LETTER

REPLY TO JIANG AND ZHANG:

Parallel transcriptomic signature of monogamy: What is the null hypothesis anyway?

Rebecca L. Young[a,b,1] and Hans A. Hofmann[a,b,c,1]

To explore whether parallel transcriptomic patterns underlie behavioral similarities across vertebrates, we compared the brain transcriptomes of 5 species pairs representing independent transitions to monogamy. We found similar expression patterns associated with monogamy across deep phylogenetic distances (1). In their letter (2), Jiang and Zhang reanalyze our publicly available data. When comparing "expression level differences of orthologous genes," they find "divergences followed the species phylogeny." Further, they find 15 orthologous gene groups (OGGs; in contrast to our 42) with concordant expression changes, concluding that "expression levels of a very small number of genes" are associated with monogamy. We thank Jiang and Zhang (2) for engaging in discourse that drives scientific advancement and respond to each point below.

Behavior is an emergent property of the organism. The neural transcriptome is closely tied to behavior (3); however, the brain also regulates many other organismal functions. Thus, only a subset of the transcriptome is likely linked to any one behavior. When comparing the whole transcriptome (or at least the 1,979 comparable OGGs), phylogeny should be the strongest signal, as confirmed by Jiang and Zhang (2). While we could have been more explicit about this expectation and result, as we have been previously (4), we disagree that a phylogenetic signal at this level is evidence against a parallel transcriptomic basis of monogamy. Importantly, our analysis embraces species diversity in life history, behavior, ecology, and evolutionary history by including an explicit test of the effect of phylogeny and ecology in determining transcriptomic similarities and finds a correlation between mating system variation and gene expression in OGGs with high interspecific variance after controlling for phylogeny (see figure 6 of ref. 1).

To identify genes with concoradant expression patterns and putatively associated with monogamy, we used several independent analyses. Jiang and Zhang (2) highlight DESeq2 and discuss the limitations of this approach, given our interspecific experimental design. We agree with their reasoning, as acknowledged in the original text. This concern motivated us to integrate diverse analyses including Rank-Rank Hypergeometric Overlap, which tests for statistical overrepresentation of concordant expression, and a comparison of $\log_2$ fold differences across lineages. Genes were considered candidates when multiple approaches indicated their involvement. For their reanalysis, Jiang and Zhang (2) applied a cutoff of ± 2 $\log_2$ fold difference between the monogamous and nonmonogamous species in all lineages, citing this as a commonly accepted "substantial expression change." However, the statistical and biological assumptions that genes with fold differences <2 $\log_2$ are equivalent (5) and do not contribute to maintenance, expression, and regulation of complex traits, respectively, are not justified (6, 7).

The difference in interpretation also deserves attention. Jiang and Zhang (2) discover 15 genes with large, concordant expression changes across lineages, which exceeds the random expectation, further validating our result. Our study shows that shared evolutionary history, evident at the genomic level, is reflected across hierarchical levels of organization and may, in part, underlie the abundance of homoplasies (8–10). Perhaps the null expectation should differ across levels, but determining the appropriate null requires examinations of evolutionary lability at multiple levels.

[a]Department of Integrative Biology, The University of Texas at Austin, Austin, TX 78712; [b]Center for Computational Biology and Bioinformatics, The University of Texas at Austin, Austin, TX 78712; and [c]Institute for Cellular and Molecular Biology, Institute for Neuroscience, The University of Texas at Austin, Austin, TX 78712

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[1]To whom correspondence may be addressed. Email: youngrl@utexas.edu or hans@utexas.edu.

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