Corrigendum

In the article by M. Xu and K. L. Shaw (*GENETICS* **211**: 1089–1104) entitled "The Genetics of Mating Song Evolution Underlying Rapid Speciation: Linking Quantitative Variation to Candidate Genes for Behavioral Isolation" the authors reported a nonsynonymous single nucleotide polymorphism (SNP) in the exon coding for the conserved cyclic nucleotide binding domain in the candidate gene *Cngl* using whole genome sequencing of two males from the intercross offspring of a 4th generation backcross line. Unfortunately, the authors discovered the location of the SNP in the gene was mislabeled. The correct location of the SNP, verified through PCR, is two nucleotides removed from the location indicated in the paper. The result is that the SNP is a synonymous variant.

To that end, several statements in the article were corrected. In the abstract, the clause, "Identification and molecular characterization of the candidate gene reveals a nonsynonymous mutation in a conserved binding domain," was deleted. On p. 1094, in *Materials and Methods*, the following sentence was also deleted, along with the reference to Choi and Chan (2015): "We evaluated the effects of any resulting amino acid substitutions in PROVEAN Protein (Choi and Chan 2015)." Additionally, the last paragraph of the *Results*, beginning with, "The putative *Laupala Cngl* gene. . .", was removed, as well as the first three sentences of the last paragraph on p. 1100: "Most intriguingly, our annotation suggests a functional consequence. . .two types of cNMP."

Figure 7 was replaced to remove sequence data for *Laupala paranigra*, and the Figure 7 legend was modified to remove references to the alleged "amino acid substitution caused by the nonsynonymous SNP in the putative *cngl* on scaffold S001371." The new figure and legend appear below. Accordingly, File S1 and Figure S6 have also been corrected, and Figure S6 appears below. Both Supplemental Material files are available on figshare: https://doi.org/10.25386/genetics.7505762.

The accuracy of the major conclusions and most of the details remain unaffected, and the results remain valid with regard to the conclusions stemming from quantitative trait loci (QTL) fine mapping, identification of *Drosophila melanogaster* song candidate gene in the *Laupala* genome, gene annotation in the QTL region, as well as evaluation of the candidate genes (including *Cngl*). The only impact of this oversight is that, with current data, the authors no longer identify a nonsynonymous SNP within *Cngl* as a candidate causal mutation for pulse rate variation between the two species. However, even without a nonsynonymous SNP, *Cngl* remains the most promising candidate gene for pulse rate variation among all genes annotated within the QTL region according to the three criteria the authors used to evaluate candidate genes.

Literature Cited

Choi, Y., and A. P. Chan, 2015 PROVEAN web server: a tool to predict the functional effect of amino acid substitutions and indels. Bioinformatics 31: 2745–2747. https://doi.org/10.1093/bioinformatics/btv195

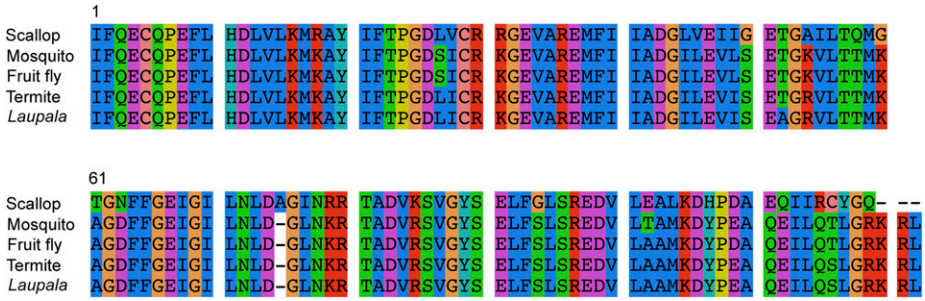

Figure 7 Multiple alignment of amino acid sequences of the cNMP binding domain, one of the domains used for building the tree in Figure 6, within putative homologous proteins of the cyclic nucleotide-gated ion channel-like protein in *D. melanogaster*. Protein sequence of the *Laupala* cNMP domain was translated from DNA sequence based on alignment to termite cNMP domain sequence in Exonerate (available in Figure S6).