

8. Hess, J.E. *et al.* (2015) Use of genotyping by sequencing data to develop a high-throughput and multifunctional SNP panel for conservation applications in Pacific lamprey. *Mol. Ecol. Resour.* 15, 187–202
9. Miller, W. *et al.* (2011) Genetic diversity and population structure of the endangered marsupial *Sarcophilus harrisii* (Tasmanian devil). *Proc. Natl. Acad. Sci. U.S.A.* 108, 12348–12353
10. Lemmon, A.R. *et al.* (2012) Anchored hybrid enrichment for massively high-throughput phylogenomics. *Syst. Biol.* 61, 727–744
11. Gustafson, R. *et al.* (2007) *Pacific Salmon Extinctions: Quantifying Lost and Remaining Diversity. Paper 438*, US Department of Commerce
12. Habicht, C. *et al.* (2012) *Harvest and Harvest Rates of Sockeye Salmon Stocks in Fisheries of the Western Alaska Salmon Stock Identification Program (WASSIP), 2006–2008. Special Publication No. 12–24*, Alaska Department of Fish and Game

## Letter

### Reply to Garner *et al.*

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The letter by Garner *et al.* [1] continued an important discussion regarding the role genomics might play in conservation biology. In general, we do not see a dichotomy between our point of view [2] and that put forth by Garner *et al.* [1]. At the heart of the issue is how to define an actual impact of genomics on applied conservation and find suitable ways to remove existing barriers limiting the use of genomics for managing wild populations. The promised gains of identifying adaptive loci and the genes underlying phenotypes [3,4] have in most systems not yet been realized and recent empirical work further highlights the challenges [5,6]. Thus, our take-home message boiled down to the application of genomics in wild populations being at an early developmental stage that is far from straightforward and far from regularly applied [2].

Garner *et al.* [1] extended the list of examples where genomics has aided the conservation and management of wild species. It is promising to see that examples are beginning to emerge and we are pleased that the authors repeated the call for increased agency–academic collaboration to enhance the application of genomics to real-world conservation issues. However, the list of case studies provided (Table S1 in [1]) underscores the absence of genomic work effectively impacting the conservation of a broad array of organisms. The majority of examples involve commercially important species in North America, most often salmonid fish populations. Other featured examples, such as the Tasmanian devil, are interesting genomic studies, but the key conservation strategy revolves around maintaining an insurance (disease-free) population, with genomic applications labeled as ongoing research [7]. The lack of taxonomic and geographic breadth and applied impact on noncommercial entities suggest that genomics has as yet not been as influential

on conservation biology as initially promised [3] or implied [1]. Examples with high commercial potential might in the best case reflect a starting point for testing the applicability of genomics more broadly.

Cooperation across the academic and practical realms is an integral part of applied conservation and increased attention in published literature does have a beneficial corollary for conservation. In that regard, we agree that reports from the grey literature are valuable and play an important role of disseminating valuable information. However, we must not lose sight of the main incentive of conservation research, which is conserving biodiversity. To truly bridge the conservation genomics gap, alternative ways to measure impact [8] and fund conservation science [2] need to be considered. We therefore echo our original call for the need to develop research-to-application frameworks that will accelerate the crossing of the conservation genomics gap that is still present for the very large number of species not commercially harvested and with limited resources.

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#### References

1. Garner, B.A. *et al.* (2016) Genomics in conservation: case studies and bridging the gap between data and application. *Trends Ecol. Evol.* 31, 81–83
2. Shafer, A.B.A. *et al.* (2015) Genomics and the challenging translation into conservation practice. *Trends Ecol. Evol.* 30, 78–87
3. Allendorf, F.W. *et al.* (2010) Genomics and the future of conservation genetics. *Nat. Rev. Genet.* 11, 697–709
4. McMahon, B.J. *et al.* (2014) How and why should we implement genomics into conservation? *Evol. Appl.* 7, 999–1007
5. Kardos, M. *et al.* (2015) Whole genome resequencing of extreme phenotypes in collared flycatchers highlights the difficulty of detecting quantitative trait loci in natural populations. *Mol. Ecol. Res.* (in press)
6. Burri, R. *et al.* (2015) Linked selection and recombination rate variation drive the evolution of the genomic landscape of differentiation across the speciation continuum of *Ficedula* flycatchers. *Genome Res.* 25, 1656–1665
7. Grueber, C.E. *et al.* (2015) Genomic insights into a contagious cancer in Tasmanian devils. *Trends Genet.* 31, 528–535
8. Sibbald, S.L. *et al.* (2015) Into the gray: a modified approach to citation analysis to better understand research impact. *J. Med. Libr. Assoc.* 103, 49–54

## Letter

# A Balanced Data Archiving Policy for Long-Term Studies

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Long-term monitoring and experiments are crucial to understanding many important questions in ecology and evolution, and, consequently, the data sets that emerge from long-term projects can be extremely valuable. It is crucial that such data are treated in a way that supports the best interests of science. We must continue to encourage researchers to engage in long-term projects, and we must also ensure that such data are widely available in perpetuity [1,2]. Balancing these sometimes opposing goals is a difficult but not insurmountable problem, and certainly one that should be resolved in a way that balances the needs of those who produced those data with the best interests of science.

In a recent article in *TREE*, Mills *et al.* [3] argued that current data accessibility policies hinder long-term studies. They raised several important issues. While many of us strongly disagree with many of the points that they raised, we do think that some changes to data-archiving policies are warranted.

The current data-archiving policies of many ecology and evolution journals have provisions to attenuate the burdens of data archiving. First, the current policies do not require archiving of the entire data set from a project; they require only that authors make available the data necessary to recreate the analyses and results in the published manuscript. Second, embargoes of public access to archived data for a year after publication are typically automatic, but longer embargoes can be allowed with the discretion of the editor. However, while we think that editorial discretion is an important tool in a fair policy, such discussions can be inefficient and lead to inconsistent policies.

Despite these existing provisions, we do agree with Mills *et al.* that, in some situations, the current data-archiving policy adopted by many ecology and evolutionary biology journals does not adequately balance the needs of scientists producing long-term data sets with the needs of the community. As some of the original framers of the joint data archiving policy [1] and current editors of ecology and evolution journals, we propose the following as a balanced way forward (in many cases echoing the suggestions of Roche *et al.* [4]):

- As Mills *et al.* [3] suggest, a longer embargo period may often be appropriate for long-term studies. We suggest that, for projects for which the key data reported in the publication have been regularly collected from a population for more than 5 years, journals should allow a 5-year embargo period upon author request. This longer embargo allows authors the opportunity to make additional use of their own data while ensuring that the data underlying results in the paper are appropriately preserved and eventually available for reuse.
- With longer embargoes, the importance of careful data management and good meta-data becomes even greater, because the data cannot be easily vetted while the potential ambiguities are fresh in the authors' minds. Authors who opt for a longer embargo should take care that the data being archived are well presented for easy and unambiguous reuse in the future.
- As Mills *et al.* also note [3], original data collectors have insights into the data that cannot be fully extracted from previous papers and metadata. Journals and researchers who reuse data should recognize that, in most cases, data will be better understood and analyzed with the cooperation or collaboration of those who collected the data. We agree that reusers of data should strongly consider consulting and, in many cases, directly collaborating with,