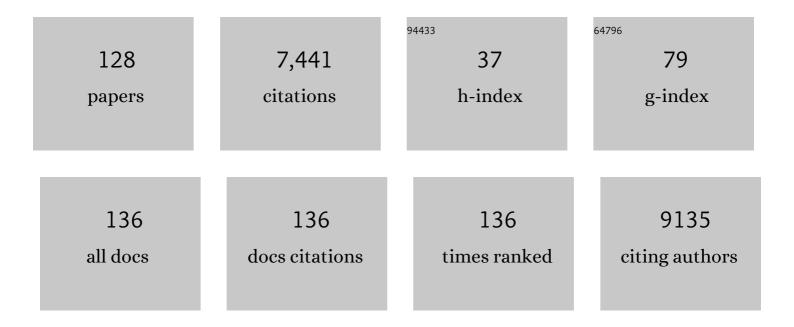
Armando Caballero

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Prediction of fitness under different breeding designs in conservation programs. Animal Conservation, 2023, 26, 86-102.	2.9	3
2	Reviewing the consequences of genetic purging on the success of rescue programs. Conservation Genetics, 2022, 23, 1-17.	1.5	19
3	Obituary in memoriam of Professor William G. (Bill) Hill. Heredity, 2022, 128, 77-78.	2.6	0
4	The estimates of effective population size based on linkage disequilibrium are virtually unaffected by natural selection. PLoS Genetics, 2022, 18, e1009764.	3.5	21
5	Prediction of the minimum effective size of a population viable in the long term. Biodiversity and Conservation, 2022, 31, 2763-2780.	2.6	14
6	An evaluation of inbreeding measures using a whole-genome sequenced cattle pedigree. Heredity, 2021, 126, 410-423.	2.6	46
7	On the estimation of inbreeding depression using different measures of inbreeding from molecular markers. Evolutionary Applications, 2021, 14, 416-428.	3.1	35
8	The value of genomic relationship matrices to estimate levels of inbreeding. Genetics Selection Evolution, 2021, 53, 42.	3.0	31
9	Neutral genetic diversity as a useful tool for conservation biology. Conservation Genetics, 2021, 22, 541-545.	1.5	49
10	Highly pleiotropic variants of human traits are enriched in genomic regions with strong background selection. Human Genetics, 2021, 140, 1343-1351.	3.8	3
11	Long-term exhaustion of the inbreeding load in Drosophila melanogaster. Heredity, 2021, 127, 373-383.	2.6	20
12	Estimates of recent and historical effective population size in turbot, seabream, seabass and carp selective breeding programmes. Genetics Selection Evolution, 2021, 53, 85.	3.0	23
13	Mate Choice Contributes to the Maintenance of Shell Color Polymorphism in a Marine Snail via Frequency-Dependent Sexual Selection. Frontiers in Marine Science, 2020, 7, .	2.5	13
14	The value of targeting recombination as a strategy against coronavirus diseases. Heredity, 2020, 125, 169-172.	2.6	6
15	Recent Demographic History Inferred by High-Resolution Analysis of Linkage Disequilibrium. Molecular Biology and Evolution, 2020, 37, 3642-3653.	8.9	141
16	GWEHS: A Genome-Wide Effect Sizes and Heritability Screener. Genes, 2019, 10, 558.	2.4	2
17	Accelerated inbreeding depression suggests synergistic epistasis for deleterious mutations in Drosophila melanogaster. Heredity, 2019, 123, 709-722.	2.6	13
18	Optimal Management of Genetic Diversity in Subdivided Populations. Frontiers in Genetics, 2019, 10, 843.	2.3	24

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19	Inferring the Nature of Missing Heritability in Human Traits Using Data from the GWAS Catalog. Genetics, 2019, 212, 891-904.	2.9	34
20	Untangling the contribution of genetic and environmental effects to shell differentiation across an environmental cline in a marine snail. Journal of Experimental Marine Biology and Ecology, 2019, 513, 27-34.	1.5	11
21	<scp>metapop</scp> 2: Reâ€implementation of software for the analysis and management of subdivided populations using gene and allelic diversity. Molecular Ecology Resources, 2019, 19, 1095-1100.	4.8	35
22	Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection. Nature Genetics, 2018, 50, 381-389.	21.4	1,332
23	Population genomics of parallel evolution in gene expression and gene sequence during ecological adaptation. Scientific Reports, 2018, 8, 16147.	3.3	12
24	The risk of forcing inbreeding in conservation programmes: a reply to Theodorou and Couvet. Heredity, 2017, 119, 51-53.	2.6	3
25	Can parallel ecological speciation be detected with phylogenetic analyses?. Molecular Phylogenetics and Evolution, 2017, 116, 149-156.	2.7	11
26	Inbreeding load and purging: implications for the short-term survival and the conservation management of small populations. Heredity, 2017, 118, 177-185.	2.6	75
27	Estimation of genetic purging under competitive conditions. Evolution; International Journal of Organic Evolution, 2016, 70, 1856-1870.	2.3	31
28	On the Consequences of Purging and Linkage on Fitness and Genetic Diversity. G3: Genes, Genomes, Genetics, 2016, 6, 171-181.	1.8	22
29	Joint Prediction of the Effective Population Size and the Rate of Fixation of Deleterious Mutations. Genetics, 2016, 204, 1267-1279.	2.9	13
30	Prediction and estimation of effective population size. Heredity, 2016, 117, 193-206.	2.6	254
31	Allelic diversity for neutral markers retains a higher adaptive potential for quantitative traits than expected heterozygosity. Molecular Ecology, 2015, 24, 4419-4432.	3.9	59
32	The Nature of Genetic Variation for Complex Traits Revealed by GWAS and Regional Heritability Mapping Analyses. Genetics, 2015, 201, 1601-1613.	2.9	58
33	THE ACTION OF STABILIZING SELECTION, MUTATION, AND DRIFT ON EPISTATIC QUANTITATIVE TRAITS. Evolution; International Journal of Organic Evolution, 2014, 68, 1974-1987.	2.3	11
34	PARALLEL EVOLUTION OF LOCAL ADAPTATION AND REPRODUCTIVE ISOLATION IN THE FACE OF GENE FLOW. Evolution; International Journal of Organic Evolution, 2014, 68, 935-949.	2.3	165
35	Impact of deep coalescence and recombination on the estimation of phylogenetic relationships among species using AFLP markers. Molecular Phylogenetics and Evolution, 2014, 76, 102-109.	2.7	3
36	Genomic distribution of AFLP markers relative to gene locations for different eukaryotic species. BMC Genomics, 2013, 14, 528.	2.8	19

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37	An experimental assessment of artificial within-family selection for fitness in conservation programs. Conservation Genetics, 2013, 14, 1149-1159.	1.5	5
38	Are transcriptional responses to inbreeding a functional response to alleviate inbreeding depression?. Fly, 2013, 7, 8-12.	1.7	9
39	Allelic Diversity and Its Implications for the Rate of Adaptation. Genetics, 2013, 195, 1373-1384.	2.9	91
40	Efficiency of Conservation Management Methods for Subdivided Populations under Local Adaptation. Journal of Heredity, 2013, 104, 554-564.	2.4	5
41	Candidate Transcriptomic Sources of Inbreeding Depression in Drosophila melanogaster. PLoS ONE, 2013, 8, e70067.	2.5	5
42	Gene-Expression Changes Caused by Inbreeding Protect Against Inbreeding Depression in <i>Drosophila</i> . Genetics, 2012, 192, 161-172.	2.9	18
43	Dietary effects on shell growth and shape in an intertidal marine snail, Littorina saxatilis. Journal of Molluscan Studies, 2012, 78, 213-216.	1.2	9
44	Analysis and Management of Gene and Allelic Diversity in Subdivided Populations Using the Software Program METAPOP. Methods in Molecular Biology, 2012, 888, 261-275.	0.9	4
45	AFLPM ax : a userâ€friendly application for computing the optimal number of amplified fragment length polymorphism markers needed in phylogenetic reconstruction. Molecular Ecology Resources, 2012, 12, 566-569.	4.8	3
46	A simulation study on the performance of differentiationâ€based methods to detect selected loci using linked neutral markers. Journal of Evolutionary Biology, 2012, 25, 1364-1376.	1.7	53
47	The relative contribution of band number to phylogenetic accuracy in AFLP data sets. Journal of Evolutionary Biology, 2011, 24, 2346-2356.	1.7	9
48	An experimental evaluation with Drosophila melanogaster of a novel dynamic system for the management of subdivided populations in conservation programs. Heredity, 2011, 106, 765-774.	2.6	8
49	Lack of early laboratory postzygotic reproductive isolation between two ecotypes of Littorina saxatilis (Mollusca, Gastropoda) showing strong premating sexual isolation. Hydrobiologia, 2011, 675, 13-18.	2.0	8
50	Management of genetic diversity of subdivided populations in conservation programmes. Conservation Genetics, 2010, 11, 409-419.	1.5	117
51	A new method for the partition of allelic diversity within and between subpopulations. Conservation Genetics, 2010, 11, 2219-2229.	1.5	36
52	Predictions of response to selection caused by angling in a wild population of Atlantic salmon (<i>Salmo salar</i>). Freshwater Biology, 2010, 55, 923-930.	2.4	29
53	Comparing three different methods to detect selective loci using dominant markers. Journal of Evolutionary Biology, 2010, 23, 2267-2276.	1.7	177
54	Homoplasy and Distribution of AFLP Fragments: An Analysis In Silico of the Genome of Different Species. Molecular Biology and Evolution, 2010, 27, 1139-1151.	8.9	24

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55	Evaluating the Relationship between Evolutionary Divergence and Phylogenetic Accuracy in AFLP Data Sets. Molecular Biology and Evolution, 2010, 27, 988-1000.	8.9	35
56	The Action of Purifying Selection, Mutation and Drift on Fitness Epistatic Systems. Genetics, 2009, 183, 299-313.	2.9	21
57	METAPOP—A software for the management and analysis of subdivided populations in conservation programs. Conservation Genetics, 2009, 10, 1097-1099.	1.5	35
58	RELATIVE ROLE OF GENETIC DETERMINATION AND PLASTIC RESPONSE DURING ONTOGENY FOR SHELL-SHAPE TRAITS SUBJECTED TO DIVERSIFYING SELECTION. Evolution; International Journal of Organic Evolution, 2009, 63, 1356-1363.	2.3	39
59	Molecular characterization of breeds and its use in conservation. Livestock Science, 2009, 120, 174-195.	1.6	140
60	A First Insight into the In Silico Evaluation of the Accuracy of AFLP Markers for Phylogenetic Reconstruction. Lecture Notes in Computer Science, 2009, , 1143-1146.	1.3	0
61	Genetic diversity and effective size of the Atlantic salmon Salmo salar L. inhabiting the River Eo (Spain) following a stock collapse. Journal of Fish Biology, 2008, 72, 1933-1944.	1.6	10
62	Impact of precocious male parr on the effective size of a wild population of Atlantic salmon. Freshwater Biology, 2008, 53, 2375-2384.	2.4	38
63	Preserving Population Allele Frequencies in Ex Situ Conservation Programs. Conservation Biology, 2008, 22, 1277-1287.	4.7	40
64	Genetic impact of the Prestige oil spill in wild populations of a poor dispersal marine snail from intertidal rocky shores. Marine Pollution Bulletin, 2008, 56, 270-281.	5.0	25
65	The relationship between hatching rate and number of embryos of the brood pouch in Littorina saxatilis. Journal of Sea Research, 2008, 60, 223-225.	1.6	10
66	Management of Subdivided Populations in Conservation Programs: Development of a Novel Dynamic System. Genetics, 2008, 179, 683-692.	2.9	108
67	Impact of Amplified Fragment Length Polymorphism Size Homoplasy on the Estimation of Population Genetic Diversity and the Detection of Selective Loci. Genetics, 2008, 179, 539-554.	2.9	129
68	Genetic discontinuity associated with an environmentally induced barrier to gene exchange in the marine snail Littorina saxatilis. Marine Ecology - Progress Series, 2008, 357, 175-184.	1.9	20
69	PHYLOGENETIC EVIDENCE FOR MULTIPLE SYMPATRIC ECOLOGICAL DIVERSIFICATION IN A MARINE SNAIL. Evolution; International Journal of Organic Evolution, 2007, 61, 1600-1612.	2.3	93
70	Genetic variation for shell traits in a direct-developing marine snail involved in a putative sympatric ecological speciation process. Evolutionary Ecology, 2007, 21, 635-650.	1.2	41
71	The accuracy of a heritability estimator using molecular information. Conservation Genetics, 2007, 8, 1189-1198.	1.5	17
72	Palliating the impact of fixation of a major gene on the genetic variation of artificially selected polygenes. Genetical Research, 2006, 88, 105-118.	0.9	11

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73	Analysis of the biases in the estimation of deleterious mutation parameters from natural populations at mutation–selection balance. Genetical Research, 2006, 88, 177.	0.9	1
74	Genetic variation in restored Atlantic salmon (Salmo salar L.) populations in the Ulla and Lérez rivers, Galicia, Spain. ICES Journal of Marine Science, 2006, 63, 1290-1296.	2.5	16
75	Relaxation of Selection With Equalization of Parental Contributions in Conservation Programs: An Experimental Test With Drosophila melanogaster. Genetics, 2006, 172, 1043-1054.	2.9	28
76	Estimation of the upper limit of the mutation rate and mean heterozygous effect of deleterious mutations. Genetical Research, 2006, 88, 137.	0.9	2
77	The evolutionary forces maintaining a wild polymorphism of Littorina saxatilis: model selection by computer simulations. Journal of Evolutionary Biology, 2005, 18, 191-202.	1.7	22
78	Comparing the estimation properties of different statistics for measuring sexual isolation from mating frequencies. Biological Journal of the Linnean Society, 2005, 85, 307-318.	1.6	46
79	Habitat-dependent Ecotype Micro-distribution at the Mid-shore in Natural Populations of Littorina saxatilis. Hydrobiologia, 2005, 548, 307-311.	2.0	16
80	The Effect of Antagonistic Pleiotropy on the Estimation of the Average Coefficient of Dominance of Deleterious Mutations. Genetics, 2005, 171, 2097-2112.	2.9	11
81	Variation After a Selective Sweep in a Subdivided Population. Genetics, 2005, 169, 475-483.	2.9	76
82	Genetic Differentiation and Estimation of Effective Population Size and Migration Rates in Two Sympatric Ecotypes of the Marine Snail Littorina saxatilis. Journal of Heredity, 2005, 96, 460-464.	2.4	10
83	Characterization and conservation of genetic diversity in subdivided populations. Philosophical Transactions of the Royal Society B: Biological Sciences, 2005, 360, 1367-1378.	4.0	208
84	Quantitative variation as a tool for detecting human-induced impacts on genetic diversity. Biological Conservation, 2005, 124, 1-13.	4.1	25
85	Analysis of the Estimators of the Average Coefficient of Dominance of Deleterious Mutations. Genetics, 2004, 168, 1053-1069.	2.9	14
86	Mutation-selection balance accounting for genetic variation for viability inDrosophila melanogasteras deduced from an inbreeding and artificial selection experiment. Journal of Evolutionary Biology, 2004, 17, 528-541.	1.7	22
87	Nonallopatric and parallel origin of local reproductive barriers between two snail ecotypes. Molecular Ecology, 2004, 13, 3415-3424.	3.9	104
88	Managing Individuals' Contributions to Maximize the Allelic Diversity Maintained in Small, Conserved Populations. Conservation Biology, 2004, 18, 1358-1367.	4.7	55
89	ON THE PERSISTENCE AND PERVASIVENESS OF A NEW MUTATION. Evolution; International Journal of Organic Evolution, 2003, 57, 2644-2646.	2.3	46
90	A parallel optimization approach for controlling allele diversity in conservation schemes. Mathematical Biosciences, 2003, 183, 161-173.	1.9	16

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91	ON THE PERSISTENCE AND PERVASIVENESS OF A NEW MUTATION. Evolution; International Journal of Organic Evolution, 2003, 57, 2644.	2.3	7
92	The mutational rate of Drosophila viability decline: tinkering with old data. Genetical Research, 2002, 80, 99-105.	0.9	15
93	Analysis of genetic diversity for the management of conserved subdivided populations. Conservation Genetics, 2002, 3, 289-299.	1.5	299
94	A comparison of management strategies for conservation with regard to population fitness. Conservation Genetics, 2001, 2, 121-131.	1.5	39
95	Accumulation of deleterious mutations and equalization of parental contributions in the conservation of genetic resources. Heredity, 2001, 86, 480-488.	2.6	30
96	Interrelations between effective population size and other pedigree tools for the management of conserved populations. Genetical Research, 2000, 75, 331-343.	0.9	362
97	ESTIMATING SEXUAL SELECTION AND SEXUAL ISOLATION EFFECTS FROM MATING FREQUENCIES. Evolution; International Journal of Organic Evolution, 2000, 54, 30-36.	2.3	126
98	Application of Reproduction Technologies to the Conservation of Genetic Resources. Conservation Biology, 2000, 14, 1831-1836.	4.7	7
99	ESTIMATING SEXUAL SELECTION AND SEXUAL ISOLATION EFFECTS FROM MATING FREQUENCIES. Evolution; International Journal of Organic Evolution, 2000, 54, 30.	2.3	48
100	Effect of linkage on the control of inbreeding in selection programmes. Genetics Selection Evolution, 2000, 32, 249-64.	3.0	13
101	Application of Reproduction Technologies to the Conservation of Genetic Resources. Conservation Biology, 2000, 14, 1831-1836.	4.7	4
102	Developments in predicting the effective size of subdivided populations. Heredity, 1999, 82, 212-226.	2.6	180
103	Properties of spontaneous mutations affecting quantitative traits. Genetical Research, 1999, 74, 341-350.	0.9	118
104	Inferences on genome-wide deleterious mutation rates in inbred populations of Drosophila and mice. Genetica, 1998, 102/103, 229-239.	1.1	22
105	Population genetics: Surviving under mutation pressure. Current Biology, 1998, 8, R235-R237.	3.9	31
106	The effect of linkage disequilibrium and deviation from Hardy–Weinberg proportions on the changes in genetic variance with bottlenecking. Heredity, 1998, 81, 174-186.	2.6	1
107	Effective Size and Polymorphism of Linked Neutral Loci in Populations Under Directional Selection. Genetics, 1998, 149, 2105-2117.	2.9	94
108	Bottleneck Effect on Genetic Variance: A Theoretical Investigation of the Role of Dominance. Genetics, 1998, 150, 435-447.	2.9	70

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109	Inferences on genome-wide deleterious mutation rates in inbred populations of Drosophila and mice. Contemporary Issues in Genetics and Evolution, 1998, , 229-239.	0.9	1
110	Genomic mutation rates for lifetime reproductive output and lifespan in <i>Caenorhabditis elegans</i> . Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 3823-3827.	7.1	256
111	Average Dominance for Polygenes: Drawbacks of Regression Estimates. Genetics, 1997, 147, 1487-1490.	2.9	29
112	Systems of mating to reduce inbreeding in selected populations. Animal Science, 1996, 62, 431-442.	1.3	93
113	Survival rates of mutant genes under artificial selection using individual and family information. Journal of Genetics, 1996, 75, 63-80.	0.7	11
114	A Note on the Change in Gene Frequency of a Selected Allele in Partial Full-Sib Mating Populations. Genetics, 1996, 142, 649-650.	2.9	3
115	Selection Response in Finite Populations. Genetics, 1996, 144, 1961-1974.	2.9	53
116	Accumulation of mutations affecting body weight in inbred mouse lines. Genetical Research, 1995, 65, 145-149.	0.9	24
117	Response to selection from new mutation and effective size of partially inbred populations. II. Experiments with Drosophila melanogaster. Genetical Research, 1995, 66, 227-240.	0.9	27
118	Response to selection from new mutation and effective size of partially inbred populations. I. Theoretical results. Genetical Research, 1995, 66, 213-225.	0.9	36
119	A note on using biased parameter values and non-random mating to reduce rates of inbreeding in selection programmes. Animal Science, 1994, 59, 465-468.	1.3	37
120	Developments in the prediction of effective population size. Heredity, 1994, 73, 657-679.	2.6	528
121	A Note on the Inbreeding Effective Population Size. Evolution; International Journal of Organic Evolution, 1992, 46, 1969.	2.3	8
122	The time of detection of recessive visible genes with non-random mating. Genetical Research, 1992, 60, 201-207.	0.9	7
123	A NOTE ON THE INBREEDING EFFECTIVE POPULATION SIZE. Evolution; International Journal of Organic Evolution, 1992, 46, 1969-1972.	2.3	7
124	Strategies for increasing fixation probabilities of recessive mutations. Genetical Research, 1991, 58, 129-138.	0.9	40
125	The cumulative effect of artificial selection on the reduction of population effective size. Journal of Animal Breeding and Genetics, 1990, 107, 180-187.	2.0	3
126	Efficiency in prediction of response in selection index experiments. Journal of Animal Breeding and Genetics, 1989, 106, 187-194.	2.0	6

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127	An experimental evaluation of the usefulness of secondary traits in index selection, using <i>Drosophila melanogaster</i> . Journal of Animal Breeding and Genetics, 1987, 104, 175-179.	2.0	5
128	Looking for a successful translocation: the case of Astragalus edulis. Mediterranean Botany, 0, 42, e68048.	0.9	2