Drs. Laura Katz and Adam Eyre-Walker

Editors-In-Chief, *Genome Biology and Evolution*

Dear Drs. Katz and Eyre-Walker,

After some delay due to the lead author’s parental leave, we are happy to re-submit the manuscript titled, “**The genomic landscape, causes, and consequences of extensive phylogenomic discordance in murine rodents**” as an Article to *Genome Biology and Evolution*. This manuscript was transferred from *Molecular Biology and Evolution*.

Evolutionary biology is based upon an understanding of the history of the genomes of our study systems and their closely related species. This history is routinely represented as a phylogeny and a single phylogeny, or species tree, can be used to summarize the speciation history of a group of species. However, we now know that different regions of the genome have undergone different evolutionary trajectories. This can be due to several biological phenomena, including incomplete sorting of ancestral polymorphisms and introgression, and is driven by recombination within evolving populations where those varying histories exist. Despite this knowledge, species trees are still routinely used when studying the evolution of individual loci within the genome. Our paper presents several new rodent genomes in order to use genome-wide data to resolve the species relationships of Old World mice and rats, and then, using the resources of the mouse reference genome, we investigate phylogenetic discordance in depth across the rodent genomes. We find that, despite recovering a well resolved species tree using conserved loci, that topology is not the most common topology across the genome. We also show that phylogenetic similarity across the genome is independent of recombination rates inferred from contemporary lab mice. Finally, we quantify the consequences of this discordance across the genome by testing how using different phylogenies affects common tests for positive selection.

In the original submission, the reviewers had only minor criticisms regarding the scope and text of the document. To accommodate these suggestions, we have re-written parts of the Introduction and Results, largely re-written the Discussion, and made other clarifications throughout the text. The only re-analysis was that of the divergence times with different calibration points, at the suggestion of Reviewer 2. We have also endeavored to make all the formatting changes required by the transfer to GBE.

In all, we are grateful for the reviewer’s suggestions and are happy to work with GBE. We hope you find the paper of interest, and we look forward to hearing from you.

Sincerely,

Gregg Thomas, for all the authors