



Reply to DeWoody et al.: Inequitable access to affordable sequencing limits the benefits from population genomic insights

Carolyn J. Hogg^{a,1} and Katherine Belov^a

DeWoody et al. (1) recently commended the Threatened Species Initiative (TSI), a project generating genomic resources for threatened species and developing accessible tools for the conservation community (2). However, their letter questions our advocacy for reduced representation sequencing (RRS), stating the economic advantages of RRS are rapidly diminishing or nonexistent [citing a 2021 New Zealand paper (3)]. Rather, DeWoody et al. (1) advocate for whole-genome resequencing (WGR), highlighting how WGR projects have progressed the field of evolutionary biology over the last decade and that biodiversity conservation genomics studies are lagging behind. Although these authors make some excellent points on the value of WGR to understanding species biology, most of which we agree with, they fail to note the current inequity that exists at a global scale in relation to access to and funding for WGR.

In 2022, WGR in the United States is ~US\$150 per sample for 30x short-read sequencing, while in Australia it costs ~US\$900 per sample. In a quick survey of conservation genomics colleagues outside of North America (Malaysia, Colombia, Australia, and India) they were unanimous in their desire to use WGR but are unable to do so, either because it is too expensive in their country or their country does not have the facilities to provide WGR data. The heavily discounted sequencing costs provided in North America/Europe are driving demand by the scientific community that researchers use WGR data. However, this is disadvantaging conservation biologists in other nations as they are unable

to generate these datasets within their countries. Our original piece highlighted that international treaty obligations (i.e., CITES, CBD, Nagoya) also limit a researcher's ability to send samples overseas for cheaper sequencing (2). So, although WGR is a useful tool and may become the sequencing of choice in the future for many conservation efforts, at this time equitable access does not exist.

It is not simply a lack of access, or high sequencing costs, but also access to conservation research funding. The 17 megadiverse nations hold ~60 to 80% of global biodiversity (4). The United States and Australia are the only two developed megadiverse economies (5). The gross domestic product per capita of the remaining 15 nations is between US\$526 and US\$16,056, compared to the United States (US\$65,095) and Australia (US\$54,875) (Fig. 1), meaning for many nations there is a lack of biodiversity conservation investment, impacting their ability to conserve their endemic species. For example, Australian investment into conservation

Author affiliations: ^aSchool of Life & Environmental Sciences, The University of Sydney, Sydney, NSW 2006, Australia

Author contributions: C.J.H. and K.B. wrote the paper.

The authors declare no competing interest.

Copyright © 2022 the Author(s). Published by PNAS. This article is distributed under Creative Commons Attribution-NonCommercial-NoDerivatives License 4.0 (CC BY-NC-ND).

¹To whom correspondence may be addressed. Email: carolyn.hogg@sydney.edu.au.

Published September 26, 2022.

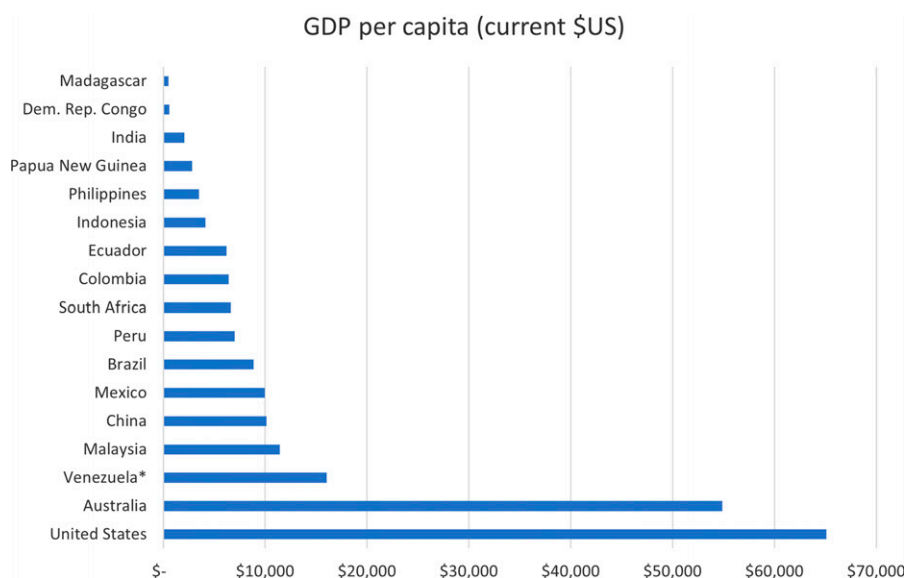


Fig. 1. The 2019 gross domestic product (GDP) per capita in current US dollars for the 17 megadiverse nations in the world; note data for Venezuela are for 2014 as later data are not available. Source: World Bank Open Data (<https://data.worldbank.org/>; accessed 26 August 2022).

activities is only an estimated \$US92 million per year, which is a tenth of the US\$1.45 billion per year investment by the US government (6).

In principle we agree with DeWoody et al. (1) on the scientific value of WGR and fully support the goals of the Earth BioGenome Project (7), but we recognize the massive inequity that currently exists in accessing this technology

across the globe. If scientists, journal editors, and funding agencies value WGR in conservation management, then responsibility rests with those in developed economies to advance tools and methodologies that permit easier access. Until we do so, the current inequity will continue, and genomics informed conservation decision-making will not be possible.

1. J. A. DeWoody *et al.*, The Threatened Species Imperative: Conservation assessments would benefit from population genomic insights. *Proc. Natl. Acad. Sci. U.S.A.* **119**, e2210685119 (2022).
2. C. J. Hogg *et al.*, Threatened Species Initiative: Empowering conservation action using genomic resources. *Proc. Natl. Acad. Sci. U.S.A.* **119**, e2115643118 (2022).
3. L. Duntsch, A. Whibley, P. Brekke, J. G. Ewen, A. W. Santure, Genomic data of different resolutions reveal consistent inbreeding estimates but contrasting homozygosity landscapes for the threatened Aotearoa New Zealand hiihi. *Mol. Ecol.* **30**, 6006–6020 (2021).
4. R. A. Mittermeier, C. G. Mittermeier, P. R. Gil, *Megadiversity: Earth's Biologically Wealthiest Nations* (CEMEX, Arlington, VA, 1997).
5. UN/DESA, *Country Classification - Data Sources, Country Classifications and Aggregation Methodology* (United Nations, 2014).
6. B. A. Wintle *et al.*, Spending to save: What will it cost to halt Australia's extinction crisis? *Conserv. Lett.* **12**, e12682 (2019).
7. H. A. Lewin *et al.*, Earth BioGenome project: Sequencing life for the future of life. *Proc. Natl. Acad. Sci. U.S.A.* **115**, 4325–4333 (2018).