 0, , 1.	1.5	2
88	From the Eurasian Steppes to the Roman Circuses: A Review of Early Development of Horse Breeding and Management. Animals, 2021, 11, 1859.	2.3	14
89	Exceptional ancient DNA preservation and fibre remains of a Sasanian saltmine sheep mummy in ChehrÄbÄd, Iran. Biology Letters, 2021, 17, 20210222.	2.3	7
90	Whole genome sequencing reveals a complex introgression history and the basis of adaptation to subarctic climate in wild sheep. Molecular Ecology, 2021, 30, 6701-6717.	3.9	12
91	Sporadic occurrence of recent selective sweeps from standing variation in humans as revealed by an approximate Bayesian computation approach. Genetics, 2021, 219, .	2.9	2
92	Whole-Genome Resequencing Points to Candidate DNA Loci Affecting Body Temperature under Cold Stress in Siberian Cattle Populations. Life, 2021, 11, 959.	2.4	8
95	Late Quaternary dynamics of Arctic biota from ancient environmental genomics. Nature, 2021, 600, 86-92.	27.8	81
96	The origins and spread of domestic horses from the Western Eurasian steppes. Nature, 2021, 598, 634-640.	27.8	142
97	Genomic regions under selection for important traits in domestic horse breeds. Frontiers of Agricultural Science and Engineering, 2017, 4, 289.	1.4	2
99	Neanderthal and Woolly Mammoth Molecular Resemblance: Genetic Similarities May Underlie Cold Adaptation Suite. Human Biology, 2018, 90, 115.	0.2	0
104	Origin and Diffusion of Equus caballus from the Archaeological and Genetic Perspectives. Anatomy & Biological Anthropology, 2020, 33, 57.	0.3	1
105	Revisiting the Evolutionary History of Pigs via De Novo Mutation Rate Estimation in A Three-generation Pedigree. Genomics, Proteomics and Bioinformatics, 2022, 20, 1040-1052.	6.9	9
106	MIS $3\hat{a}\in 1$ fauna from Krosinko: Implications for the past biogeography, chronology and palaeoenvironments of Poland. Quaternary International, 2022, , .	1.5	2
107	Assessing the impact of USERâ€ŧreatment on hyRAD capture applied to ancient DNA. Molecular Ecology Resources, 2022, 22, 2262-2274.	4.8	2
110	Radiocarbon and genomic evidence for the survival of Equus Sussemionus until the late Holocene. ELife, 2022, 11, .	6.0	6

ARTICLE

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112	IN SEARCH OF MYTH AND REAL HISTORICAL EVENTS. Siberian Research, 2022, 7, 38-44.	0.1	0
114	mapDATAge: a ShinyR package to chart ancient DNA data through space and time. Bioinformatics, 2022, 38, 3992-3994.	4.1	3
115	Genome-wide analysis reveals selection signatures for body size and drought adaptation in Liangzhou donkey. Genomics, 2022, 114, 110476.	2.9	5
116	Genome-wide analysis identified candidate variants and genes associated with heat stress adaptation in Egyptian sheep breeds. Frontiers in Genetics, 0, 13, .	2.3	6
117	Genomic and transcriptomic analyses reveal genetic adaptation to cold conditions in the chickens. Genomics, 2022, 114, 110485.	2.9	5
118	Animal board invited review: Genomic-based improvement of cattle in response to climate change. Animal, 2022, 16, 100673.	3.3	11
119	Markhor-derived Introgression of a Genomic Region Encompassing <i>PAPSS2</i> Confers High-altitude Adaptability in Tibetan Goats. Molecular Biology and Evolution, 2022, 39, .	8.9	9
121	Unlocking Horse Y Chromosome Diversity. Genes, 2022, 13, 2272.	2.4	3
122	Wholeâ€genome identification of transposable elements reveals the equine repetitive element insertion polymorphism in Chinese horses. Animal Genetics, 0, , .	1.7	0
123	187. Markhor-derived introgression of <i>PAPSS2</i> confers high-altitude adaptability in Tibetan goats. , 2022, , .		0
124	747. Selection signatures in South African indigenous sheep using the HAPFLK approach. , 2022, , .		0
125	Early dispersal of domestic horses into the Great Plains and northern Rockies. Science, 2023, 379, 1316-1323.	12.6	8
126	Evolutionary rescue in a fluctuating environment: periodic versus quasi-periodic environmental changes. Proceedings of the Royal Society B: Biological Sciences, 2023, 290, .	2.6	3
127	A method to generate capture baits for targeted sequencing. Nucleic Acids Research, 2023, 51, e69-e69.	14.5	1
128	New genomic insights into the conformation of Lipizzan horses. Scientific Reports, 2023, 13, .	3.3	1
130	Genetic diversity and signatures of selection in four indigenous horse breeds of Iran. Heredity, 2023, 131, 96-108.	2.6	2
131	Imputed genomes of historical horses provide insights into modern breeding. IScience, 2023, 26, 107104.	4.1	2

IF CITATIONS ARTICLE # Genetic variation and domestication of horses revealed by 10 chromosomeâ€level genomes and 132 4.8 2 wholeâ€genome resequencing. Molecular Ecology Resources, 0, , . Equid Adaptations to Cold Environments. Fascinating Life Sciences, 2023, , 209-246. On Humanity and Equids: Ecologies, Trajectories, and Relationships. Fascinating Life Sciences, 2023, , 134 0.9 0 379-410. The Characteristics, Distribution, Function, and Origin of Alternative Lateral Horse Gaits. Animals, The Genetic Diversity of Horse Native Breeds in Russia. Genes, 2023, 14, 2148. 137 2.4 0 Genome-wide selection signatures address trait specific candidate genes in cattle indigenous to arid regions of India. Animal Biotechnology, 2024, 35, . 1.5 Modeling Climate Change Effects on Genetic Diversity of an Endangered Horse Breed Using Canonical 139 2.3 0 Correlations. Animals, 2024, 14, 659.

CITATION REPORT