

No evidence that selection has been less effective at removing deleterious mutations in Europeans than in Africans

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Characteristics of Neutral and Deleterious Protein-Coding Variation among Individuals and Populations. <i>American Journal of Human Genetics</i> , 2014, 95, 421-436.	2.6	89
2	Genetic diversity in humans and non-human primates and its evolutionary consequences. <i>Genes and Genetic Systems</i> , 2015, 90, 133-145.	0.2	27
3	A General Model of the Relationship between the Apportionment of Human Genetic Diversity and the Apportionment of Human Phenotypic Diversity. <i>Human Biology</i> , 2015, 87, 313.	0.4	19
4	Secondary findings and carrier test frequencies in a large multiethnic sample. <i>Genome Medicine</i> , 2015, 7, 54.	3.6	47
6	Dominance of Deleterious Alleles Controls the Response to a Population Bottleneck. <i>PLoS Genetics</i> , 2015, 11, e1005436.	1.5	78
7	Global diversity, population stratification, and selection of human copy-number variation. <i>Science</i> , 2015, 349, aab3761.	6.0	293
8	Whole-Genome Sequencing of Six Mauritian Cynomolgus Macaques (<i>Macaca fascicularis</i>) Reveals a Genome-Wide Pattern of Polymorphisms under Extreme Population Bottleneck. <i>Genome Biology and Evolution</i> , 2015, 7, 821-830.	1.1	37
9	Origin and dynamics of admixture in Brazilians and its effect on the pattern of deleterious mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8696-8701.	3.3	206
10	Estimating the mutation load in human genomes. <i>Nature Reviews Genetics</i> , 2015, 16, 333-343.	7.7	233
11	The Accumulation of Deleterious Mutations as a Consequence of Domestication and Improvement in Sunflowers and Other Compositae Crops. <i>Molecular Biology and Evolution</i> , 2015, 32, 2273-2283.	3.5	139
12	A global reference for human genetic variation. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
13	The role of climate and out-of-Africa migration in the frequencies of risk alleles for 21 human diseases. <i>BMC Genetics</i> , 2015, 16, 81.	2.7	7
14	Expansion load: recessive mutations and the role of standing genetic variation. <i>Molecular Ecology</i> , 2015, 24, 2084-2094.	2.0	152
15	Selection and explosive growth alter genetic architecture and hamper the detection of causal rare variants. <i>Genome Research</i> , 2016, 26, 863-873.	2.4	63
16	Understanding rare and common diseases in the context of human evolution. <i>Genome Biology</i> , 2016, 17, 225.	3.8	76
17	Secondary structure impacts patterns of selection in human lncRNAs. <i>BMC Biology</i> , 2016, 14, 60.	1.7	43
18	When Is Selection Effective?. <i>Genetics</i> , 2016, 203, 451-462.	1.2	73
19	Genetics of Type 2 Diabetes: the Power of Isolated Populations. <i>Current Diabetes Reports</i> , 2016, 16, 65.	1.7	25

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20	The Genetic Cost of Neanderthal Introgression. <i>Genetics</i> , 2016, 203, 881-891.	1.2	342
21	Genetic surfing in human populations: from genes to genomes. <i>Current Opinion in Genetics and Development</i> , 2016, 41, 53-61.	1.5	48
22	Evolutionary History, Selective Sweeps, and Deleterious Variation in the Dog. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2016, 47, 73-96.	3.8	37
23	Population Genomics Reveals Low Genetic Diversity and Adaptation to Hypoxia in Snub-Nosed Monkeys. <i>Molecular Biology and Evolution</i> , 2016, 33, 2670-2681.	3.5	69
24	Variation in the molecular clock of primates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10607-10612.	3.3	189
25	The Simons Genome Diversity Project: 300 genomes from 142 diverse populations. <i>Nature</i> , 2016, 538, 201-206.	13.7	1,216
26	Characterization of Greater Middle Eastern genetic variation for enhanced disease gene discovery. <i>Nature Genetics</i> , 2016, 48, 1071-1076.	9.4	314
28	A continuum of admixture in the Western Hemisphere revealed by the African Diaspora genome. <i>Nature Communications</i> , 2016, 7, 12522.	5.8	136
29	Challenges and disparities in the application of personalized genomic medicine to populations with African ancestry. <i>Nature Communications</i> , 2016, 7, 12521.	5.8	68
30	Recent demography drives changes in linked selection across the maize genome. <i>Nature Plants</i> , 2016, 2, 16084.	4.7	111
31	The impact of recent population history on the deleterious mutation load in humans and close evolutionary relatives. <i>Current Opinion in Genetics and Development</i> , 2016, 41, 150-158.	1.5	89
32	Patterns of deleterious variation between human populations reveal an unbalanced load. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 809-811.	3.3	2
33	Human Knockout Carriers: Dead, Diseased, Healthy, or Improved?. <i>Trends in Molecular Medicine</i> , 2016, 22, 341-351.	3.5	31
34	Health and population effects of rare gene knockouts in adult humans with related parents. <i>Science</i> , 2016, 352, 474-477.	6.0	272
35	The Limits of Natural Selection in a Nonequilibrium World. <i>Trends in Genetics</i> , 2016, 32, 201-210.	2.9	98
36	Distance from sub-Saharan Africa predicts mutational load in diverse human genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E440-9.	3.3	224
37	Bottlenecks and selective sweeps during domestication have increased deleterious genetic variation in dogs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 152-157.	3.3	265
38	Europeans have a higher proportion of high-frequency deleterious variants than Africans. <i>Human Genetics</i> , 2016, 135, 1-7.	1.8	15

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39	Local Adaptation Interacts with Expansion Load during Range Expansion: Maladaptation Reduces Expansion Load. <i>American Naturalist</i> , 2017, 189, 368-380.	1.0	88
40	Deleterious variants in Asian rice and the potential cost of domestication. <i>Molecular Biology and Evolution</i> , 2017, 34, msw296.	3.5	68
41	The Effect of an Extreme and Prolonged Population Bottleneck on Patterns of Deleterious Variation: Insights from the Greenlandic Inuit. <i>Genetics</i> , 2017, 205, 787-801.	1.2	54
42	An evolutionary medicine perspective on Neandertal extinction. <i>Journal of Human Evolution</i> , 2017, 108, 62-71.	1.3	16
43	Estimating the selective effects of heterozygous protein-truncating variants from human exome data. <i>Nature Genetics</i> , 2017, 49, 806-810.	9.4	157
44	Genetic Diversity and the Efficacy of Purifying Selection across Plant and Animal Species. <i>Molecular Biology and Evolution</i> , 2017, 34, 1417-1428.	3.5	142
45	Living in an adaptive world: Genomic dissection of the genus <i>Homo</i> and its immune response. <i>Journal of Experimental Medicine</i> , 2017, 214, 877-894.	4.2	34
46	Gene Discovery for Complex Traits: Lessons from Africa. <i>Cell</i> , 2017, 171, 261-264.	13.5	27
47	A Temporal Perspective on the Interplay of Demography and Selection on Deleterious Variation in Humans. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1027-1037.	0.8	14
48	Range Expansion Compromises Adaptive Evolution in an Outcrossing Plant. <i>Current Biology</i> , 2017, 27, 2544-2551.e4.	1.8	75
49	Accumulation of Deleterious Mutations During Bacterial Range Expansions. <i>Genetics</i> , 2017, 207, 669-684.	1.2	74
50	Inference of the Distribution of Selection Coefficients for New Nonsynonymous Mutations Using Large Samples. <i>Genetics</i> , 2017, 206, 345-361.	1.2	170
51	The impact of recombination on human mutation load and disease. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160465.	1.8	31
52	Enrichment of low-frequency functional variants revealed by whole-genome sequencing of multiple isolated European populations. <i>Nature Communications</i> , 2017, 8, 15927.	5.8	64
53	Rapid evolution of the human mutation spectrum. <i>ELife</i> , 2017, 6, .	2.8	144
54	Bioinformatically predicted deleterious mutations reveal complementation in the interior spruce hybrid complex. <i>BMC Genomics</i> , 2017, 18, 970.	1.2	16
55	The interplay of demography and selection during maize domestication and expansion. <i>Genome Biology</i> , 2017, 18, 215.	3.8	172
56	Natural selection interacts with recombination to shape the evolution of hybrid genomes. <i>Science</i> , 2018, 360, 656-660.	6.0	314

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57	Elevated Proportions of Deleterious Genetic Variation in Domestic Animals and Plants. <i>Genome Biology and Evolution</i> , 2018, 10, 276-290.	1.1	75
58	On the decidability of population size histories from finite allele frequency spectra. <i>Theoretical Population Biology</i> , 2018, 120, 42-51.	0.5	16
59	The demographic history and mutational load of African hunter-gatherers and farmers. <i>Nature Ecology and Evolution</i> , 2018, 2, 721-730.	3.4	38
60	Slightly deleterious genomic variants and transcriptome perturbations in Down syndrome embryonic selection. <i>Genome Research</i> , 2018, 28, 1-10.	2.4	36
61	Relaxed Selection During a Recent Human Expansion. <i>Genetics</i> , 2018, 208, 763-777.	1.2	49
62	Deleterious variation shapes the genomic landscape of introgression. <i>PLoS Genetics</i> , 2018, 14, e1007741.	1.5	95
63	Patterns of variation in cis-regulatory regions: examining evidence of purifying selection. <i>BMC Genomics</i> , 2018, 19, 95.	1.2	8
64	Frequency of genetic variants associated with arrhythmogenic right ventricular cardiomyopathy in the genome aggregation database. <i>European Journal of Human Genetics</i> , 2018, 26, 1312-1318.	1.4	31
65	Human demographic history has amplified the effects of background selection across the genome. <i>PLoS Genetics</i> , 2018, 14, e1007387.	1.5	71
66	Nearly Neutral Evolution across the <i>Drosophila melanogaster</i> Genome. <i>Molecular Biology and Evolution</i> , 2018, 35, 2685-2694.	3.5	32
67	Direct Evidence of an Increasing Mutational Load in Humans. <i>Molecular Biology and Evolution</i> , 2019, 36, 2823-2829.	3.5	12
68	Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. <i>Cell</i> , 2019, 179, 984-1002.e36.	13.5	152
69	Linked Mutations at Adjacent Nucleotides Have Shaped Human Population Differentiation and Protein Evolution. <i>Genome Biology and Evolution</i> , 2019, 11, 759-775.	1.1	9
70	Allele frequency of pathogenic variants related to adult-onset Mendelian diseases. <i>Clinical Genetics</i> , 2019, 96, 226-235.	1.0	4
71	Applicability of the Mutation-Selection Balance Model to Population Genetics of Heterozygous Protein-Truncating Variants in Humans. <i>Molecular Biology and Evolution</i> , 2019, 36, 1701-1710.	3.5	27
72	Stability of petal color polymorphism: the significance of anthocyanin accumulation in photosynthetic tissues. <i>BMC Plant Biology</i> , 2019, 19, 496.	1.6	18
73	Population size influences the type of nucleotide variations in humans. <i>BMC Genetics</i> , 2019, 20, 93.	2.7	2
74	Multiple episodes of interbreeding between Neanderthal and modern humans. <i>Nature Ecology and Evolution</i> , 2019, 3, 39-44.	3.4	148

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75	Exploring rare and low-frequency variants in the Saguenayâ€“Lac-Saint-Jean population identified genes associated with asthma and allergy traits. <i>European Journal of Human Genetics</i> , 2019, 27, 90-101.	1.4	15
76	Impact of Mutation Rate and Selection at Linked Sites on DNA Variation across the Genomes of Humans and Other Homininae. <i>Genome Biology and Evolution</i> , 2020, 12, 3550-3561.	1.1	18
77	From Drift to Draft: How Much Do Beneficial Mutations Actually Contribute to Predictions of Ohtaâ€™s Slightly Deleterious Model of Molecular Evolution?. <i>Genetics</i> , 2020, 214, 1005-1018.	1.2	25
78	The spatial Mullerâ€™s ratchet: Surfing of deleterious mutations during range expansion. <i>Theoretical Population Biology</i> , 2020, 135, 19-31.	0.5	5
79	Mitochondrial DNA Sequence Diversity in Mammals: A Correlation between the Effective and Census Population Sizes. <i>Genome Biology and Evolution</i> , 2020, 12, 2441-2449.	1.1	13
80	Inference of natural selection from ancient DNA. <i>Evolution Letters</i> , 2020, 4, 94-108.	1.6	58
81	The Temporal Dynamics of Background Selection in Nonequilibrium Populations. <i>Genetics</i> , 2020, 214, 1019-1030.	1.2	23
82	The influence of evolutionary history on human health and disease. <i>Nature Reviews Genetics</i> , 2021, 22, 269-283.	7.7	133
83	Deleterious variants in genes regulating mammalian reproduction in Neanderthals, Denisovans and extant humans. <i>Human Reproduction</i> , 2021, 36, 734-755.	0.4	5
84	Probing the aggregated effects of purifying selection per individual on 1,380 medical phenotypes in the UK Biobank. <i>PLoS Genetics</i> , 2021, 17, e1009337.	1.5	2
85	The inflated significance of neutral genetic diversity in conservation genetics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	222
86	The Counteracting Effects of Demography on Functional Genomic Variation: The Roma Paradigm. <i>Molecular Biology and Evolution</i> , 2021, 38, 2804-2817.	3.5	14
87	Genetic load has potential in large populations but is realized in small inbred populations. <i>Evolutionary Applications</i> , 2021, 14, 1540-1557.	1.5	58
88	Cutaneous and hepatic vascular lesions due to a recurrent somatic GJA4 mutation reveal a pathway for vascular malformation. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100028.	1.0	12
92	Authorsâ€™ Reply to Letter to the Editor: Neutral genetic diversity as a useful tool for conservation biology. <i>Conservation Genetics</i> , 2021, 22, 547-549.	0.8	0
93	Genome of PeÅŸtera Muierii skull shows high diversity and low mutational load in pre-glacial Europe. <i>Current Biology</i> , 2021, 31, 2973-2983.e9.	1.8	18
97	The genetic consequences of dog breed formationâ€“Accumulation of deleterious genetic variation and fixation of mutations associated with myxomatous mitral valve disease in cavalier King Charles spaniels. <i>PLoS Genetics</i> , 2021, 17, e1009726.	1.5	12
98	Bottleneckâ€“associated changes in the genomic landscape of genetic diversity in wild lynx populations. <i>Evolutionary Applications</i> , 2021, 14, 2664-2679.	1.5	7

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99	Demographic history and patterns of molecular evolution from whole genome sequencing in the radiation of Galapagos giant tortoises. <i>Molecular Ecology</i> , 2021, 30, 6325-6339.	2.0	7
100	Genomic signatures of inbreeding and mutation load in a threatened rattlesnake. <i>Molecular Ecology</i> , 2021, 30, 5454-5469.	2.0	20
101	Maintenance of Adaptive Dynamics and No Detectable Load in a Range-Edge Outcrossing Plant Population. <i>Molecular Biology and Evolution</i> , 2021, 38, 1820-1836.	3.5	24
119	The Strength of Selection against Neanderthal Introgression. <i>PLoS Genetics</i> , 2016, 12, e1006340.	1.5	257
120	Inference of Candidate Germline Mutator Loci in Humans from Genome-Wide Haplotype Data. <i>PLoS Genetics</i> , 2017, 13, e1006549.	1.5	22
121	Genetic Variants in DNA Double-Strand Break Repair Genes and Risk of Salivary Gland Carcinoma: A Case-Control Study. <i>PLoS ONE</i> , 2015, 10, e0128753.	1.1	4
122	Evolutionary genomics of epidemic visceral leishmaniasis in the Indian subcontinent. <i>ELife</i> , 2016, 5, .	2.8	147
123	The comparative population genetics of <i>Neisseria meningitidis</i> and <i>Neisseria gonorrhoeae</i> . <i>PeerJ</i> , 2019, 7, e7216.	0.9	20
143	Whole-exome analysis in Tunisian Imazighen and Arabs shows the impact of demography in functional variation. <i>Scientific Reports</i> , 2021, 11, 21125.	1.6	4
144	Not out of the woods yet: Signatures of the prolonged negative genetic consequences of a population bottleneck in a rapidly re-expanding wader, the black-faced spoonbill <i>Platalea minor</i> . <i>Molecular Ecology</i> , 2022, 31, 529-545.	2.0	3
146	Genomic evidence for inbreeding depression and purging of deleterious genetic variation in Indian tigers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	80
147	Overcoming constraints on the detection of recessive selection in human genes from population frequency data. <i>American Journal of Human Genetics</i> , 2022, 109, 33-49.	2.6	5
148	Genomic analyses reveal range-wide devastation of sea otter populations. <i>Molecular Ecology</i> , 2023, 32, 281-298.	2.0	12
149	Haplotype-based inference of the distribution of fitness effects. <i>Genetics</i> , 2022, 220, .	1.2	1
150	Dominance Can Increase Genetic Variance After a Population Bottleneck: A Synthesis of the Theoretical and Empirical Evidence. <i>Journal of Heredity</i> , 2022, 113, 257-271.	1.0	2
151	Genetic load: genomic estimates and applications in non-model animals. <i>Nature Reviews Genetics</i> , 2022, 23, 492-503.	7.7	82
152	Purging of deleterious burden in the endangered Iberian lynx. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2110614119.	3.3	32
153	Ancient Demographics Determine the Effectiveness of Genetic Purging in Endangered Lizards. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	22

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155	The critically endangered vaquita is not doomed to extinction by inbreeding depression. <i>Science</i> , 2022, 376, 635-639.	6.0	49
158	Evaluating the persistence and utility of five wild <i>Vitis</i> species in the context of climate change. <i>Molecular Ecology</i> , 2022, 31, 6457-6472.	2.0	7
159	Deleterious Variation in Natural Populations and Implications for Conservation Genetics. <i>Annual Review of Animal Biosciences</i> , 2023, 11, 93-114.	3.6	32
162	Insights into the differentiation and adaptation within Circaeasteraceae from <i>Circaeaster agrestis</i> genome sequencing and resequencing. <i>IScience</i> , 2023, 26, 106159.	1.9	0
163	An evolutionary perspective on genetic load in small, isolated populations as informed by whole genome resequencing and forward-time simulations. <i>Evolution; International Journal of Organic Evolution</i> , 2023, 77, 690-704.	1.1	13
164	The efficacy of selection may increase or decrease with selfing depending upon the recombination environment. <i>Evolution; International Journal of Organic Evolution</i> , 2023, 77, 394-408.	1.1	3
165	Inbreeding depression explains killer whale population dynamics. <i>Nature Ecology and Evolution</i> , 2023, 7, 675-686.	3.4	24
166	Population genomic analysis provides evidence of the past success and future potential of South China tiger captive conservation. <i>BMC Biology</i> , 2023, 21, .	1.7	3