Corrigendum: Distinguishing genomic homogenization from parapatric speciation in an elevationally replacing pair of Ramphocelus tanagers

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Abstract

Geographically connected species pairs with weakly differentiated genomes could either represent cases of genomic homogenization in progress or of incipient parapatric speciation. Discriminating between these processes is difficult because intermediate stages of either may produce weakly differentiated genomes that diverge at few locations. We used coalescent modelling applied to a genome-wide sample of SNPs to discriminate between speciation with gene flow and genomic homogenization in two phenotypically distinct but genomically weakly diverged species of elevationally replacing Ramphocelus tanagers, forming a hybrid zone in the Andean foothills. We found overwhelming support for a model of genomic homogenization following secondary contact. Simulating under this model suggested that our species pair was differentiated (FST = 0.30) at secondary contact but that most of the genome has rapidly homogenized during 254 Ky of high gene flow towards the present (FST = 0.02). Despite extensive genome-wide homogenization, plumage remains distinctive with a narrower than expected geographic cline width, indicating divergent selection on colour. We found two SNPs significantly associated with plumage colour, which retain moderately high FST. We conclude that the majority of the genome has fused, but that divergent selection on select loci probably maintains the geographically structured colour differences between these incipient species.

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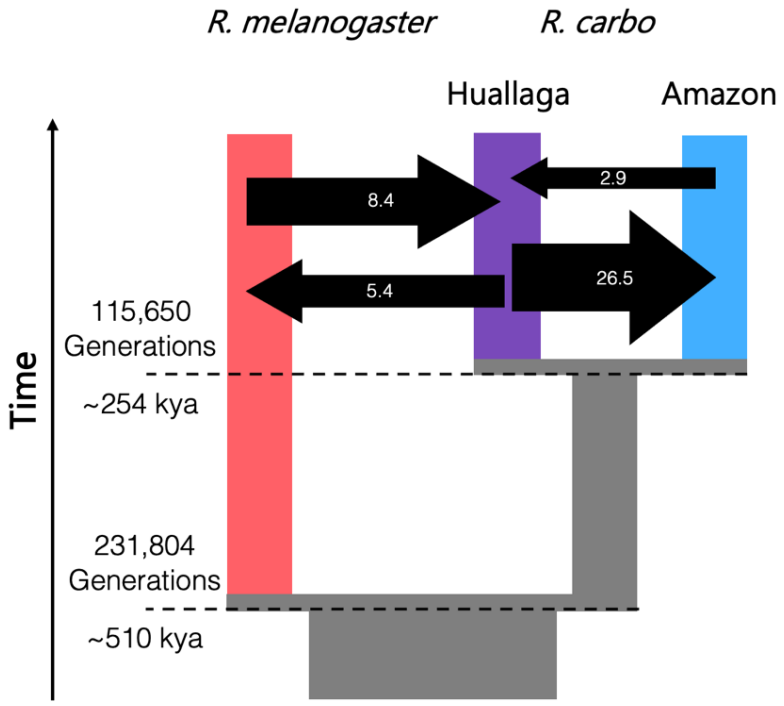
The authors would like to correct an error in the calculation of the number of migrants per generation reported for the best fit demographic model. The demographic model estimates migration rates backwards in time under a coalescent process. These rates represent a per capita rate back in time. We incorrectly multiplied this rate by the effective population size of the recipient population to calculate the number of migrants per generation. Instead, the effective population size of the source population should have been used. This error had no impact on model fit (i.e. AIC and Akaike Weights) and model choice, because the error does not affect any of the parameters estimated by the model. Instead, the error simply impacts the number of migrants per generation calculated from per capita migration rate and effective population size parameters of the model. Also, we now divide these migration rates by two, reflecting the number of diploid individual migrants, whereas we previously reported the number of haploid migrants.

Corrected version of Figure 4:



Our results remain largely unchanged. The number of migrants per generation remain much higher than one between *Ramphocelus melanogaster* and *R. carbo* , as expected if these populations are merging genomically. Previously, our incorrectly calculated number of migrants had suggested much higher movement of individuals into *R. melanogaster* from *R. carbo* than in the reverse. Instead, we now find that the number of migrants moving into *R. carbo* from*R. melanogaster* is slightly higher than in the reverse. Here we show an updated Figure 4 with the correct number of migrants per generation, and we update Table S4 to have the correct parameter values for this model. Coded model files used for demographic analyses deposited in Figshare (dx.doi.org/10.6084/m9.figshare.14981556) have also been updated.

The authors apologize for any inconvenience this may have caused.