CORRIGENDUM

Mitochondrial genomes and thousands of ultraconserved elements resolve the taxonomy and historical biogeography of the *Euphonia* and *Chlorophonia* finches (Passeriformes: Fringillidae)

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The following errors have been identified in this manuscript, but they do not substantially alter the findings of the study in any way.

In the Introduction, the authors introduce the euphonias and chlorophonias as members of the true-finch family. This family, Fringillidae, is misspelled as “Friingillidae”, and should be corrected.

In the Taxonomic Sampling section, the authors state the number of tissue samples that were included in the study, but the number of species represented in each genus was reported incorrectly. The statement:

“We obtained loans of frozen or ethanol-preserved tissue samples for all 5 Chlorophonia species and for 23 of 27 Euphonia species…”

Should read:

“We obtained loans of frozen or ethanol-preserved tissue samples for 4 Chlorophonia species and for 24 of 27 Euphonia species…”

In the Mitochondrial Phylogeny section of the results, the authors describe topological differences between the phylogenies inferred from mitogenomes versus those inferred from UCE loci. They failed to report a third difference in the mitogenome-based phylogeny, and the proportion of UCE gene trees supporting the other two differences in the mitogenome-based phylogeny were reported incorrectly.

The last paragraph of this section:

“Two additional points in the mitogenome tree support relationships that were not found in any of the UCE-based phylogenies. First, *E. chrysopasta* was found to be sister to the set of 3 small *Euphonia* clades. This placement has only 74% bootstrap support in the mitochondrial phylogeny, but its placement in the 2 concatenated trees as the sister to (minuta, [chalybea, {violacea, (hirundinacea, laniirostris)]]) had 100% bootstrap support. Its placement in the ASTRAL species tree matched that of the 2 other UCE-based phylogenies, but had moderate to low concordance factor and IC support (gCF = 18.5, sCF = 47.7, IC = 0.093). We searched the individual gene tree topologies containing this relationship to find the frequency at which the UCE sequences supported this relationship and found that only 18.1% (701/3,867) of gene trees did. Second, *E. jamaica* and *saturata* are sister species in the mitochondrial tree with reasonably high bootstrap support (84%), whereas *jamaica* is sister to all other species in its lineage with high support in both the ASTRAL species tree (gCF = 34.9, sCF = 70.0, IC = 0.322) and the incomplete RAxML phylogeny (bootstrap = 100%), and *saturata* is sister to all other species within its clade in the complete, concatenated RAxML phylogeny with full bootstrap support. Only 19.1% (772/4,053) of individual UCE gene trees supported a sister relationship between the 2 species. Overall, we found evidence for only 2 instances of phylogenetic discordance between the mitochondrial and the nuclear UCE sequence data, with only moderate support.”

Should read:

“Three additional points in the mitogenome tree support relationships that were not found in any of the UCE-based phylogenies. First, *E. chrysopasta* was found to be sister to the set of 3 small *Euphonia* clades. This placement has only 74% bootstrap support in the mitochondrial phylogeny, but its placement in the 2 concatenated trees as the sister to (minuta, [chalybea, {violacea, (hirundinacea, laniirostris)]}) had 100% bootstrap support. Its placement in the ASTRAL species tree matched that of the 2 other UCE-based phylogenies, but had moderate to low concordance factor and IC support (gCF = 18.5, sCF = 47.7, IC = 0.093). We searched the individual gene tree topologies containing this relationship to find the frequency at which the UCE sequences supported this relationship and found that only 18.1% (701/3,867) of gene trees did. Second, *E. jamaica* and *saturata* are sister species in the mitochondrial tree with reasonably high bootstrap support (84%), whereas *jamaica* is sister to all other species in its lineage with high support in both the ASTRAL species tree (gCF = 34.9, sCF = 70.0, IC = 0.322) and the incomplete RAxML phylogeny (bootstrap = 100%), and *saturata* is sister to all other species within its clade in the complete, concatenated RAxML phylogeny with full bootstrap support. Only 19.1% (772/4,053) of individual UCE gene trees supported a sister relationship between the 2 species. Overall, we found evidence for only 2 instances of phylogenetic discordance between the mitochondrial and the nuclear UCE sequence data, with only moderate support.”

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laniirostris)) had 100% bootstrap support. Its placement in the ASTRAL species tree matched that of the 2 other UCE-based phylogenies, but had moderate to low concordance factor and IC support (gCF = 18.5, sCF = 47.7, IC = 0.093). We searched the individual gene tree topologies containing this relationship to find the frequency at which the UCE sequences supported this relationship and found that only 6.9% (107/1,558) of gene trees did. Second, E. jamaica and saturata are sister species in the mitochondrial tree with reasonably high bootstrap support (84%), whereas jamaica is sister to all other species in its lineage with high support in both the ASTRAL species tree (gCF = 34.9, sCF = 70.0, IC = 0.322) and the incomplete RAxML phylogeny (bootstrap = 100%), and saturata is sister to all other species within its clade in the complete, concatenated RAxML phylogeny (bootstrap = 100%).

In the third paragraph of this section, the sentence:

“The only variable placements of any species in this clade are the oldest divergences defining the placement of E. jamaica and saturata.”

This sentence should reflect the corrected results of the mitogenome phylogeny and read:

“The only variable placements of any species in this clade are the oldest divergences defining the placement of E. jamaica, saturata, and chlorotica.”

Lastly, in the section Paraphyly of Euphonia and Historical Precedent for Three Genera of Euphoniine Finches, the authors discuss the previous taxonomic assignment of three euphonia species in the genus Cyanophonia.

The second-to-last sentence of the legend for Figure 3 reads:

“White arrows point to 3 points on this phylogeny that differ from all of the UCE-based phylogenies: the sister relationship of E. jamaica and saturata, the placement of E. chrysopasta, and the relationships among E. fulvicrissa, imitans, and gouldi.”

This sentence should read:

“White arrows point to 3 points on this phylogeny that differ from all of the UCE-based phylogenies: the sister relationship of E. jamaica and saturata, the placement of E. chrysopasta, and the placement of E. chlorotica.”

There were additional issues in Figure 3, which presented the results of their phylogenomic analyses to traditional classifications of species groups within the subfamily that were based on phenotypic characteristics. In the third paragraph of this section, the sentence:

“The only variable placements of any species in this clade are the oldest divergences defining the placement of E. jamaica and saturata.”

This sentence should reflect the corrected results of the mitogenome phylogeny and read:

“The only variable placements of any species in this clade are the oldest divergences defining the placement of E. jamaica, saturata, and chlorotica.”

When quoting Charles Lucien Bonaparte’s manuscript from 1851 to provide support for a proposed revision, they state:

“The third proposal stems from the fact that, in the same work in which he created the name Chlorophonia, Bonaparte also designated a separate genus for E. musica and cyanocephala (then described as aurita)...”

The previous name for this taxon was “aureata”, and “aurita” should be corrected to reflect this fact.

The authors sincerely regret these errors in the original manuscript.