

Alma Mater Studiorum Università di Bologna
Archivio istituzionale della ricerca

Reply to D'Huy et al.: Navigating biases and charting new ground in the cultural diffusion of folktales

This is the final peer-reviewed author's accepted manuscript (postprint) of the following publication:

Published Version:

Bortolini, E., Pagani, L., Crema, E.R., Sarno, S., Barbieri, C., Boattini, A., et al. (2017). Reply to D'Huy et al.: Navigating biases and charting new ground in the cultural diffusion of folktales. PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, 114(41), E8556-E8556 [10.1073/pnas.1715139114].

Availability:

This version is available at: <https://hdl.handle.net/11585/609103> since: 2020-02-28

Published:

DOI: <http://doi.org/10.1073/pnas.1715139114>

Terms of use:

Some rights reserved. The terms and conditions for the reuse of this version of the manuscript are specified in the publishing policy. For all terms of use and more information see the publisher's website.

This item was downloaded from IRIS Università di Bologna (<https://cris.unibo.it/>).
When citing, please refer to the published version.

(Article begins on next page)

This is the final peer-reviewed accepted manuscript of:

Bortolini, E., Pagani, L., Crema, E., Sarno, S., Barbieri, C., Boattini, A., Sazzini, M., et al. (2017). Reply to d'Huy et al.: Navigating biases and charting new ground in the cultural diffusion of folktales. *Proceedings of the National Academy of Sciences of the United States of America*, 114 (41), E8556-E8556

The final published version is available online at:

<https://doi.org/10.1073/pnas.1715139114>

Rights / License:

The terms and conditions for the reuse of this version of the manuscript are specified in the publishing policy. For all terms of use and more information see the publisher's website.

This item was downloaded from IRIS Università di Bologna (<https://cris.unibo.it/>)

When citing, please refer to the published version.

Navigating biases and charting new ground in the cultural diffusion of folktales

Eugenio Bortolini, a) Department of Cultural Heritage, University of Bologna, 48121 Ravenna, Italy; b) Department of Humanities, Universitat Pompeu Fabra, 08005 Barcelona, Spain

Luca Pagani, c) Estonian Biocentre, 51010 Tartu, Estonia; d) Department of Biology, University of Padova, 35131 Padua, Italy

Enrico R. Crema, d) Department of Archaeology and Anthropology, University of Cambridge, CB2 3DZ Cambridge, United Kingdom

Stefania Sarno, e) Laboratory of Molecular Anthropology, Department of Biological, Geological, and Environmental Sciences, University of Bologna, 40126 Bologna, Italy

Chiara Barbieri, f) Department of Linguistic and Cultural Evolution, Max Planck Institute for the Science of Human History, 07745 Jena, Germany

Alessio Boattini, e) Laboratory of Molecular Anthropology, Department of Biological, Geological, and Environmental Sciences, University of Bologna, 40126 Bologna, Italy

Marco Sazzini, e) Laboratory of Molecular Anthropology, Department of Biological, Geological, and Environmental Sciences, University of Bologna, 40126 Bologna, Italy

Sara Graca da Silva, g) Institute for the Study of Literature and Tradition, Faculty of Social Sciences and Humanities, New University of Lisbon, 1069-061 Lisbon, Portugal

Gessica Martini, h) Centre for the Coevolution of Biology and Culture, Department of Anthropology, Durham University, DH1 3LE Durham, United Kingdom

Mait Metspalu, c) Estonian Biocentre, 51010 Tartu, Estonia

Davide Pettener, e) Laboratory of Molecular Anthropology, Department of Biological, Geological, and Environmental Sciences, University of Bologna, 40126 Bologna, Italy

Donata Luiselli, e) Laboratory of Molecular Anthropology, Department of Biological, Geological, and Environmental Sciences, University of Bologna, 40126 Bologna, Italy

Jamshid J. Tehrani, h) Centre for the Coevolution of Biology and Culture, Department of Anthropology, Durham University, DH1 3LE Durham, United Kingdom

In their letter (1), d'Huy et al. challenge the novelty of our study (2), and question the reliability of some of our results in the light of previous folkloric research and geographic biases in the ATU index (3). In our reply we explain how their criticisms are already largely addressed in the paper, or based on misunderstandings that we clarify below.

As we make clear in the paper, the idea that the diffusion of folktales might be linked to migration histories is in fact a very old one, and certainly not one we claim for ourselves. However, ours is the first study to investigate this issue at the genomic level rather than using single genetic markers. We show how newly available whole genome sequences from diverse human populations can be used to tease apart the effects of demic movements and cultural diffusion on the international distribution of folktales at different geographic scales. Our results demonstrate that it is particularly difficult to disentangle the explanatory power of genetic variability from spatial proximity beyond ~4,000 km due to the smothering effects of isolation by distance. D'Huy et al. overlook this finding, which has significant implications for the studies they cite and highlights the importance of comparing multiple models to draw inferences about the processes that have generated cross-cultural patterns.

D'Huy et al.'s criticisms concerning the Eurocentric bias of the ATU Index simply reiterate limitations that are already explicitly stated in our paper (and prominently displayed in our Figure 1), and ignore the steps taken to ameliorate them. These involved establishing a minimum threshold of folktale richness for inclusion in the dataset, excluding Africa from the correlation models with genomic variability, and ensuring a uniform geographic distribution of sampled populations across Eurasia. Consequently, the correlations we report between folktale, genomic and spatial distances controlling for linguistic barriers – which form the core part of our results – are not biased by the underrepresentation of African populations in the ATU Index.

The rest of d'Huy et al.'s letter disputes reconstructions of the spread of a few individual tales which are presented in a small and openly tentative section of our Results. Like us, they draw attention to discrepancies between some of our results and those of previous studies (ironically, in light of the above, ours suggest a *less* Eurocentric view of folktale diffusion, as pointed out in SI Appendix page 20). Notably d'Huy et al. do not engage with (or object to) our methodological approach except for making the point that the results might be improved with more data. Of course we agree, and in fact outline potential strategies to test our findings in future research (Discussion, SI Appendix page 20). Moreover, by making our research fully replicable, we would welcome efforts by d'Huy et al. and other researchers to extend our analyses, and capitalize on the rich opportunities for inferring patterns of cultural diffusion in the genomic era.

- 1) d'Huy, J., Le Quellec, J.L., Berezkin, Y., Lajoye, P., Uther, H.J. (submitted) Substantial biases in the paper of Bortoloni et al., *Proceedings of the National Academy of Sciences of the United States of America*
- 2) Bortolini, E., Pagani, L., Crema, E.R., Sarno, S., Barbieri, C., Boattini, A., Sazzini, M., da Silva, S. G., Martini, G., Metspalu, M., Pettener, D., Luiselli, D., Tehrani, J.J., (2017) Inferring patterns of folktale diffusion using genomic data, *Proceedings of the National Academy of Sciences of the United States of America* 114(34):9140-9145

- 3) Uther HJ (2004) *The Types of International Folktales: A Classification and Bibliography. Based on the System of Antti Aarne and Stith Thompson* (Suomalainen Tiedeakatemia, Helsinki).