





The long-standing significance of genetic diversity in conservation

J. Andrew DeWoody¹  | Avril M. Harder²  | Samarth Mathur³  |
Janna R. Willoughby² 

¹Department of Forestry and Natural Resources, Department of Biological Sciences, Purdue University, West Lafayette, Indiana, USA

²School of Forestry and Wildlife Sciences, Auburn University, Auburn, Alabama, USA

³Department of Evolution, Ecology and Organismal Biology, The Ohio State University, Columbus, Ohio, USA

Correspondence

J. Andrew DeWoody, Department of Forestry and Natural Resources, Purdue University, West Lafayette, IN, USA.
Email: dewoody@purdue.edu

Funding information

JAD was supported in part by USDA-NIFA.

Abstract

Since allozymes were first used to assess genetic diversity in the 1960s and 1970s, biologists have attempted to characterize gene pools and conserve the diversity observed in domestic crops, livestock, zoos and (more recently) natural populations. Recently, some authors have claimed that the importance of genetic diversity in conservation biology has been greatly overstated. Here, we argue that a voluminous literature indicates otherwise. We address four main points made by detractors of genetic diversity's role in conservation by using published literature to firmly establish that genetic diversity is intimately tied to evolutionary fitness, and that the associated demographic consequences are of paramount importance to many conservation efforts. We think that responsible management in the Anthropocene should, whenever possible, include the conservation of ecosystems, communities, populations and individuals, and their underlying genetic diversity.

KEYWORDS

conservation biology, conservation genetics, population genetics – empirical, population genetics – theoretical

Genetic diversity, along with species and ecosystem diversity, is one of the three main pillars of biodiversity. The realization of genetic diversity's role in the conservation of biodiversity was fuelled by the discovery and characterization of widespread protein variation and the long-observed notion that close inbreeding was associated with declines in fitness (Brown, 1978; Lewontin, 1974). Historically, genetic diversity was characterized using allozyme and later microsatellite loci, and was typically reported as observed heterozygosity, mean allelic diversity and (in allozymes) the proportion of polymorphic loci. More recently, single nucleotide polymorphisms (SNPs) have largely replaced microsatellites. Because SNPs are typically biallelic due to mutation-drift equilibrium, genetic diversity at the nucleotide level is reported as observed heterozygosity or as SNP density. In addition, the distribution of structural variants is emerging as an orthologous measure of

genetic diversity (e.g., Weissensteiner et al., 2020). Whether one considers allozymes, microsatellites, SNPs or structural variants, population geneticists use these empirical assessments of genetic diversity to support one of the core goals of conservation genetics: maintaining genetic diversity across individuals in ways that support persistence of populations and species, even in the face of ongoing threats such as fragmentation and global climate change (Crandall et al., 2000; Moritz, 2002).

Recently, Teixeira and Huber (2021) argued against the perceived importance of neutral genetic diversity for the conservation of wild populations and species. While we respect their Perspective, a deeper dive into decades of conservation genetics literature contradicts many of their arguments. Here, we address four key points made by Teixeira and Huber that are counter to a robust literature focused on the genetics of wild and captive populations.

TABLE 1 Exemplar studies demonstrating positive relationships between genetic diversity and fitness

Species	Ecosystem	GD marker	GD estimator	Reference
Reproductive success				
Atlantic salmon (<i>Salmo salar</i>)	Diadromous	Microsatellite	r	Garant et al. (2005)
Kangaroo rat (<i>Dipodomys spectabilis</i>)	Terrestrial	Pedigree	F, r	Willoughby et al. (2019)
Black stilt (<i>Himantopus novaeseelandiae</i>)	Terrestrial	Microsatellite	H	Hagen et al. (2011)
Grey seal (<i>Halichoerus grypus</i>)	Marine	Microsatellite	r	Pomeroy et al. (2001)
Helmeted honeyeater (<i>Lichenostomus melanops</i>)	Terrestrial	SNP	F	Harrisson et al. (2019)
Kakapo (<i>Strigops habroptilus</i>)	Terrestrial	Microsatellite	r	White et al. (2015)
Leadbeater's possum (<i>Gymnobelideus leadbeateri</i>)	Terrestrial	SNP	H	Zilko et al. (2020)
Little spotted kiwi (<i>Apteryx owenii</i>)	Terrestrial	Microsatellite	H, F, A	Taylor et al. (2017)
Long-finned pilot whale (<i>Globicephala melas</i>)	Marine	Microsatellite	H, r	Amos et al. (2001)
Mandrill (<i>Mandrillus sphinx</i>)	Terrestrial	Microsatellite	H, r	Charpentier et al. (2005)
Mysid shrimp (<i>Americamysis bahia</i>)	Estuarine	Pedigree, AFLP	H, A	Markert et al. (2010)
Red-breasted flycatcher (<i>Ficedula parva</i>)	Terrestrial	Microsatellite	H	Mitrus et al. (2020)
Red deer (<i>Cervus elaphus</i>)	Terrestrial	SNP	F	Huisman et al. (2016)
Wandering albatross (<i>Diomedea exulans</i>)	Terrestrial	Microsatellite	H, r	Amos et al. (2001)
Viability/survival (adults and juveniles)				
Alpine marmot (<i>Marmota m. flaviventris</i>)	Terrestrial	Microsatellite	H	Silva et al. (2006)
Chalk-hill blue butterfly (<i>Polyommatus coridon</i>)	Terrestrial	Microsatellite	H, A	Vandewoestijne et al. (2008)
Chatham Island black robin (<i>Petroica nigra</i>)	Terrestrial	Pedigree	F	Kennedy et al. (2014)
Chinook salmon (<i>Oncorhynchus tshawytscha</i>)	Diadromous	Microsatellite	H	Rosengrave et al. (2016)
Common frog (<i>Rana temporaria</i>)	Terrestrial	Microsatellite	H, A, r	Lesbarreres et al. (2005)
Common toad (<i>Bufo bufo</i>)	Terrestrial	Allozyme	H, A	Hitchings and Beebee (1998)
European tree frog (<i>Hyla arborea</i>)	Terrestrial	Microsatellite	H, F	Andersen et al. (2004)
Florida panther (<i>Puma concolor coryi</i>)	Terrestrial	Microsatellite	H	Johnson et al. (2010)
Glanville fritillary butterfly (<i>Melitaea cinxia</i>)	Terrestrial	Allozyme	H	Saccheri et al. (1998)
Golden eagle (<i>Aquila chrysaetos</i>)	Terrestrial	SNP	H	Doyle et al. (2016)
Golden lion tamarin (<i>Leontopithecus rosalia</i>)	Terrestrial	Pedigree	F	Dietz et al. (2000)
Great reed warbler (<i>Acrocephalus arundinaceus</i>)	Terrestrial	Microsatellite	H, A	Hansson et al. (2001)
Great tit (<i>Parus major</i>)	Terrestrial	Pedigree	F	Szulkin et al. (2007)
Harbor seal (<i>Phoca vitulina</i>)	Marine	Microsatellite, SNP	H	Hoffman et al. (2014)
Harp seal (<i>Phoca groenlandica</i>)	Marine	Microsatellite	A	Kretzmann et al. (2006)
Imperial eagle (<i>Aquila nguilla</i>)	Terrestrial	SNP	H	Doyle et al. (2019)
North Island robin (<i>Petroica longipes</i>)	Terrestrial	Pedigree	F	Jamieson et al. (2007)
Red flour beetle (<i>Tribolium castaneum</i>)	Terrestrial	Microsatellite	H	Szűcs et al. (2017)
Rock iguana (<i>Cyclura n. n. n.</i>)	Terrestrial	Pedigree	H, F	Moss et al. (2019)
Wolf (<i>Canis lupus</i>)	Terrestrial	Pedigree	F	Liberg et al. (2005)
Size, weight, growth rate				
American crow (<i>Corvus brachyrhynchos</i>)	Terrestrial	Microsatellite	H, r	Townsend et al. (2010)
American oyster (<i>Crassostrea virginica</i>)	Marine	Allozyme	H	Singh and Zouros (1978)

(Continues)

TABLE 1 (Continued)

Species	Ecosystem	GD marker	GD estimator	Reference
Blue mussel (<i>Mytilus edulis</i>)	Freshwater	Allozyme	H, F	Koehn and Gaffney (1984)
Common fruit fly (<i>Drosophila melanogaster</i>)	Terrestrial	SNP	F	Ørsted et al. (2019)
European eel (<i>Anguilla nguilla</i>)	Diadromous	Allozyme	H, A	Pujolar et al. (2005)
Gilthead sea bream (<i>Sparus aurata</i>)	Freshwater	Microsatellite	H, A	Borrell et al. (2011)
Rainbow trout (<i>Oncorhynchus mykiss</i>)	Freshwater	Allozyme	H	Danzmann et al. (1987)
Scots pine (<i>Pinus sylvestris</i>)	Terrestrial	Pedigree	F	Mullin et al. (2019)
Springtail (<i>Orchesella cincta</i>)	Terrestrial	AFLP	A	Ellers et al. (2011)
Tiger salamander (<i>Ambystoma tigrinum</i>)	Terrestrial	Allozyme	H	Mitton et al. (1986)
White-footed mouse (<i>Peromyscus leucopus</i>)	Terrestrial	Pedigree, SNP	H	Willoughby et al. (2017)
Disease/pathogen resistance				
Guppy (<i>Poecilia reticulata</i>)	Freshwater	Pedigree	F	Smallbone et al. (2016)
California sea lion (<i>Zalophus californianus</i>)	Marine	Microsatellite	R	Acevedo-Whitehouse et al. (2006)
House finch (<i>Carpodacus mexicanus</i>)	Terrestrial	Microsatellite	H	Hawley et al. (2005)
Soay sheep (<i>Ovis aries</i>)	Terrestrial	Microsatellite	H	Coltman et al. (1999)
Gamete quality				
Bladder campion (<i>Silene vulgaris</i>)	Terrestrial	AFLP	A	Keller and Taylor (2010)
European rabbit (<i>Oryctolagus cuniculus</i>)	Terrestrial	Microsatellite	H	Gage et al. (2006)
Flour beetle (<i>Tribolium castaneum</i>)	Terrestrial	Pedigree	F	Michalczyk et al. (2010)
Guppy (<i>Poecilia reticulata</i>)	Freshwater	Pedigree	F	Zajitschek and Brooks (2010)
Wild gourd (<i>Cucurbita pepo</i>)	Terrestrial	Pedigree	F	Hayes et al. (2005)

Note: Genetic diversity was measured as indicated by the “GD” marker column using relatedness (*r*), inbreeding coefficient (F), heterozygosity (H) or allelic diversity (A) as listed in the estimator column. Fitness-associated traits are indicated by subheadings within the table. These references do not represent a systematic or comprehensive survey of the literature, but are intended to provide the reader with a glimpse of the breadth and depth of the topical literature. There is ample evidence that as genetic diversity increases, fitness tends to increase as well, which leads to a reduced risk of extinction.

The first alleged problem with the use of genetic diversity in conservation is the lack of supporting evidence for the idea that higher levels of genetic diversity lead to an increase in fitness and long-term survival with a concomitant reduction in species extinction risk. Indeed, Teixeira and Huber (2021) write that “no simple general relationship exists between neutral genetic diversity and the risk of species extinction.” Notwithstanding the paradoxical view of neutrality, such sweeping statements mischaracterize an impressive literature that spans decades. Textbook examples of the positive relationship between genetic diversity and fitness abound, including examples in fruit flies (*Drosophila melanogaster*) (Frankham, 1995), monkeyflower (*Mimulus guttatus*) (Willis, 1993) and field mice (*Peromyscus leucopus*) (Lacy et al., 2013), as well as many other diverse organisms that occupy a variety of ecosystems (Table 1; see also Chapman et al., 2009; Hedrick & Kalinowski, 2000). In one recent example, Scott et al. (2020) showed that individual heterozygosity predicted translocation success in threatened desert tortoises (Figure 1; Scott et al., 2020). While there is obviously variation in survival that is not explained by heterozygosity (Reed & Frankham, 2003), this does not undermine the

position that reduced genetic variability often imparts a substantial and negative effect on fitness in this and many other examples (Table 1).

The second criticism of using genetic diversity as a metric for identifying species of conservation concern is that endangered species do not always have less genetic diversity than species of lesser conservation need. Teixeira and Huber (2021) posit that “if genetic diversity is indeed a major factor affecting the health and survival of populations in the wild, then one would expect endangered species to show, on average, lower levels of diversity.” Although there are many species-specific traits that can influence genetic diversity irrespective conservation need (e.g., fecundity, mutation rate, breeding system), we have previously identified and reported the reduction of genetic diversity in threatened vs. nonthreatened species (Willoughby et al., 2015) as have Li et al. (2016)—see Figure 2—despite the fact that species of conservation concern are not identified based on any genetic diversity criteria. We continue to argue that identification of this trend, despite the influence of outlier species, suggests that genetic diversity should be considered in conjunction with other listing criteria and

we have made explicit recommendations to this end (Willoughby et al., 2015). For example, range size has long been used by the International Union for the Conservation of Nature (IUCN) to ascribe conservation status but does not completely capture conservation need, particularly during this time of globally shifting climates (Rattis et al., 2018; Runge et al., 2015). The evaluation of several lines of evidence, including genetic diversity, is needed to accurately identify species that most require conservation action in order to prevent extinctions.

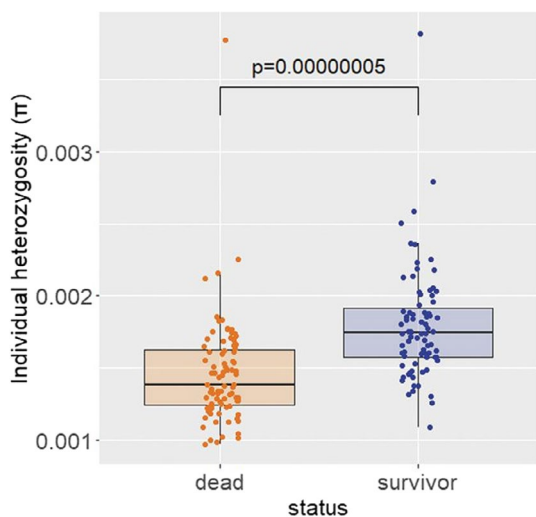


FIGURE 1 Genetic diversity in Mojave desert tortoises (*Gopherus agassizii*) that survived translocation was significantly higher than in individuals that did not survive. Individual heterozygosity was measured using ~6.7 million SNPs from RADSeq data sequenced for 87 dead (orange) and 79 surviving (blue) tortoises. Hence, lower genetic diversity was related to reduced fitness which contributes to extirpations and extinctions. Figure reproduced from Scott et al. (2020) [Colour figure can be viewed at wileyonlinelibrary.com]

A third claim that purportedly undermines the utility of genetic diversity in conservation is that neutral diversity does not predict adaptive potential (Teixeira & Huber, 2021). Geneticists have long recognized that neutral diversity, which is now often measured as mean genome-wide diversity, is related to and correlated with functional diversity (Borrell et al., 2011; Fernandez-Fournier et al., 2021; Mackintosh et al., 2019; Nam et al., 2020; Willoughby et al., 2017). For example, Fernandez-Fournier et al. (2021) rank-ordered populations of yellow warblers (*Setophaga petechia*) and lodgepole pines (*Pinus contorta*) by mean genome-wide genetic diversity as well as by adaptive genetic diversity and found no difference in the rankings. This traditional conservation genetics framework, whereby adaptive diversity is characterized by neutral or genome-wide diversity, makes sense because adaptive loci often represent a small proportion of the genome or consist of many loci of small effect (Benestan et al., 2016; Mathur & DeWoody, 2021; Sella & Barton, 2019). Furthermore, many perturbations which threaten population persistence (fragmentation, bottlenecks, etc.) are expected to affect neutral and adaptive diversity similarly because drift overwhelms selection in small populations. Finally, diversity which may be neutral now could become adaptive in the future (Harrison et al., 2014). Excluding genetic diversity (neutral and/or functional) from conservation practice seems short-sighted and potentially catastrophic for species on the brink, particularly because we have only just begun to compile whole-genome data sets in these nonmodel species.

The fourth point used to dismiss the usefulness of conserving genetic diversity is that to do so requires a better understanding of functional genetic diversity, demographic history and ecological relationships for conservation (Teixeira & Huber, 2021). We think this is a straw man; one would be hard pressed to find a respectable conservation geneticist who thought otherwise. Indeed, we have argued elsewhere (Brüniche-Olsen et al., 2019; Willoughby et al., 2015) that the IUCN should incorporate measures of genetic/

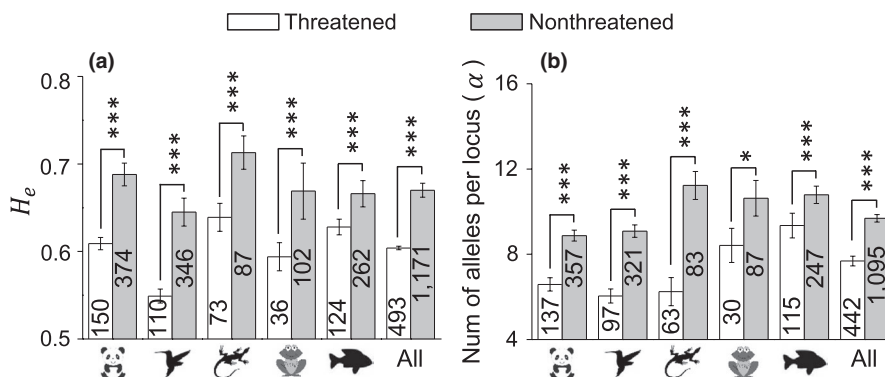


FIGURE 2 Threatened and endangered species have, on average, significantly lower levels of genetic diversity than nonthreatened species (from left to right: mammals, birds, reptiles, amphibians, fishes, all groups combined). Significance was estimated using permutation tests on expected heterozygosity (H_e ; left) and number of alleles (α ; right) per microsatellite locus between nonthreatened and threatened species with a null hypothesis that mean genetic diversity of nonthreatened species is equal to that of threatened species. Column number indicates the numbers of species compared in each category, and the one-tailed p values of the test are shown above the columns. * $p < .05$, *** $p < .01$. Figure from Li et al. (2016)

genomic diversity (e.g., heterozygosity or effective population size) as explicit criteria in Red Listing decisions to more accurately indicate the likelihood of future extinction and the associated need for conservation. However, it would be folly to suggest that demographic, environmental or ecological factors should be ignored or subsumed by genetic concerns as all are clearly integral to population persistence.

We agree with Teixeira and Huber (2021) that the global conservation emergency has “fostered the development and implementation of imperfect ... conservation strategies.” Our perspective—one shared by others (e.g. Hoban et al., 2020; Peart et al., 2020)—is that the consideration of genetic diversity in conservation has a strong theoretical justification, is backed by decades of empirical research and literature, and is empirically tractable for many species given current data and technological limitations. Furthermore, genetic diversity has predictive value (Scott et al., 2020) and, in the absence of knowledge of what variants are adaptive, approximates standing genetic variation and adaptive potential. We recognize that no one approach will be perfectly suited to characterizing all species and ecosystems, but we see no need to disregard informative data sets and thus we strongly support the use of genetics in establishing conservation priorities.

ACKNOWLEDGEMENTS

We thank two anonymous peer reviewers for valuable feedback.

CONFLICT OF INTEREST

None known, other than two of the authors are on the journal's Editorial Board.

AUTHOR CONTRIBUTIONS

All authors contributed similarly to the contents of this manuscript.

DATA AVAILABILITY STATEMENT

Not applicable.

ORCID

J. Andrew DeWoody  <https://orcid.org/0000-0002-7315-5631>

Avril M. Harder  <https://orcid.org/0000-0001-7371-4002>

Samarth Mathur  <https://orcid.org/0000-0002-6446-5718>

Janna R. Willoughby  <https://orcid.org/0000-0002-0176-1878>

REFERENCES

- Acevedo-Whitehouse, K., Spraker, T. R., Lyons, E., Melin, S. R., Gulland, F., Delong, R. L., & Amos, W. (2006). Contrasting effects of heterozygosity on survival and hookworm resistance in California sea lion pups. *Molecular Ecology*, 15(7), 1973–1982. <https://doi.org/10.1111/j.1365-294X.2006.02903.x>
- Amos, W., Wilmer, J. W., Fullard, K., Burg, T. M., Croxall, J. P., Bloch, D., & Coulson, T. (2001). The influence of parental relatedness on reproductive success. *Proceedings of the Royal Society*, B268(1480), 2021–2027.
- Andersen, L. W., Fog, K., & Damgaard, C. (2004). Habitat fragmentation causes bottlenecks and inbreeding in the European tree frog (*Hyla arborea*). *Proceedings of the Royal Society*, B271(1545), 1293–1302.
- Benestan, L., Quinn, B. K., Maaroufi, H., Laporte, M., Clark, F. K., Greenwood, S. J., & Bernatchez, L. (2016). Seascape genomics provides evidence for thermal adaptation and current-mediated population structure in American lobster (*Homarus americanus*). *Molecular Ecology*, 25(20), 5073–5092.
- Borrell, Y. J., Carleos, C. E., Sánchez, J. A., Vázquez, E., Gallego, V., Asturiano, J. F., & Blanco, G. (2011). Heterozygosity-fitness correlations in the gilthead sea bream *Sparus aurata* using microsatellite loci from unknown and gene-rich genomic locations. *Journal of Fish Biology*, 79, 1111–1129. <https://doi.org/10.1111/j.1095-8649.2011.03099.x>
- Brown, A. H. D. (1978). Isozymes, plant population genetic structure, and genetic conservation. *Theoretical and Applied Genetics*, 52, 145–157. <https://doi.org/10.1007/BF00282571>
- Brüniche-Olsen, A., Kellner, K. N., & DeWoody, J. A. (2019). Island area, body size and demographic history shape genomic diversity in Darwin's finches and related tanagers. *Molecular Ecology*, 28, 4914–4925. <https://doi.org/10.1111/mec.15266>
- Chapman, J. R., Nakagawa, S., Coltman, D. W., Slate, J., & Sheldon, B. C. (2009). A quantitative review of heterozygosity-fitness correlations in animal populations. *Molecular Ecology*, 18(13), 2746–2765. <https://doi.org/10.1111/j.1365-294X.2009.04247.x>
- Charpentier, M., Setchell, J. M., Prugnolle, F., Knapp, L. A., Wickings, E. J., Peignot, P., & Hossaert-McKey, M. (2005). Genetic diversity and reproductive success in mandrills (*Mandrillus sphinx*). *Proceedings of the National Academy of Sciences of the United States of America*, 102(46), 16723–16728. <https://doi.org/10.1073/pnas.0507205102>
- Coltman, D. W., Pilkington, J. G., Smith, J. A., & Pemberton, J. M. (1999). Parasite-mediated selection against inbred Soay sheep in a free-living, island population. *Evolution; International Journal of Organic Evolution*, 53(4), 1259. <https://doi.org/10.2307/2640828>
- Crandall, K. A., Bininda-Emonds, O. R. P., Mace, G. M., & Wayne, R. K. (2000). Considering evolutionary processes in conservation biology. *Trends in Ecology and Evolution*, 15, 290–295. [https://doi.org/10.1016/S0169-5347\(00\)01876-0](https://doi.org/10.1016/S0169-5347(00)01876-0)
- Danzmann, R. G., Ferguson, M. M., & Allendorf, F. W. (1987). Heterozygosity and oxygen-consumption rate as predictors of growth and developmental rate in rainbow trout. *Physiological Zoology*, 60(2), 211–220. <https://doi.org/10.1086/physzool.60.2.30158645>
- Dietz, J. M., Baker, A. J., & Ballou, J. D. (2000). Demographic evidence of inbreeding depression in wild golden lion tamarins. In A. G. Young, & G. M. Clarke (Eds.), *Genetics, demography and viability of fragmented populations* (pp. 203–212). Cambridge University Press.
- Doyle, J. M., Katzner, T. E., Roemer, G. W., Cain, J. W., Millsap, B. A., McIntyre, C. L., Sonsthagen, S. A., Fernandez, N. B., Wheeler, M., Bulut, Z., Bloom, P. H., & Andrew DeWoody, J. (2016). Genetic structure and viability selection in the golden eagle (*Aquila chrysaetos*), a vagile raptor with a Holarctic distribution. *Conservation Genetics*, 17(6), 1307–1322. <https://doi.org/10.1007/s10592-016-0863-0>
- Doyle, J. M., Willoughby, J. R., Bell, D. A., Bloom, P. H., Bragin, E. A., Fernandez, N. B., Katzner, T. E., Leonard, K., & DeWoody, J. A. (2019). Elevated heterozygosity in adults relative to juveniles provides evidence of viability selection on eagles and falcons. *The Journal of Heredity*, 110(6), 696–706. <https://doi.org/10.1093/jhered/esz048>
- Ellers, J., Rog, S., Braam, C., & Berg, M. P. (2011). Genotypic richness and phenotypic dissimilarity enhance population performance. *Ecology*, 92(8), 1605–1615. <https://doi.org/10.1890/10-2082.1>
- Fernandez-Fournier, P., Lewthwaite, J. M. M., & Mooers, A. Ø. (2021). Do we need to identify adaptive genetic variation when prioritizing populations for conservation? *Conservation Genetics*, <https://doi.org/10.1007/s10592-020-01327-w>

- Frankham, R. (1995). Inbreeding and extinction: A threshold effect. *Conservation Biology: The Journal of the Society for Conservation Biology*, 9(4), 792–799. <https://doi.org/10.1046/j.1523-1739.1995.09040792.x>
- Gage, M. J. G., SurrIDGE, A. K., Tomkins, J. L., Green, E., Wiskin, L., Bell, D. J., & Hewitt, G. M. (2006). Reduced heterozygosity depresses sperm quality in wild rabbits, *Oryctolagus cuniculus*. *Current Biology*, 16(6), 612–617. <https://doi.org/10.1016/j.cub.2006.02.059>
- Garant, D., Dodson, J. J., & Bernatchez, L. (2005). Offspring genetic diversity increases fitness of female Atlantic salmon (*Salmo salar*). *Behavioral Ecology and Sociobiology*, 57(3), 240–244. <https://doi.org/10.1007/s00265-004-0854-x>
- Hagen, E. N., Hale, M. L., Maloney, R. F., & Steeves, T. E. (2011). Conservation genetic management of a critically endangered New Zealand endemic bird: minimizing inbreeding in the Black Stilt *Himantopus novaezelandiae*. *Ibis*, 153(3), 556–561. <https://doi.org/10.1111/j.1474-919X.2011.01137.x>
- Hansson, B., Bensch, S., Hasselquist, D., & Akesson, M. (2001). Microsatellite diversity predicts recruitment of sibling great reed warblers. *Proceedings. Biological Sciences*, 268(1473), 1287–1291.
- Harrisson, K. A., Magrath, M. J. L., Yen, J. D. L., Pavlova, A., Murray, N., Quin, B., Menkhorst, P., Miller, K. A., Cartwright, K., & Sunnucks, P. (2019). Lifetime fitness costs of inbreeding and being inbred in a critically endangered bird. *Current Biology*, 29(16), 2711–2717.e4. <https://doi.org/10.1016/j.cub.2019.06.064>
- Harrisson, K. A., Pavlova, A., Telonis-Scott, M., & Sunnucks, P. (2014). Using genomics to characterize evolutionary potential for conservation of wild populations. *Evolutionary Applications*, 7, 1008–1025. <https://doi.org/10.1111/eva.12149>
- Hawley, D. M., Sydenstricker, K. V., Kollias, G. V., & Dhondt, A. A. (2005). Genetic diversity predicts pathogen resistance and cell-mediated immunocompetence in house finches. *Biology Letters*, 1(3), 326–329. <https://doi.org/10.1098/rsbl.2005.0303>
- Hayes, C. N., Winsor, J. A., & Stephenson, A. G. (2005). Multigenerational effects of inbreeding in *Cucurbita pepo* ssp. *texana* (Cucurbitaceae). *Evolution; International Journal of Organic Evolution*, 59(2), 276–286. <https://doi.org/10.1111/j.0014-3820.2005.tb00988.x>
- Hedrick, P. W., & Kalinowski, S. T. (2000). Inbreeding depression in conservation biology. *Annual Review of Ecology and Systematics*, 31(1), 139–162. <https://doi.org/10.1146/annurev.ecolsys.31.1.139>
- Hitchings, S. P., & Beebee, T. J. C. (1998). Loss of genetic diversity and fitness in Common Toad (*Bufo bufo*) populations isolated by inimical habitat. *Journal of Evolutionary Biology*, 11(3), 269–283.
- Hoban, S., Campbell, C., da Silva, J., Ekblom, R., Funk, W. C., Garner, B., Hunter, M. E. (2020). An analysis of genetic diversity actions, indicators and targets in 114 National Reports to the Convention on Biological Diversity. *bioRxiv*. <https://doi.org/10.1101/2020.08.28.254672>
- Hoffman, J. I., Simpson, F., David, P., Rijks, J. M., Kuiken, T., Thorne, M. A. S., Lacy, R. C., & Dasmahapatra, K. K. (2014). High-throughput sequencing reveals inbreeding depression in a natural population. *Proceedings of the National Academy of Sciences of the United States of America*, 111(10), 3775–3780. <https://doi.org/10.1073/pnas.1318945111>
- Huisman, J., Kruuk, L. E. B., Ellis, P. A., Clutton-Brock, T., & Pemberton, J. M. (2016). Inbreeding depression across the lifespan in a wild mammal population. *Proceedings of the National Academy of Sciences of the United States of America*, 113(13), 3585–3590. <https://doi.org/10.1073/pnas.1518046113>
- Jamieson, I. G., Tracy, L. N., Fletcher, D., & Armstrong, D. P. (2007). Moderate inbreeding depression in a reintroduced population of North Island robins. *Animal Conservation*, 10(1), 95–102. <https://doi.org/10.1111/j.1469-1795.2006.00078.x>
- Johnson, W. E., Onorato, D. P., Roelke, M. E., Land, E. D., Cunningham, M., Belden, R. C., McBride, R., Jansen, D., Lotz, M., Shindle, D., Howard, J., Wildt, D. E., Penfold, L. M., Hostetler, J. A., Oli, M. K., & O'Brien, S. J. (2010). Genetic restoration of the Florida panther. *Science*, 329(5999), 1641–1645. <https://doi.org/10.1126/science.1192891>
- Keller, S. R., & Taylor, D. R. (2010). Genomic admixture increases fitness during a biological invasion. *Journal of Evolutionary Biology*, 23(8), 1720–1731. <https://doi.org/10.1111/j.1420-9101.2010.02037.x>
- Kennedy, E. S., Grueber, C. E., Duncan, R. P., & Jamieson, I. G. (2014). Severe inbreeding depression and no evidence of purging in an extremely inbred wild species—the chatham island black robin. *Evolution; International Journal of Organic Evolution*, 68(4), 987–995. <https://doi.org/10.1111/evo.12315>
- Koehn, R. K., & Gaffney, P. M. (1984). Genetic heterozygosity and growth rate in *Mytilus edulis*. *Marine Biology*, 82(1), 1–7. <https://doi.org/10.1007/BF00392757>
- Kretzmann, M., Mentzer, L., DiGiovanni, R. Jr, Leslie, M. S., & Amato, G. (2006). Microsatellite diversity and fitness in stranded juvenile harp seals (*Phoca groenlandica*). *The Journal of Heredity*, 97(6), 555–560. <https://doi.org/10.1093/jhered/esl043>
- Lacy, R. C., Alaks, G., & Walsh, A. (2013). Evolution of *Peromyscus leucopus* mice in response to a captive environment. *PLoS One*, 8(8), e72452. <https://doi.org/10.1371/journal.pone.0072452>
- Lesbarrères, D., Primmer, C. R., Laurila, A., & Merilä, J. (2005). Environmental and population dependency of genetic variability–fitness correlations in *Rana temporaria*. *Molecular Ecology*, 14, 311–323. <https://doi.org/10.1111/j.1365-294X.2004.02394.x>
- Lewontin, R. C. (1974). *The genetic basis of evolutionary change*. Columbia University Press.
- Li, H., Xiang-Yu, J., Dai, G., Gu, Z., Ming, C., Yang, Z., Ryder, O. A., Li, W.-H., Fu, Y.-X., & Zhang, Y.-P. (2016). Large numbers of vertebrates began rapid population decline in the late 19th century. *Proceedings of the National Academy of Sciences of the United States of America*, 113(49), 14079–14084. <https://doi.org/10.1073/pnas.1616804113>
- Liberg, O., Andrén, H., Pedersen, H.-C., Sand, H., Sejberg, D., Wabakken, P., & Bensch, S. (2005). Severe inbreeding depression in a wild wolf (*Canis lupus*) population. *Biology Letters*, 1(1), 17–20.
- Mackintosh, A., Laetsch, D. R., Hayward, A., Charlesworth, B., Waterfall, M., Vila, R., & Lohse, K. (2019). The determinants of genetic diversity in butterflies. *Nature Communications*, 10(1), 3466. <https://doi.org/10.1038/s41467-019-11308-4>
- Markert, J. A., Champlin, D. M., Gutjahr-Gobell, R., Gear, J. S., Kuhn, A., McGreevy, T. J., Roth, A., Bagley, M. J., & Nacci, D. E. (2010). Population genetic diversity and fitness in multiple environments. *BMC Evolutionary Biology*, 10(1), 205. <https://doi.org/10.1186/1471-2148-10-205>
- Mathur, S., & DeWoody, J. A. (2021). Genetic load has potential in large populations but is realized in small inbred populations. *Evolutionary Applications*, 14, 1540–1557. <https://doi.org/10.1111/eva.13216>
- Michalczyk, L., Martin, O. Y., Millard, A. L., Emerson, B. C., & Gage, M. J. G. (2010). Inbreeding depresses sperm competitiveness, but not fertilization or mating success in male *Tribolium castaneum*. *Proceedings of the Royal Society*, B277(1699), 3483–3491.
- Mitrus, C., Mitrus, J., & Rutkowski, R. (2020). Individual heterozygosity influences arrival times and mating success of male Red-breasted Flycatchers *Ficedula parva*. *Zoological Studies (Taipei, Taiwan)*, 59, e12.
- Mitton, J. B., Carey, C., & Kocher, T. D. (1986). The relation of enzyme heterozygosity to standard and active oxygen consumption and body size of tiger salamanders, *Ambystoma tigrinum*. *Physiological Zoology*, 59(5), 574–582. <https://doi.org/10.1086/physzool.59.5.30156122>
- Moritz, C. (2002). Strategies to protect biological diversity and the evolutionary processes that sustain it. *Systematic Biology*, 51, 238–254. <https://doi.org/10.1080/10635150252899752>

- Moss, J. B., Gerber, G. P., & Welch, M. E. (2019). Heterozygosity-fitness correlations reveal inbreeding depression in neonatal body size in a critically endangered rock iguana. *The Journal of Heredity*, 110(7), 818–829. <https://doi.org/10.1093/jhered/esz060>
- Mullin, T. J., Persson, T., Abrahamsson, S., & Andersson Gull, B. (2019). Effects of inbreeding depression on seed production in Scots pine (*Pinus sylvestris*). *Canadian Journal of Forest Research*, 49(7), 854–860.
- Nam, K., Nhim, S., Robin, S., Bretaudeau, A., Nègre, N., & d'Alençon, E. (2020). Positive selection alone is sufficient for whole genome differentiation at the early stage of speciation process in the fall armyworm. *BMC Evolutionary Biology*, 20(1), 152. <https://doi.org/10.1186/s12862-020-01715-3>
- Ørsted, M., Hoffmann, A. A., Sverrisdóttir, E., Nielsen, K. L., & Kristensen, T. N. (2019). Genomic variation predicts adaptive evolutionary responses better than population bottleneck history. *PLoS Genetics*, 15(6), e1008205. <https://doi.org/10.1371/journal.pgen.1008205>
- Peart, C. R., Tusso, S., Pophaly, S. D., Botero-Castro, F., Wu, C.-C., Aurióles-Gamboá, D., Baird, A. B., Bickham, J. W., Forcada, J., Galimberti, F., Gemmill, N. J., Hoffman, J. I., Kovacs, K. M., Kunasranta, M., Lydersen, C., Nymán, T., de Oliveira, L. R., Orr, A. J., Sanvito, S., ... Wolf, J. B. W. (2020). Determinants of genetic variation across eco-evolutionary scales in pinnipeds. *Nature Ecology & Evolution*, 4(8), 1095–1104. <https://doi.org/10.1038/s41559-020-1215-5>
- Pomeroy, P. P., Wilmer, J. W., Amos, W., & Twiss, S. D. (2001). Reproductive performance links to fine-scale spatial patterns of female grey seal relatedness. *Proceedings of the Royal Society*, B268(1468), 711–717.
- Pujolar, J. M., Maes, G. E., Vancoillie, C., & Volckaert, F. A. M. (2005). Growth rate correlates to individual heterozygosity in the European eel, *Anguilla anguilla* L. *Evolution; International Journal of Organic Evolution*, 59(1), 189–199.
- Rattis, L., Dobrovolski, R., Talebi, M., & Loyola, R. (2018). Geographic range-scale assessment of species conservation status: A framework linking species and landscape features. *Perspectives in Ecology and Conservation*, 16(2), 97–104. <https://doi.org/10.1016/j.pecon.2018.01.001>
- Reed, D. H., & Frankham, R. (2003). Correlation between fitness and genetic diversity. *Conservation Biology: the Journal of the Society for Conservation Biology*, 17(1), 230–237. <https://doi.org/10.1046/j.1523-1739.2003.01236.x>
- Rosengrave, P., Montgomerie, R., & Gemmill, N. (2016). Cryptic female choice enhances fertilization success and embryo survival in chinook salmon. *Proceedings of the Royal Society*, B283(1827), 20160001. <https://doi.org/10.1098/rspb.2016.0001>
- Runge, C. A., Tulloch, A., Hammill, E., Possingham, H. P., & Fuller, R. A. (2015). Geographic range size and extinction risk assessment in nomadic species. *Conservation Biology: the Journal of the Society for Conservation Biology*, 29(3), 865–876. <https://doi.org/10.1111/cobi.12440>
- Saccheri, I., Kuussaari, M., Kankare, M., Vikman, P., Fortelius, W., & Hanski, I. (1998). Inbreeding and extinction in a butterfly metapopulation. *Nature*, 392(6675), 491–494.
- Scott, P. A., Allison, L. J., Field, K. J., Averill-Murray, R. C., & Shaffer, H. B. (2020). Individual heterozygosity predicts translocation success in threatened desert tortoises. *Science*, 370(6520), 1086–1089. <https://doi.org/10.1126/science.abb0421>
- Sella, G., & Barton, N. H. (2019). Thinking about the evolution of complex traits in the era of genome-wide association studies. *Annual Review of Genomics and Human Genetics*, 20(1), 461–493. <https://doi.org/10.1146/annurev-genom-083115-022316>
- Silva, A. D., Luikart, G., Yoccoz, N. G., Cohas, A., & Allainé, D. (2006). Genetic diversity-fitness correlation revealed by microsatellite analyses in European alpine marmots (*Marmota marmota*). *Conservation Genetics*, 7(3), 371–382. <https://doi.org/10.1007/s10592-005-9048-y>
- Singh, S. M., & Zouros, E. (1978). Genetic variation associated with growth rate in the American oyster (*Crassostrea virginica*). *Evolution; International Journal of Organic Evolution*, 32(2), 342. <https://doi.org/10.2307/2407602>
- Smallbone, W., van Oosterhout, C., & Cable, J. (2016). The effects of inbreeding on disease susceptibility: *Gyrodactylus turnbulli* infection of guppies, *Poecilia reticulata*. *Experimental Parasitology*, 167, 32–37. <https://doi.org/10.1016/j.exppara.2016.04.018>
- Szűcs, M., Melbourne, B. A., Tuff, T., Weiss-Lehman, C., & Hufbauer, R. A. (2017). Genetic and demographic founder effects have long-term fitness consequences for colonising populations. *Ecology Letters*, 20(4), 436–444. <https://doi.org/10.1111/ele.12743>
- Szulkin, M., Garant, D., McCleery, R. H., & Sheldon, B. C. (2007). Inbreeding depression along a life-history continuum in the great tit. *Journal of Evolutionary Biology*, 20(4), 1531–1543. <https://doi.org/10.1111/j.1420-9101.2007.01325.x>
- Taylor, H. R., Colbourne, R. M., Robertson, H. A., Nelson, N. J., Allendorf, F. W., & Ramstad, K. M. (2017). Cryptic inbreeding depression in a growing population of a long-lived species. *Molecular Ecology*, 26(3), 799–813. <https://doi.org/10.1111/mec.13977>
- Teixeira, J. C., & Huber, C. D. (2021). The inflated significance of neutral genetic diversity in conservation genetics. *Proceedings of the National Academy of Sciences of the United States of America*, 118(10), e2015096118. <https://doi.org/10.1073/pnas.2015096118>
- Townsend, A. K., Clark, A. B., & McGowan, K. J. (2010). Direct benefits and genetic costs of extrapair paternity for female American crows (*Corvus brachyrhynchos*). *The American Naturalist*, 175(1), E1–E9.
- Vandewoestijne, S., Schtickzelle, N., & Baguette, M. (2008). Positive correlation between genetic diversity and fitness in a large, well-connected metapopulation. *BMC Biology*, 6(1), 46. <https://doi.org/10.1186/1741-7007-6-46>
- Weissensteiner, M. H., Bunikis, I., Catalan, A., Francoijs, K.-J., Knief, U., Heim, W., Peona, V., Pophaly, S. D., Sedlazeck, F. J., Suh, A., Warmuth, V. M., & Wolf, J. B. W. (2020). Discovery and population genomics of structural variation in a songbird genus. *Nature Communications* 11, 3403. <https://doi.org/10.1038/s41467-020-17195-4>
- White, K. L., Eason, D. K., Jamieson, I. G., & Robertson, B. C. (2015). Evidence of inbreeding depression in the critically endangered parrot, the kakapo. *Animal Conservation*, 18(4), 341–347. <https://doi.org/10.1111/acv.12177>
- Willis, J. H. (1993). Effects of different levels of inbreeding on fitness components in *Mimulus guttatus*. *Evolution; International Journal of Organic Evolution*, 47(3), 864.
- Willoughby, J. R., Ivy, J. A., Lacy, R. C., Doyle, J. M., & DeWoody, J. A. (2017). Inbreeding and selection shape genomic diversity in captive populations: Implications for the conservation of endangered species. *PLoS One*, 12(4), e0175996. <https://doi.org/10.1371/journal.pone.0175996>
- Willoughby, J. R., Sundaram, M., Wijayawardena, B. K., Kimble, S. J. A., Ji, Y., Fernandez, N. B., Antonides, J. D., Lamb, M. C., Marra, N. J., & DeWoody, J. A. (2015). The reduction of genetic diversity in threatened vertebrates and new recommendations regarding IUCN conservation rankings. *Biological Conservation*, 191, 495–503. <https://doi.org/10.1016/j.biocon.2015.07.025>
- Willoughby, J. R., Waser, P. M., Brüniche-Olsen, A., & Christie, M. R. (2019). Inbreeding load and inbreeding depression estimated from lifetime reproductive success in a small, dispersal-limited population. *Heredity*, 123(2), 192–201. <https://doi.org/10.1038/s41437-019-0197-z>
- Zajitschek, S. R. K., & Brooks, R. C. (2010). Inbreeding depression in male traits and preference for outbred males in *Poecilia reticulata*.

Behavioral Ecology: Official Journal of the International Society for Behavioral Ecology, 21(4), 884–891. <https://doi.org/10.1093/beheco/arq077>

Zilko, J. P., Harley, D., Hansen, B., Pavlova, A., & Sunnucks, P. (2020). Accounting for cryptic population substructure enhances detection of inbreeding depression with genomic inbreeding coefficients: an example from a critically endangered marsupial. *Molecular Ecology*, 29(16), 2978–2993. <https://doi.org/10.1111/mec.15540>

How to cite this article: DeWoody, J. A., Harder, A. M., Mathur, S., & Willoughby, J. R. (2021). The long-standing significance of genetic diversity in conservation. *Molecular Ecology*, 30, 4147–4154. <https://doi.org/10.1111/mec.16051>