

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

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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).