

AOS Classification Committee – North and Middle America

Proposal Set 2021-C

8 March 2021, rev. 23 March 2021

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Revise the classification of the Antillean Piculet *Nesocittes micromegas*

Background:

The Antillean Piculet *Nesocittes micromegas* was first described in the genus *Picumnus* by Sundevall (1866), who placed all piculets in that genus. Hargitt (1890) separated *Sasia* and *Verreauxia* from *Picumnus* and erected the monospecific genus *Nesocittes* for the Antillean Piculet, based on its large size for a piculet and differences from other piculets in wing, bill, and foot structure and proportions. For most of the 20th century, *Nesocittes* was thought of as closely related to the other piculets, particularly *Picumnus* (e.g., Peters 1948, Cruz 1974). Goodge (1972), based on detailed anatomical study of 47 species of woodpeckers spanning the diversity of the family, remarked that “*Nesocittes* is perhaps closer to the ancestral members of the Picinae [than to other piculets]”, but didn’t make any taxonomic changes.

Short (1974) cataloged a variety of morphological and behavioral differences between the Antillean Piculet and other piculets, including its much larger size, passerine-like foraging and locomotory behaviors (foraging primarily by gleaning, sometimes probing, and only rarely tapping, and perching and moving with the body at right angles or diagonally to branches, rather than clinging to trunks and branches with the body parallel like typical piculets or woodpeckers; Short described it as almost vireo-like in the field, and Bond (1928) described it as acting very much like *Xenops*), and distinctive vocalizations (including antiphonal duetting and a lack of drumming). He accordingly advocated placing the Antillean Piculet in its own tribe, Nesocittini*, separate from the rest of the piculets (Picumnini) within Picumninae, pending further systematic study.

In the sixth edition of the AOU Checklist, the first to include the birds of the Caribbean, the Antillean Piculet was placed in a monospecific tribe Nesocittini within Picumninae, where it remains to this day (AOU 1983, Chesser et al. 2020).

New Information:

Several recent molecular phylogenetic studies have corroborated earlier ideas based on morphology that the Antillean Piculet is more closely related to typical woodpeckers than it is to other piculets. The first molecular phylogeny of woodpeckers to include *Nesocittes* was published by Benz et al. (2006), who sequenced 2 mitochondrial genes and 1 nuclear gene from 46 species of woodpeckers, including representatives of all piculet genera and most typical woodpecker genera (but not the Asian genus *Hemicircus* - see below). Benz et al. recovered the Antillean Piculet as sister to Picinae with strong support (see tree on next page), and accordingly, taking into account the various morphological and behavioral differences between it and typical woodpeckers, tentatively recommended that it be placed in a monogeneric subfamily Nesocittinae.

*Nesocittini was not formally named until 1976, by Wolters in *Die Vogelarten der Erde* (Bock 1994)

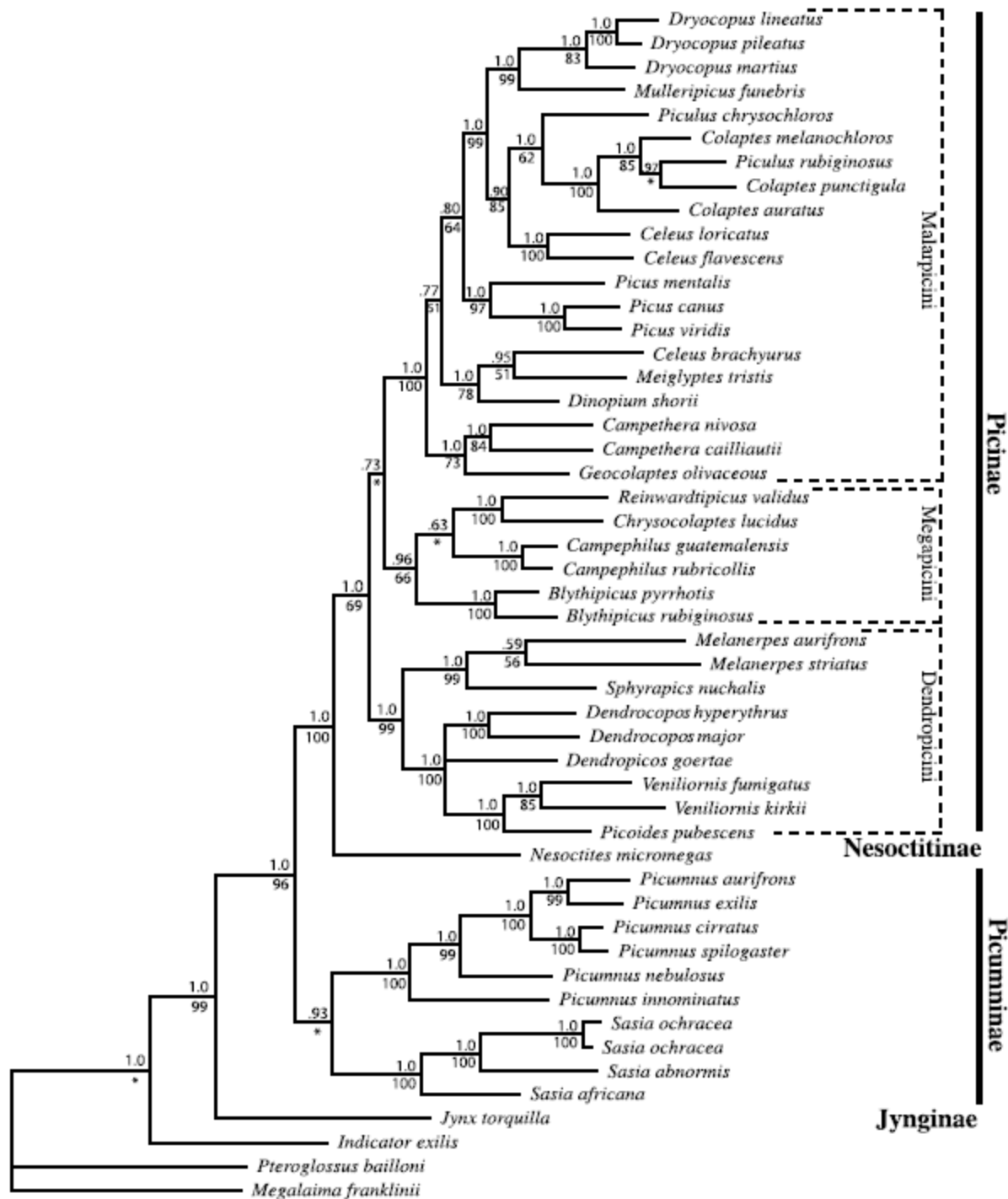


Fig. 1. Phylogenetic results depicting the evolutionary history of the woodpeckers and allies, as inferred from a seven-partition Bayesian analysis using the GTR + I + G model. Numbers above each node represent posterior probabilities, while Maximum Likelihood bootstrap values are indicated below each node, with * indicating less than 50% bootstrap support.

Dufort (2016) constructed a supermatrix phylogeny of 172 picid taxa using a subset of 25 loci (10 mitochondrial, 12 autosomal, 3 Z-linked) and again recovered *Nesocitites* as more closely

related to typical woodpeckers than to other piculets, with strong support. The relationships among *Nesocittes*, *Hemicircus*, and the rest of the woodpeckers were poorly resolved:

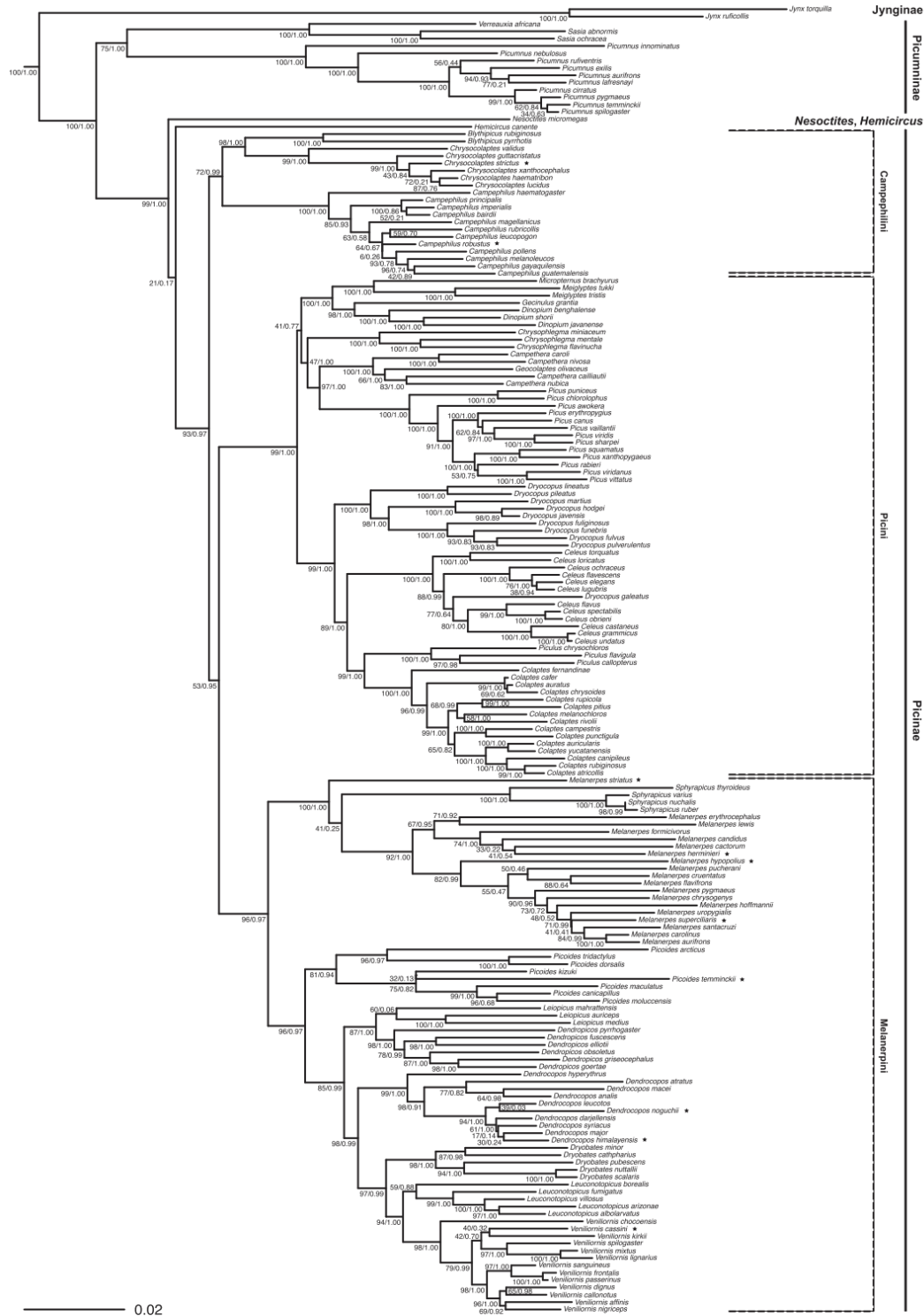


Fig. 2. Phylogenetic relationships of Picidae inferred from maximum likelihood analysis of the concatenated alignment of all loci in RAxML. Numbers at nodes indicate percentage of bootstrap replicates and posterior probabilities for the descendant clade. Stars indicate taxa identified by *RogueNaRok* as rogues in the ML analyses. Bars and labels at right indicate named subfamilies, tribes, and genera that do not fit into existing groupings.

Shakya et al. (2017) sequenced 2 mitochondrial loci and 3 nuclear loci (2 autosomal, 1 Z-linked) from 203 picid species. Again, *Nesoctites* was strongly supported as more closely related to typical woodpeckers than to other piculets; the relationships among *Nesoctites*, *Hemicircus*, and the rest of the woodpeckers were poorly resolved; and piculet monophyly (excluding *Nesoctites*) was uncertain.

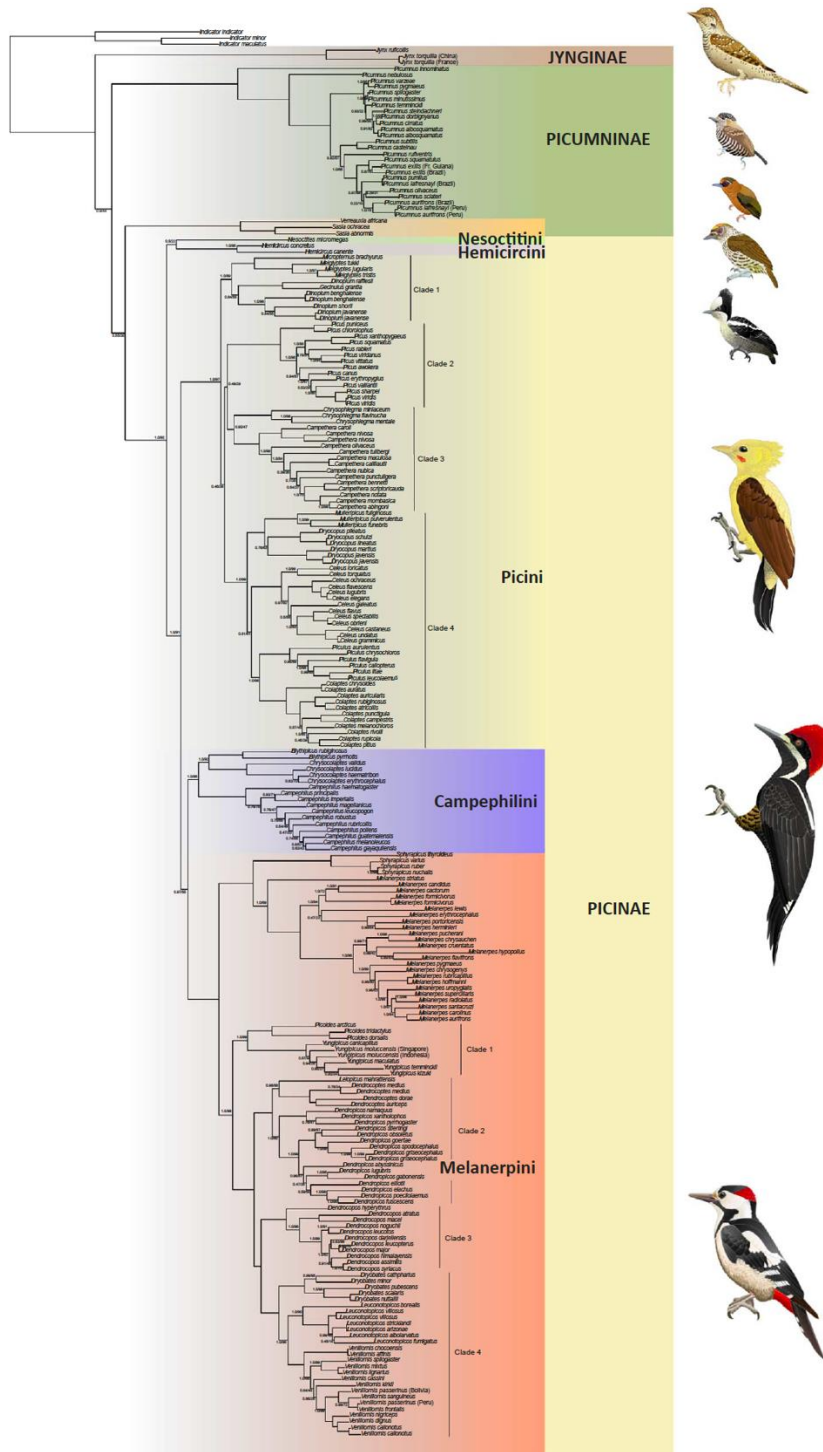


Fig. 1. Bayesian tree showing relationships among woodpeckers based on mtDNA and nuclear sequences. Posterior probabilities less than 1.0 and bootstrap values less than 100% are shown above or below branches, respectively. Subfamily and tribes are indicated by colored shading. Exemplar taxa of each subfamily and tribe are illustrated on the right. (Illustrations by Subir B. Shakya).

Regardless of the precise relationships among the “typical” piculet lineages and between *Nesocittes*, *Hemicircus*, and the rest of the woodpeckers, it is clear that *Nesocittes* is more closely related to Picinae *sensu* Chesser et al. (2020) than it is to *Picumnus*, and accordingly it must be removed from Picumninae (in agreement with the variety of morphological and behavioral differences between it and all other piculets).

Recommendations:

Given that the Antillean Piculet is strongly supported in multiple molecular phylogenetic studies as more closely related to Picinae than to *Picumnus*, it must be removed from Picumninae. Whether to place the Antillean Piculet in Picinae or in its own subfamily Nesocittinae is more subjective. Given the striking morphological and behavioral differences between the Antillean Piculet and typical woodpeckers (including a lack of stiffened rectrices and a lack of adaptations for drilling into hard substrates), as well as its phylogenetic position sister to the typical woodpeckers (or sister to *Hemicircus* and together sister to the typical woodpeckers), I tentatively recommend placing Antillean Piculet in Nesocittinae (which in the latter scenario requires recognizing Hemicircinae as a subfamily as well, although that’s outside the purview of this committee).

Please vote on (a) removing *N. micromegas* from Picumninae, and (b) recognizing the monospecific subfamily Nesocittinae. YES votes on both parts of this proposal would move Antillean Piculet to a monogeneric Nesocittinae, placed in linear sequence between Picumninae and Picinae. A YES vote on Part A but a NO vote on Part B would move Antillean Piculet (and tribe Nesocittini) to the beginning of Picinae.

Literature Cited:

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Submitted by: Max T. Kirsch

Date of Proposal: 8 February 2021

Transfer Flammulated Flycatcher *Deltarhynchus flammulatus* to *Ramphotricon*

Effect on NACC:

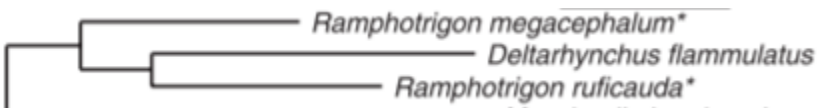
If approved, this proposal would subsume *Deltarhynchus* into *Ramphotricon*, transferring *Deltarhynchus flammulatus* to *Ramphotricon* and resulting in the addition of one genus (*Ramphotricon*) and deletion of another (*Deltarhynchus*) from the checklist.

Background:

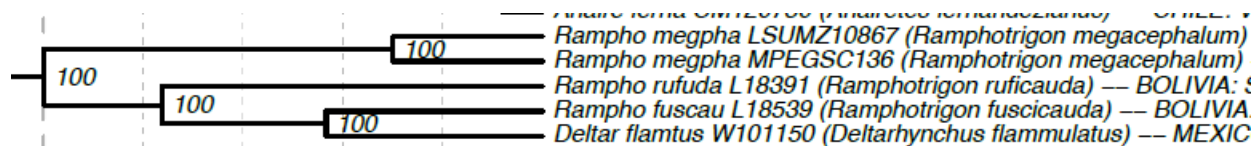
Myiarchus flammulatus, described by Lawrence in 1875, was transferred by Ridgway to the new monotypic genus *Deltarhynchus* in 1893, based on its bill shape, wing shape, and partly streaked underparts. Lanyon (1982) studied the behavior and morphology of this species and concluded that it belongs to the myiarchine flycatchers, but that it is sufficiently different from *Myiarchus* to warrant a separate genus. Later, Lanyon (1985, 1988) proposed that *Deltarhynchus* is most closely related to *Ramphotricon*, a genus consisting of three species endemic to South America: *R. ruficauda*, the type species, *R. fuscicauda*, and *R. megacephalum*. We currently place *flammulatus* in *Deltarhynchus*.

New Information:

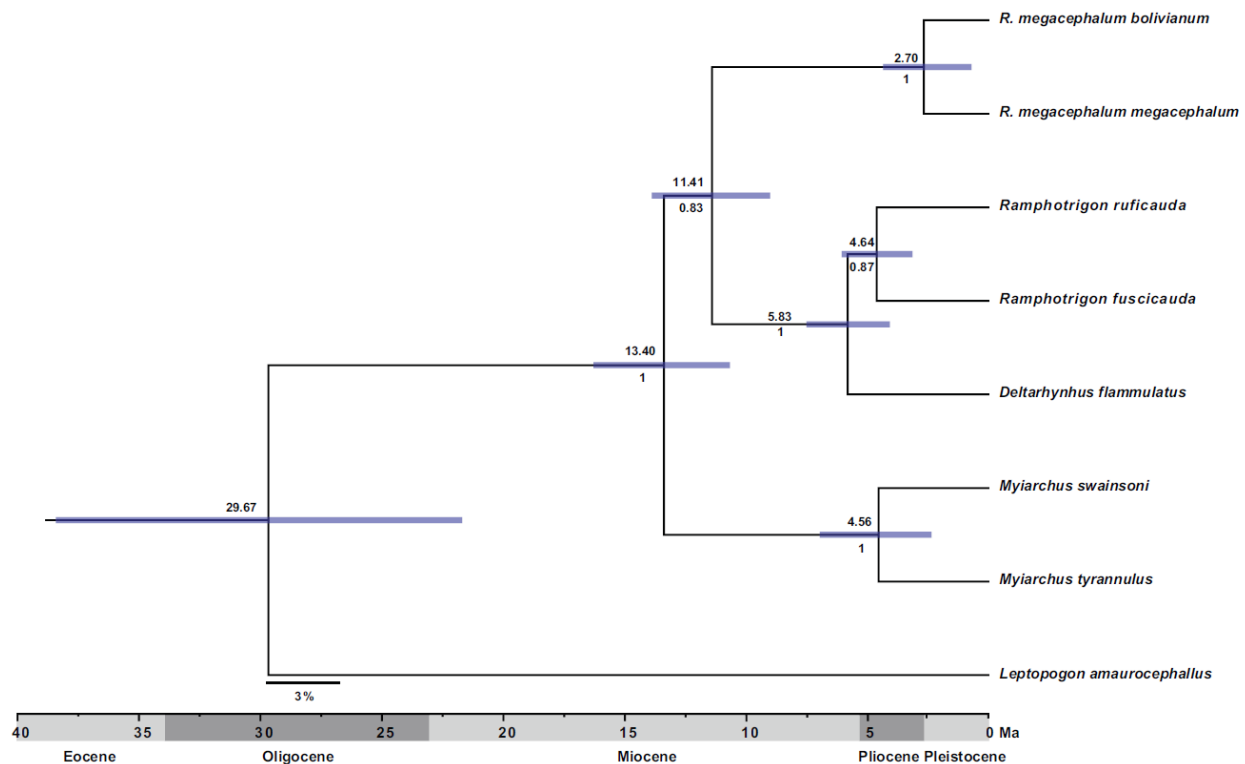
Molecular phylogenies have shed new light on the relationships of *D. flammulatus*, consistently grouping it with *Ramphotricon*. Ohlson et al. (2008), in a study of the Tyrannidae based on sequences from four nuclear introns and one exon, sampled *D. flammulatus* and two species of *Ramphotricon* and found *D. flammulatus* to be sister to *R. ruficauda* and *R. megacephalum* to be sister to *flammulatus-ruficauda*:



More recently, Lavinia et al. (2020; see next page), using sequences from three mitochondrial genes and one nuclear intron, and Harvey et al. (2020; see tree excerpt below) using sequences from 2389 genomic regions (UCEs and exons), sampled *D. flammulatus* and all three species of *Ramphotricon*. Both studies concluded that *D. flammulatus* is nested within *Ramphotricon*. In the Harvey et al. (2020) tree, *D. flammulatus* is sister to *R. fuscicauda*, with *ruficauda* sister to *flammulatus-fuscicauda*, and *R. megacephalum* sister to *flammulatus-fuscicauda-ruficauda*, all nodes receiving 100% bootstrap support:



In the Lavinia et al. (2020) tree, *R. fuscicauda* and *R. ruficauda* were sister species, although with only 0.87 posterior probability, and *D. flammulatus* sister to them, and *R. megacephalum* again sister to *flammulatus-fuscicauda-ruficauda*. Lavinia et al. (2020) also suggested, based not only on the genetic evidence but on morphological differences between *R. megacephalum* and the other three species, which were very similar morphologically, that *Ramphotricon* might be split, placing *megacephalum* in a new genus, but that is an issue for the SACC.



Recommendation:

I recommend that the committee transfer *D. flammulatus* to *Ramphotricon*.

Literature Cited:

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Submitted by: Terry Chesser

Date of Proposal: 9 February 2021

Treat *Cistothorus stellaris* as a separate species from *C. platensis***Background:**

NACC currently considers the Sedge Wren *Cistothorus platensis* to be a single species distributed from Canada to extreme southern South America. AOU (1998) recognized three groups within the species: Sedge Wren *C. stellaris*, consisting of migratory populations breeding in the US and Canada and wintering mainly in the southern US and northern Mexico, as well as sedentary populations from Mexico south to Panama; and Western Grass-Wren *C. platensis* and Eastern Grass-Wren, both resident in South America. The recognition of two groups of grass-wrens was apparently based on the morphological study of Traylor (1988). AOU (1998) also noted that *C. platensis* forms a superspecies with two other species of restricted distribution in the Colombian and Venezuelan Andes, the Paramo Wren or Merida Wren *C. meridae* and Apolinar's Wren *C. apolinari*. Dickinson and Christidis (2014) and the Clements list (2019) divided *C. platensis* into 18 subspecies.

The current species-level NACC treatment is in keeping with those of Hellmayr (1934) and Peters (Mayr and Greenway 1960), who treated all populations of *C. platensis* as a single species. Ridgway (1904), however, considered the populations in North America to constitute two species and the South American populations to be specifically distinct from these. He grouped the migratory populations breeding in the US and Canada as *C. stellaris* and the sedentary populations in Mexico and Central America as *C. polyglottus*.

New Information:

Robbins & Nyári (2014) sequenced the mitochondrial ND2 gene for 53 individuals of *C. platensis*, three individuals of *C. apolinari*, and two individuals of *C. meridae*. Sampling was conducted throughout the range of *C. platensis* but samples were not identified to subspecies; they were categorized instead by the names of species candidates identified using the GYMC molecular method. Sampling for North America included 20 individuals: two from Canada, eight from the US, five from Mexico, two from Guatemala, and three from Costa Rica. In addition, two nuclear introns were sequenced for a small subset of individuals, apparently numbering 13, including two individuals of subspecies *stellaris* from the US and Canada and three other samples from the sedentary populations in Mexico, but not including samples of *C. apolinari* or *C. meridae*.

The likelihood and Bayesian analyses of Robbins and Nyári (2014; see their Fig. 2 below) indicated that samples of *C. platensis* formed eight major clades, and that *C. apolinari* and *C. meridae* were nested within *C. platensis*. All individuals of subspecies *stellaris* (from the US and Canada) grouped together as sister to the remaining samples of *C. platensis*, *C. apolinari*, and *C. meridae*. Among samples in the sister group to *stellaris*, the samples of *meridae* and *apolinari* formed a clade that was sister to all other individuals of *C. platensis*. Thus, *C. platensis* was not monophyletic, although this result was entirely based on the mtDNA sequences. Clade A in the phylogeny below corresponds to *stellaris*, clades B and C are *meridae* and *apolinari*, respectively, and clades D-J are the remaining individuals of *C. platensis*. Clade D, consisting of

all samples from Mexico, Guatemala, and Costa Rica, was sister to clades E-J, which consisted of individuals from South America, including the Falkland Islands and Tierra del Fuego. Support values on the trees are tiny and difficult to read, but support for *stellaris* as sister to all other individuals appears to be 0.99 posterior probability and 78% bootstrap, which is moderately strong. The time calibration at the bottom of the tree indicated that the separation of *stellaris* from the rest occurred some 3-3.5 mya.

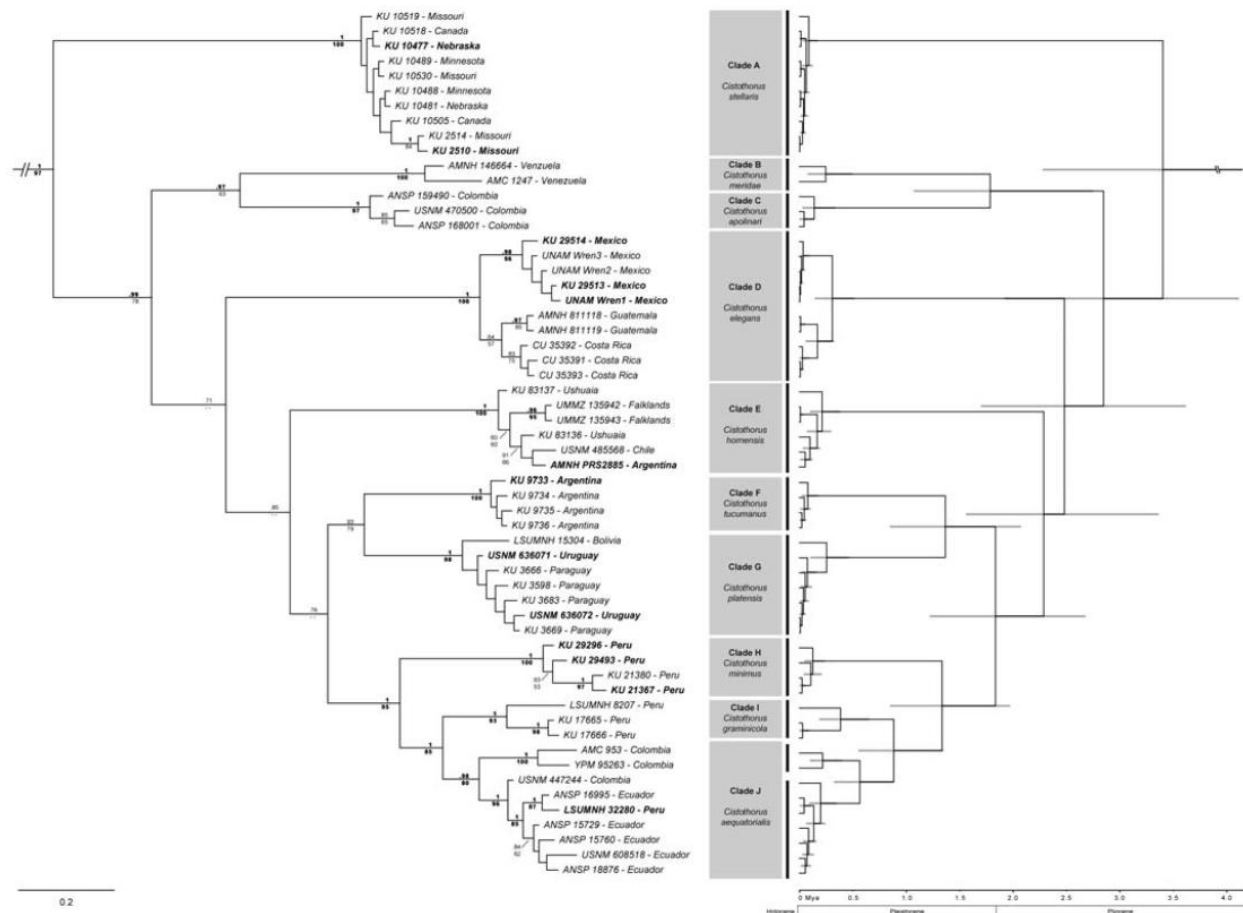


FIG. 2. Phylogenetic relationship of Sedge Wren (*Cistothorus platensis*) populations based on Bayesian and Maximum likelihood analyses. Individuals are represented by catalog number acronyms and country of provenance. The tree was rooted with *Cistothorus palustris* and *Troglodytes aedon* (omitted for display purposes). Taxa with bold font were sequenced for the nuclear introns Fib5 and TGFb2 in addition to the mitochondrial ND2 gene. Nodal support in form of Bayesian posterior probabilities (BPP) is presented above branches, while ML bootstrap support (MLBS) is indicated below each branch. Support values of BPP above 95 and MLBS above 80 are in bold and considered significant, whereas support values below 50 are indicated with a double dash. Clade names and letters follow details in the Results and Discussion sections. At right, a chronogram with 95% confidence intervals around node heights was derived from the ultrametric tree generated in the program BEAST and calibrated using a normally distributed prior ($2.0 \times 10^{-8} \pm 1$ substitutions/site/year/lineage) on the ND2 mutation rates. Dark vertical bars to the right of the gray clade name boxes indicate the distinct species delimited by the GMYC algorithm (see Methods).

Robbins and Nyári (2014) also examined recordings of the various species and subspecies (seven songs of *stellaris*, three of *C. meridae*, six of *C. apolinari*, and some 100+ songs from the

rest of *C. platensis*), but no results of these investigations were presented in their paper. This was explained in the Discussion, where it was attributed to difficulties in assessing which song features are useful in species recognition and to difficulties in understanding individual repertoires in these oscine birds. Qualitative assessments, some based on the studies of Kroodsma (1999a, b, 2001, 2002), were instead conducted and qualitative differences noted between a few of the taxa.

In sum, Robbins and Nyári (2014) concluded that, except for the songs of *C. meridae* and *C. apolinari*, which differ greatly from those of *C. platensis* as well as from those of each other, “it appears that song is conserved in the complex of Sedge Wrens, presumably related to constraints of phylogenetic inertia and transmission of song in an open, windy environment. Indeed, with the exception of *meridae* and *apolinari*, it is easy to recognize song of a member of this complex regardless if one is in Canada or at the tip of South America.” Nevertheless, Robbins and Nyári (2014) further noted that Kroodsma and colleagues found *stellaris* to be “unique in being polygynous, migratory, non-site specific, and by improvising its song, whereas all other *Cistothorus* taxa appear to be monogamous, non-migratory, site specific, and imitate adjacent male’s songs (Kroodsma et al. 1999a,b, 2001, 2002).”

More recently, Boesman (2016) reviewed the vocalizations of *C. platensis*, the specific purpose of which was to compare songs of subspecies *stellaris* to those of all other forms of this species. He characterized the songs of *stellaris* as “fairly uniform and simple over its entire range: a few “tsik” notes followed by a rattled series of notes”, whereas the songs of all other subspecies were “much more complex, combining many different phrases which consist of several note types within each phrase.” As to specific characters, Boesman concluded that the songs of *stellaris*, when compared to those of the other subspecies, consist of fewer different phrases within a song series, contain fewer notes within phrases, and lack notes of long duration. Examples of the songs of *stellaris* and other populations of *C. platensis* (ranging from Mexico to Argentina) are available in the pdf of Boesman’s report at https://static.birdsoftheworld.org/on285_sedge_wren.pdf, as well as at online sites such as xeno-canto.org.

SACC, curiously, recently considered a proposal to split subspecies *stellaris* from the rest of *platensis* (SACC Proposal 820; <https://www.museum.lsu.edu/~Remsen/SACCprop820.htm>) without consulting the NACC about this North American endemic and without sending the proposal through the NACC, a circumstance noted in the SACC comments attached below (one member of SACC voted NO based on this being primarily a NACC issue). Despite this, and despite misgivings of some members due to the lack of published data (e.g., the small amount of sequence data almost exclusively from mtDNA, the lack of a published analysis of songs, and the small number of *stellaris* songs reviewed by Boesman), the proposal passed 8-1. This split has also been implemented in the IOC list (Gill et al. 2021).

Recommendation:

I agree with the SACC members who expressed frustration with the data marshalled in support of this split. Nevertheless, I think that the differences in song and other behavior identified by Kroodsma and Boesman, supplemented to some extent by the genetic data showing *stellaris* to be a distinct lineage, are sufficient to recommend that we treat *stellaris* as a separate species. It

seems highly likely that *stellaris* is truly reproductively isolated from the rest of *C. platensis*. As to English names, Sedge Wren is well-established for *stellaris*, either as a subspecies or a group, and Grass Wren for populations of *platensis* in South America (e.g., AOU 1998) and sometimes beyond (e.g. Gill et al. 2021), and I recommend that these names be retained.

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Submitted by: Terry Chesser

Date of Proposal: 11 February 2021

Comments on SACC Proposal 820:

Comments from Stiles: “YES. Splitting *stellaris* from *platensis* (really a decision for NACC) is an obvious YES. However, this dodges the issue for SACC, because the genetic data clearly justify several splits for the South American taxa. although some degree of conservatism might

be justified where vocal data are scarce or lacking, at least three splits seem perfectly justified. Over to you, Mark!

Comments from Pacheco: “YES. The data available justifies the decision.”

Comments from Zimmer: “YES”. This one is long overdue, as suggested by vocal, morphological and behavioral (migratory versus sedentary) differences, and, as confirmed by the genetic data, which establishes that *C. platensis*, as currently recognized, is not monophyletic. We still need to deal with species-limits within the South American “Grass/Sedge” Wrens – a stickier and more complicated proposition.”

Comments from Jaramillo: “YES – this is a given, now on to the more complex issues within South America. By the way, I recall reading in one of the popular books that D. Kroodsma wrote he noted that *stellaris* was a “random song generator” in that within the very basic pattern that they use, that each song is slightly different, and created on the spot seemingly. Different from other wrens in this respect. I do not think this is published anywhere else, and I could not find where I had read it. So, take it as hearsay, or poor recollection if I am wrong.”

Comments from Remsen: “YES, but somewhat reluctantly because no matter how obvious this split seems to everyone, the published evidence for it is weak. A rather small sample of genes indicate that *platensis* as traditionally recognized is paraphyletic with respect to two South American taxa traditionally treated as species, but at the species level, peripheral speciation predicts paraphyletic species. As for voice, the published data are strongly suggestive but fall far short of a rigorous analysis. As for migratory vs. sedentary, that *stellaris* is migratory is in itself not a species-level marker, because individuals in the same population of some species can be migratory or sedentary, some individuals of some species can be migratory in some years, not in others, and within many monotypic species, the higher-latitude population can be highly migratory and the lower-latitude population sedentary (a familiar North American example being *Mimus polyglottos*).”

Comments from Areta: “A hesitant YES. This one is, to me, one of this thought-to-be obvious cases in which no one has taken the time to do a proper and careful comparative analysis and publish it. The “work” by Boesman has few samples of *stellaris* and cannot be considered by any means a thorough vocal analysis, and I believe that it cannot be used as a justification of range-wide vocal consistency or even as a good description of vocal features of *stellaris*. Kroodsma’s papers provide much better insights, even though they were not in general focusing on continent-wide geographic variation in vocalizations and their importance in taxonomy. I echo all of Van’s concerns on the other points, and so my hesitation.”

Comments from Bonaccorso: “YES. Well-supported reciprocal monophyly of *Cistothorus stellaris* and *C. platensis* (mt DNA), two nuclear introns recovering the same topology (according to Robbins and Nyari 2014, not shown), differences in song, and migratory behavior in *C. stellaris*, suggest reproductive isolation.”

Comments from Ribas: “YES. I agree with the proposal that *C. stellaris* should be treated as distinct from *C. platensis*. Even considering that the genetic evidence comes almost only from ND2, the combined geographical, vocal and behavioral evidence end up being strong in my

opinion for considering them distinct species. In addition, support for the (*C. meridae*, *C. apolinar*) clade as sister to all other *C. platensis* except *C. stellaris* is high, and this would hardly change with additional genetic sampling.”

Comments from Stotz: “NO. I think that *stellaris* is a distinct species from *platensis* (although published data are on the weak side). I am voting NO because I think this is a decision that should be made first by NACC since *stellaris* is extralimital to South America, and whether these are split or lumped, South American birds would still be *C. platensis*.”

Elevate *Turdus rufopalliatus graysoni* to species rank**Background:**

Turdus rufopalliatus (Rufous-backed Robin) occurs in western Mexico from Sonora to Chiapas and on the Tres Mariás archipelago. Dickinson & Christidis (2014) recognized three subspecies: (1) nominate *rufopalliatus* from Sonora to Puebla, (2) *interior* in the Balsas basin, from Michoacán to Puebla, and (3) *graysoni* on the Tres Mariás, and also in coastal Nayarit according to A. R. Phillips (1981, 1991), where sympatry with nominate *rufopalliatus* was used by Phillips (1981) to elevate *graysoni* to species rank. The latter was treated as a separate species (Grayson's Robin) by Ridgway (1907), but Hellmayr (1934) treated it as a subspecies of *rufopalliatus* with the following statement:

"This is merely a pale, large-billed race of the mainland bird. Certain individuals of the latter in worn breeding plumage closely approach it in coloration, and it is no doubt on such a specimen that Nelson's record of *T. r. graysoni* from Santiago, Nayarit, was based."

Subsequently, all standard references have followed Hellmayr, including those after Phillips (1981), except for Sibley and Monroe (1990) and Howell and Webb (1995; Mexico field guide), who tentatively treated it as a separate species "*Turdus (rufopalliatus?) graysoni*" but clearly were cautious ("Status needs further study" and "may be resident" on mainland). I wrote a NACC proposal in 1999 to recognize *graysoni* as a separate species based on Phillips's paper, with the following conclusion:

"Recommendation: I think that the case for a syntopic, resident mainland population of *graysoni* is weak. So far, we do not even have specimen evidence of year-round presence on the mainland, much less breeding. Yes, the number of specimens rules out casual wandering in my opinion, but until *graysoni* is shown to breed there, I think the conservative treatment is to consider it a non-breeding visitor there, with one anomalous late June record. If this is correct, then their seasonal overlap is irrelevant to species limits. Also, the absence of any comparative information on voice or anything else other than plumage prevents any real analysis of differentiation of *graysoni* vs. *rufopalliatus*. As for the plumage difference, the degree of paleness of *graysoni* vs. *rufopalliatus* is roughly comparable to the paleness of the isolated southern Baja population of Am. Robin (*T. m. confinis*) relative to "regular" Am. Robin. As long as we continue to treat *confinis* (San Lucas Robin) as a subspecies of Am. Robin (right or wrong), then treating *graysoni* as a subspecies of *rufopalliatus* represents a consistent philosophy in treatment of isolated, pale thrushes. In other words, I find it difficult to justify treating *confinis* as a subspecies (at least for which tantalizing vocal differences were noted by Howell and Webb) but *graysoni* as a species. All in all, I regard the case for splitting them as weak, especially because I do not think that there are any other Tres Mariás endemics ranked as species."

The proposal did not pass. Phillips (1981) himself pointed out that the Tres Marías representative of *Parula*, *P. p. insularis*, migrates to the mainland, so another species shows a pattern of migrating from the islands to the mainland; Phillips treated *insularis* as subspecies of *P. pitiayumi*. The difference in his treatment of *graysoni* as a species is based largely, as far as I can tell, on his conclusion that the June specimen from mainland Nayarit represented a breeding bird. Even Phillips noted the tenuous nature of this conclusion (8 specimens 4 Feb. to 12 May, 1 on 20 June).

Incidentally, *graysoni* shows the typical pattern of an insular representative: duller, less dimorphic, and larger-billed than its mainland counterpart (and was certainly one of the examples that P. R. Grant used in his classic paper on island differentiation patterns).

A quick Google Lit search revealed no published data that I can find on the vocalizations of *Turdus graysoni*, but I have not searched in depth. There were no recordings of *graysoni* in xeno-canto or Macaulay Library when I searched (11 Feb. 2021).

New Information:

Montaño-Rendon et al. (2015) did a great job of elucidating the characters of *graysoni* versus the mainland taxa, and established that *graysoni* is the most distinctive taxon (morphometrics and mtDNA in addition to well-known plumage differences) in the *T. rufopalliatu*s complex, and that *graysoni* is only taxon in the group (nominate plus two other described subspecies) that is reciprocally monophyletic (sequence data [cyt-b, ND2] from 12 *graysoni*, 4 *grisior*, 9 *interior*, 19 nominate *rufopalliatu*s). They found a deep divergence between island samples and all mainland samples, including coastal Nayarit. The two groups were reciprocally monophyletic (but in my opinion, with N=14, statements concerning reciprocal monophyly are premature).

They made their case for species rank as follows:

“Insular populations of *T. rufopalliatu*s in the Tres Marías Islands are distinguished by a particular combination of traits (Nelson 1899; Ridgway 1907; Hellmayr 1934; Stager 1957; Grant & Cowan 1964; Grant 1965; Phillips 1981; Navarro-Sigüenza & Peterson 2004, this study). Both sexes in the islands are similarly colored, and are duller than their mainland counterpart, where females have duller plumage than males, but still brighter than island birds (Grant 1965). This coloration pattern, in which the mainland birds are brighter than the island ones (see Peterson 1996), is also present in other birds in the Tres Marías Islands (Grant 1965; Cortés-Rodríguez et al. 2008). Coloration and other diagnostic characters including size (Grant 1965, this study) and mtDNA (this study), suggest that the insular populations of *T. rufopalliatu*s could be treated as a distinct evolutionary unit under both the Phylogenetic (McKittrick & Zink 1988) and Evolutionary (Wiley & Mayden 2000) species concepts. Moreover, Phillips (1981) reported not having found any hybrids on scientific collections or in birds in coastal Nayarit, where insular and continental forms apparently are occasionally found in sympatry. Evidence also suggests that both island and mainland groups could also conform to the Biological Species Concept definition (Mayr 1963); however, such a decision must wait until data on potential hybridization are available (Mayr 1963; Gill 2014).”

Analysis and Recommendation:

I recommend a NO on this one for several reasons. First, the evidence for sympatry on the mainland is highly tenuous and requires substantiation. Second, vocalizations have not been studied. Song and call note differences led to the split of *Catharus bicknelli* from *C. minimus*, which differ less in terms of phenotype from each other than do the two taxa under consideration (although I have lingering doubts about this split). In contrast, Hermit Thrush (*C. guttatus*) subspecies differ more in terms of size and plumage than the two taxa under consideration, yet are maintained as one species because, as far as is known, all populations have extremely similar calls and call notes. (By the way, we need to evaluate all the recent evidence from Kristen Ruegg's research for a two-way split in *C. ustulatus*). Third, unless sympatry can be confirmed, I don't think the genetic data can be interpreted either way in terms of taxonomy. The Tres Mariás and the mainland are separated by 100 km of ocean and (acc. to references cited by Montaña-Rendon et al.) were submerged until ca. 120,000 years ago. I would be surprised, even with occasional migrants or wanderers to the mainland, if some genetic differences did not accrue post-colonization of the Tres Mariás, particularly given the tendency for small island populations to differentiate rapidly. Certainly the phenotypic differences, likely products of selection, must have a genetic basis as well. Whether *graysoni* has diverged to the level associated with species rank in thrushes is an open question. The bar for this is very low in phenotype (as in Bicknell's Thrush), so a study of vocalizations is what is needed, in my opinion, or, of course, documentation that there is a breeding population of *graysoni* on the mainland.

What we have here is the classic problem of taxon rank for somewhat differentiated allotaxa. Where to draw the line? Certainly for thrushes, vocalizations are the standard by which allotaxa are evaluated, and I recommend that we wait for such data.

As to English names, Grayson's Robin is the English name associated with this taxon, but if the proposal passes, then I recommend a separate proposal.

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Submitted by: Van Remsen

Date of Proposal: 11 February 2021

Treat Eurasian Blackbird *Turdus merula* as four species

Background:

The Eurasian Blackbird *Turdus merula* was long treated as incorporating multiple Eurasian taxa of black or gray thrushes with yellow bills and legs, to the exclusion of any New World or Pacific island taxa with similar suites of characters, at least since Ripley (1952) revised the subfamily and later contributed the chapter on the group to Peters' check-list (Ripley 1964). In neither of these works was the justification provided, but as was generally the case at the time in ornithology, this inclusive treatment was followed nearly universally by authors for many years. Wolters (1980; date from Mlíkovský 2012), however, recognized two species in the complex, *Turdus merula* and *T. simillimus*, the latter for the taxa of sub-Himalayan India and Sri Lanka.

New Information:

More recently it has become clear that the complex includes several obviously disparate taxa that are not closely related to one another. In fact, the song of the Tibetan form *maximus* has been described as being comprised of repetitive metallic call-notes, unpleasant screeches and slurred guttural caws (Rasmussen and Anderton 2005), a description not at all likely to be bestowed on any of the other taxon groups, which all sing beautifully. Rasmussen and Anderton (2005) considered, on the basis of morphology (including plumage and soft parts, proportions, and wing formula), song, egg color and then-preliminary molecular phylogenetic analyses by Alström and colleagues, that there are four species in the complex (Western Palearctic *T. merula*, Himalayan *T. maximus*, mainly Chinese *T. mandarinus*, and sub-Himalayan *T. simillimus*), as did Collar (2005). The mtDNA and nuclear DNA phylogeny of Nylander et al. (2008; see Fig. 1 below) confirmed that four disparate lineages had been subsumed under *T. merula*, each falling within different clades and each being sister to taxa never considered part of the complex. Although more densely sampled corroborating analyses would be desirable, it is clear that there is no basis for the highly polytypic *T. merula* of Ripley (1952, 1964), and the four-species treatment is now widely followed (Dickinson and Christidis 2014, del Hoyo and Collar 2016, Clements et al. 2019, Fjeldså et al. 2020, BirdLife International 2021, Gill et al. 2021). In fact, I am unaware of any major source that continues to recognize an inclusive *Turdus merula*, with the treatment in the Check-List (AOU 1998) being a holdover from the Peters era for this regionally extremely rare vagrant, surely because the issue has not been addressed recently and is directly not relevant to the listing of the species on the NACC list as *Turdus merula*.

Effect on AOS-CLC area:

The Eurasian Blackbird *Turdus merula* is only a rare vagrant to the AOS-NACC area, including to Greenland. A split of the complex would not involve any changes to species composition of the Check-list. The changes needed would be to the Distribution and Notes statements, including to the reference to two groups (*merula* and *simillimus* groups). Also, to my knowledge no member of the *simillimus* group has occurred in northern south-east Asia, while migratory

mandarinus (considered by Wolters 1980 at least as a member of the *merula* group) regularly does in winter.

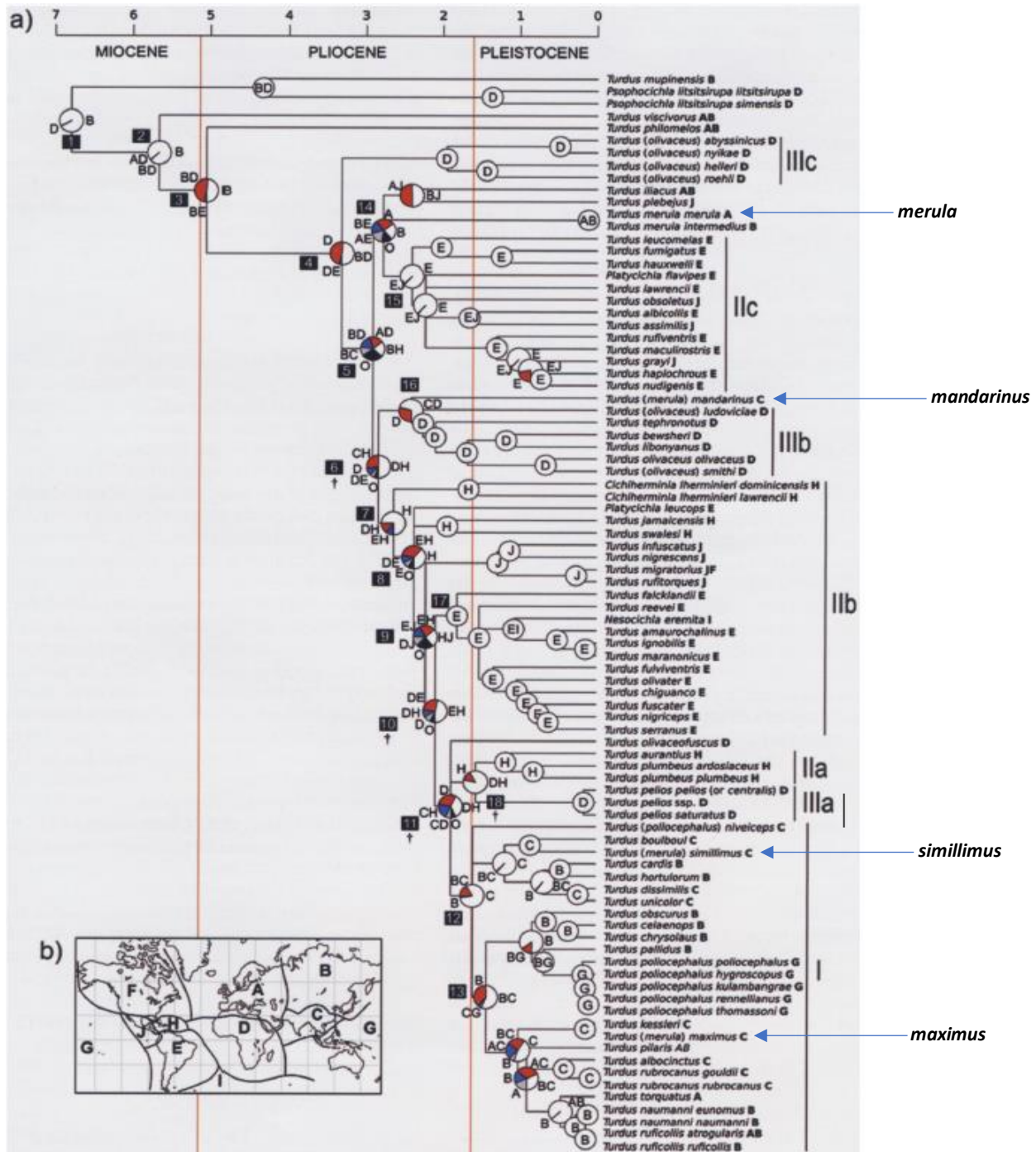


Fig. 1 of *Turdus* from Nylander et al. (2008), with arrows pointing to taxa long considered part of the *T. merula* complex.

McNeil and Cyr (1971) summarized the few North American records up to that time (essentially a probable released captive and a few Greenland records) in a short note on a bird they netted and then collected in Montreal (specimen then at University of Montreal). They considered that the Montreal bird showed no signs of captivity, but they could not rule out ship-assisted transport. DeBenedictis (1991; not seen) questioned the provenance of this record. However, it is included in the main list of the Check-list, and more recently there have been a few other reports: one in Ontario, the first record for the province and second for North America, <https://ebird.org/checklist/S12086116>, published in the 1983 OBRC annual report (not seen). Another was found dying on a lawn in Newfoundland and died five days later in November 1994; this was published in Birders Journal 3(6; not seen), <https://ebird.org/checklist/S1329605>. There are multiple records from Greenland, and the species is now common in parts of Iceland.

Although it seems highly likely that all the North American records pertain to the nominate or at least one of the members of that group, as does the Quebec specimen (AOU 1998), this should be ascertained insofar as is possible for the others. It is extremely unlikely that either the Tibetan *Turdus maximus* or Indian subcontinent *T. simillimus* complex would be a natural vagrant to the NACC region, but it is within the realm of possibility that the slightly migratory *T. mandarinus*, which occurs north to about Beijing, could be a vagrant to the Pacific coast. Fortunately, each major group (now species) is distinctive enough morphologically that any specimens or photos should be readily identifiable.

Recommendation:

I strongly recommend that we accept this non-controversial split for a species that is only an extremely rare vagrant to our area. Exactly how many species should be recognized in the complex is slightly less certain, but on present knowledge using integrative taxonomy, it seems clear that there are four species.

English names:

The name Eurasian Blackbird has been widely if not universally retained for *T. merula sensu stricto*; in my opinion any other English name would be destabilizing, and this species does have the largest range of the complex.

Voting options:

- A)** Yes, adopt the four-species treatment (strongly recommended).
- A1) If voting for split, keep English name of Eurasian Blackbird (strongly recommended).
- A2) If voting for split but not for A1, suggest alternative name.
- B)** No, do not split the *Turdus merula* complex.

Note that I have not provided an option for splitting the complex into a lower number of species because I don't know of any source that currently follows such a course and the evidence for a 4-way split does not seem ambiguous.

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Submitted by: Pamela C. Rasmussen, Michigan State University

Date of proposal: 12 February 2021

Revise the taxonomy of the Estrildidae

Background:

Estrildidae is a family of some 140 species of small finches that occur naturally in tropical areas of the Old World and in Australasia. We recognize twelve species of estrildid finch, all of which have been introduced, as established in the NACC area. The current linear sequence and generic assignments (Chesser et al. 2020) for these species are:

Lavender Waxbill *Estrilda caerulescens*
Orange-cheeked Waxbill *Estrilda melpoda*
Black-rumped Waxbill *Estrilda troglodytes*
Common Waxbill *Estrilda astrild*
Red Avadavat *Amandava amandava*
Bronze Mannikin *Spermestes cucullata*
Indian Silverbill *Euodice malabarica*
African Silverbill *Euodice cantans*
Java Sparrow *Lonchura oryzivora*
Scaly-breasted Munia *Lonchura punctulata*
Tricolored Munia *Lonchura malacca*
Chestnut Munia *Lonchura atricapilla*

New Information:

Olsson and Alström (2020) produced a dated multi-locus phylogeny (screenshot below, with species in our area highlighted in red) of the Estrildidae using 2 mtDNA and 3 nuclear markers from 103 species (70% of all species) and a mtDNA-only phylogeny with an additional 14 species (80% of all species). The multi-locus phylogeny was generally well supported and produced a very different linear sequence from that adopted in Chesser et al. (2019). Many unsampled species are considered subspecies by some authors, and the phylogeny includes all but one of the species in our area (*Lonchura malacca*). However, *Lonchura atricapilla* (which was sampled) was long considered conspecific with *L. malacca* by most authors until the publication of Restall (1996), and still is by some (Dickinson and Christidis 2014), and is almost certainly closely related, evidently hybridizing in parts of the eastern Indian peninsula (Rasmussen and Anderton 2005; but see Restall in SACC #368, which incorrectly states the apparent hybrids are in the AMNH, when the ones PCR has examined are in BMNH, as stated in Rasmussen and Anderton 2005).

The mtDNA-only phylogeny in Olsson and Alström (2020) was largely in agreement with the multi-locus phylogeny and was mostly used to place samples from GenBank that were not sampled in the multi-locus phylogeny. The taxa with topological disagreements between the two phylogenies, as well as the mtDNA-only samples, are all extralimital to our area and thus do not affect this proposal.

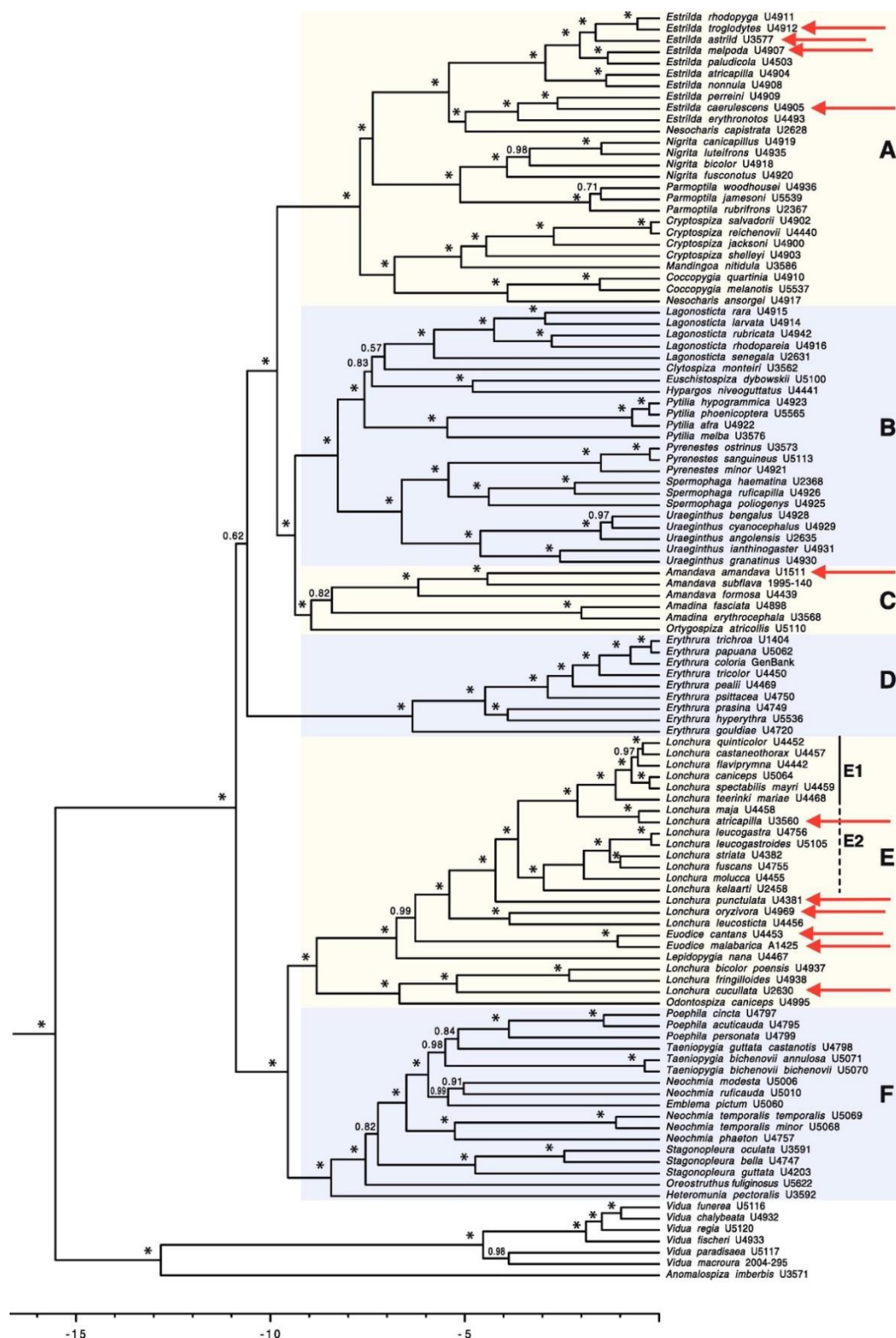


Fig. 1 from Olsson and Alström (2020). Phylogeny of Estrildidae inferred by BEAST based on sequences of the mitochondrial genes cytochrome *b* and ND2, and the nuclear introns fib5, G3P, myoglobin, ODC, and TGF. Red arrows indicate species present in the NACC area. One species in our area, *Lonchura malacca*, was not sampled but is closely related to *L. atricapilla*.

Olsson and Alström (2020) found non-monophyly at the genus level and deep divergences within recognized genera. They recommend generic reassignments to rectify the genus-level paraphyly and for divergent groups greater than ~4 million years old. All relationships described here received high support. Two cases are relevant to the species in our area:

Lonchura: The generic revisions of taxa in *Lonchura* Sykes, 1832; *Spermestes* Swainson, 1837; and *Euodice* Reichenbach, 1863, were considered by the committee in 2014 (proposal 2014-B-12). That proposal was based on more limited taxon sampling and less well-supported trees, but led to the splitting of *Spermestes* and *Euodice* from *Lonchura*, and the merging of *Padda* Reichenbach, 1850, into *Lonchura*. Most of those conclusions are supported by the data in Olsson and Alström (2020), except a previously hypothesized sister relationship between *Lonchura oryzivora* and *L. punctulata* (Amaiz-Villena et al. 2009). These genera, along with extralimital monotypic genera *Lepidopygia* and *Odontospiza* (both sometimes subsumed in *Lonchura*), all form clade E. Although one option would be to place these genera in an expanded *Lonchura*, this would make the genus old (9 Ma) and quite morphologically diverse among Estrildidae. Olsson and Alström (2020) recommend recognizing *Spermestes*, *Euodice*, *Lepidopygia*, and *Odontospiza*, and also resurrecting *Padda* for the two morphologically distinctive species *oryzivora* and *fuscata* (the latter not sampled, but sister species according to Stryjewski 2015) and *Mayrimunia* Wolters, 1949 for the extralimital *leucosticta* and *tristissima* (the latter not sampled, but sister species according to Stryjewski 2015). In Olsson and Alström (2020), *oryzivora* is sister to *leucosticta*, and these are in turn sister to core *Lonchura*. Splitting *Padda* and *Mayrimunia* from *Lonchura* thus rests on the age of the clade (~5.5 Ma from core *Lonchura*) and the morphological distinctiveness of these species. The two species of *Padda* are relatively large and have prominent white cheek patches. The two species of *Mayrimunia* have contrasting pale buff rumps and streaked heads that are lacking in core *Lonchura*, and are vocally divergent, but are otherwise similar to *Lonchura* in size, shape, and color.

Estrilda: The Gray-headed Oliveback, *Nesocharis capistrata*, is embedded within *Estrilda*, and is sister to a clade of three predominantly gray-bodied species (*caerulescens*, *perreini*, and the unsampled *thomensis*) and two black-masked species (*erythronotos* and the unsampled *charmosyna*). This clade is sister to the remainder of *Estrilda*. Olsson and Alström (2020) recommend resurrecting *Glaucestrilda* Roberts, 1922, for the gray-bodied *Estrilda*, which for our area would change *Estrilda caerulescens* to *Glaucestrilda caerulescens*, as has already been done in Gill et al. (2020). The two other species of *Nesocharis* (including the type species) fall elsewhere in the phylogeny, and Olsson and Alström (2020) recommend resurrecting *Delacourella* Wolters, 1949, for *capistrata* and *Brunhilda* Reichenbach, 1862, for the two black-masked species, both recommendations also already enacted in Gill et al. (2020). The split between the proposed *Glaucestrilda* and *Brunhilda* is fairly shallow (~4 Ma), but the two clades do differ in morphology (largely gray-bodied vs pinkish-brown-bodied with black masks). An argument could be made for considering this a single genus, in which case *Brunhilda* has priority.

Effect on AOS-CLC area:

Following the recommendations below would lead to a new taxonomic arrangement and linear sequence, as follows:

Bronze Mannikin *Spermestes cucullata*
African Silverbill *Euodice cantans*
Indian Silverbill *Euodice malabarica*
Java Sparrow *Padda oryzivora*
Scaly-breasted Munia *Lonchura punctulata*
Tricolored Munia *Lonchura malacca*
Chestnut Munia *Lonchura atricapilla*
Red Avadavat *Amandava amandava*
Lavender Waxbill *Glaucustrilda caerulescens*
Orange-cheeked Waxbill *Estrilda melpoda*
Common Waxbill *Estrilda astrild*
Black-rumped Waxbill *Estrilda troglodytes*

There is a final issue related to the spelling of *Estrilda* [*Glaucustrilda*] *caerulescens*. According to a recent paper by David and Dickinson (2016), the specific epithet must be spelled *coerulescens*, as it is to be considered the original spelling after correction of the ligature, as verified by magnification. This has been adopted by del Hoyo and Collar (2016), but not by Gill et al. (2020) or A. Peterson of zoonomen.net. Other names affected by the proposed change have already been considered and voted down by SACC (#716) in favor of stability, given issues such as mistakes, apparent randomness, difficulties of interpretation of intent, differing fonts, and an opinion that if all such changes were adopted consistently, we would have to start referring to Linnaeus' "*Systema Naturae*"! Therefore, established usage can be invoked here to retain the spelling *caerulescens*. Note also that the same nomenclatural issue applies to *Geranoospiza caerulescens*, but that species was not voted on in SACC #716. (Thanks to David Donsker for information.)

Recommendation:

Votes are required on the following issues:

- a) Adopt the new linear sequence
- b) Transfer *oryzivora* to *Padda*
- c) Transfer *caerulescens* to *Glaucustrilda*
- d) Revert to the original spelling *coerulescens*

We recommend YES votes on a) adopting the new sequence, b) transferring *oryzivora* to *Padda*, and c) transferring *caerulescens* to *Glaucustrilda*. However, we recommend voting NO on d) reverting to the spelling *coerulescens* for *Glaucustrilda* [*Estrilda*] *caerulescens*.

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Submitted by: Oscar Johnson, Louisiana State University, and Pamela C. Rasmussen, Michigan State University

Date of proposal: 23 February 2021

Add Amazilia Hummingbird *Amazilis amazilia* to the Main List

Note from Chair: This proposal was briefly considered by the committee as a late addition to Proposal Set 2020-D, but the vote was postponed so that the committee could fully consider issues raised and discussed in the two appendices that follow the photos at the end of the proposal. If *Amazilia amazilia* is not added to the Main List, it will be added instead to the Checklist Appendix.

Background:

Amazilia Hummingbird *Amazilis amazilia* has not previously been reported to occur in North America.

New Information:

A hummingbird was observed feeding on flowers of a *Samanea saman* tree near Juan Hombrón, Coclé Province, Panamá, on 16 March 2016, by James and Susan Hengeveld, and several photographs (attached) were obtained by the latter.

The following additional notes were provided in an email by J. Hengeveld (9 December 2016) to the submitter:

- size - small to medium (3.5 - 4 inches)
- bright hot pink bill with a black tip, broad-based
- dark green head and back with a dark throat
- white post-ocular spot
- white chest with abrupt border with dark throat; rufous lower breast/upper belly; lighter (grayish or whitish) lower belly & under tail coverts (latter from photos only)
- very prominent white leg “boots”
- rufous tail with hint of darker terminal band (in the photos it looks like it’s only the central rectrices)
- rufous mixed with green upper tail coverts & rump (from the photos only)

The photos and description match no hummingbird known to occur in Panama, but instead show characteristics of Amazilia Hummingbird *Amazilis amazilia* of western South America, notably a white chest patch, white postocular spot, “booted” legs with elongated white feathers, a pale rufous tail and upper tail coverts, and back with a bronzy cast, showing no strong contrast between tail and back.

Rufous-tailed Hummingbird *Amazilia tzacatl* is common in Panama and bears some similarities to the photographed bird, including green head and back, rufous tail, red bill, and white leg feathers. Therefore, the possibility that the individual could have been an aberrant *A. tzacatl* with white feathers on the chest was considered.

To resolve the identification, the submitter examined the series of specimens of *Amazilis amazilia* and its subspecies at the American Museum of Natural History, including *A. amazilia amazilia*, *A. a. leucophoea*, *A. a. dumerilii*, and *A. a. alticola*, as well specimens of *A. tzacatl*.

The photos closely match *A. amazilia leucophoea*. Of other subspecies of *A. amazilia*, the nominate and *dumerilii* have mostly green tails, and the white breast spot of *alticola* (if present) is smaller.

Diagnostic features distinguishing *A. a. leucophoea* from *A. tzacatl* that are evident in the photos include:

- white breast patch (photo A)
- distinct white postocular spot (photo A)
- "booted" legs (photos A, B, C). *A. amazilia* has elongated white feathers on the legs that extend down to the foot joint and are about as long as the foot. Although *A. tzacatl* has white leg feathers, they do not extend to the foot and are much shorter than it. Photos comparing the leg feathering of *A. amazilia* and *A. tzacatl* are attached.
- tail/back color and contrast between them. In *A. tzacatl*, the tail is chestnut, as are the upper tail coverts. These contrast with the emerald green to bronzy green back. In *A. a. leucophoea*, the tail is a somewhat lighter tawny, as are the upper tail coverts. The back is golden green to bronzy green, with no abrupt contrast between tail and back. In photos A and B, the back is bronzy well above the upper tail coverts, and there is little contrast with the tail.

In addition, bill length and breadth are suggestive but not definitive. *A. amazilia* has a much shorter bill with a relatively broader base than *A. tzacatl*. The bill is shorter and wider (almost like a *Hylocharis*) than is typical for *A. tzacatl*.

Based on this information, the record was reviewed and accepted by the Panama Records Committee of the Panama Audubon Society. The record and photos A and C were published in *North American Birds* (van Dort and Komar 2019).

Amazilia amazilia occurs in dry forest and other arid areas from western Ecuador to southwestern Peru. Subspecies *leucophoea* is found in northwestern Peru, about 1400 km from where the bird was observed. This instance of vagrancy is exceptional but could have been prompted by a strong ENSO event that took place in 2015/2016. The bird was observed in a dry region of Panama, in a habitat similar to that occupied by the species in Peru.

Recommendation:

Add Amazilia Hummingbird *Amazilia amazilia* to the main list as a vagrant.

Literature Cited:

van Dort, John, and Oliver Komar. 2019. Central America. Spring/Summer 2016. *North American Birds* 70(3/4): 394-396.

Submitted by: George R. Angehr, Smithsonian Tropical Research Institute, and Chair, Panama Records Committee, Panama Audubon Society

Date of proposal: 30 March 2020, appendices added by Terry Chesser 23 February 2021

Figures below:

Photos by Susan Hengeveld, near Juan Hombrón, Coclé Province, Panamá, 16 March 2016



Photo A.



Photo B.



Photo C.

Comparison of leg feathers of *A. amazilia* and *A. tzacatl*.



Amazilia amazilia



Amazilia tzacatl

Appendix 1: email exchange between NACC chair Terry Chesser and George Angehr, author of this proposal

1. Chesser email to Angehr, 6 April 2020

One of our committee members has pointed out that the site in Panama where the *Amazilia* Hummingbird was found is not too far from the Panama Canal, and that Talara, in Piura, Peru, part of the species' native range, is a big oil producer and has tankers coming and going. It seems to this committee member that it is more likely that someone kept an individual on board a tanker and let it go as they were about to go through the canal. I don't know how likely this is but it seems like a possible explanation for the bird appearing where it did. I also don't know whether this view will find other support on the committee, but it might.

I'm wondering whether your committee considered something like this, given that finding a restricted-range non-migratory species 1500 km out of range (with no records for Colombia), is so extraordinary, or whether you have any comment on this.

2. Angehr reply to Chesser, 6 April 2020

Frankly, that sounds even more far-fetched to me than natural vagrancy. I'm not aware that people (other than zoos or specialized aviarists) keep hummingbirds in captivity. I've kept hummingbirds in captivity for research and they're not easy to maintain. You can't keep them alive on just sugar water; they need a nutritionally complete diet including protein, fat, vitamins, and minerals. That means either supplementing their sugar water with a nutrient powder or providing small insects like fruit flies. That a crew member on an oil tanker would have a pet hummingbird and be able to maintain it in healthy condition for any length of time seems extremely unlikely to me.

In addition, Juan Hombron isn't anywhere near the Panama Canal. It's more than 100 km away. The suggestion might be a little more plausible if the record was from Panama City or another site near the Canal, but Juan Hombron is a rural agricultural area about two hours' drive west of the Canal.

The Panama Records Committee routinely considers the possibility that a vagrant could have been ship assisted, and in fact the Panama Checklist has an appendix that includes such species. However, in this case no committee member suggested it, probably because it was so implausible for a hummingbird.

Unless there is some actual evidence that the species is commonly kept in captivity in Ecuador I would dismiss that idea.

Appendix 2: further discussion of the proposal by NACC members

Committee member Van Remsen wrote to several colleagues in Peru seeking information regarding the frequency of hummingbirds kept in cage bird markets in the Lima area. Replies indicated that there had been a breeding center for *Amazilia amazilia* in Lima, which began with some 15 individuals and was intended for exportation to zoos in Europe, but that it did not work out and the project was abandoned and there are no longer any hummingbirds at that facility. Another person in Lima was rumored to be keeping hummingbirds in captivity for exportation,

because zoos in Europe were toying with the idea of hummingbird houses, but there were questions of legality and not much was known about this operation.

This information resulted in the following further discussion of the proposal within the NACC:

1. The specific mention of amazilias being the subject of this breeding attempt in Peru for purposes of shipment abroad introduces considerable doubt into natural vagrancy as the most likely explanation. (Thanks, Van, for checking on that.) We don't necessarily have to invoke ship-assistance, either. There's also the issue of how a non-migratory hummingbird could possibly make such a trip across water, even if blown off course, since it wouldn't have put on a lot of fat beforehand like a Rubythroat. And if it followed the coastline it would have had to cross a lot of highly unsuitable habitat.

Should we be voting on whether to add it to the Appendix, rather than a straight yes or no?

2. Because the record is published, with photos, it automatically goes in Appendix, right?

I'm still on the fence, but it is worrisome that the one species for which we know there have been captive breeding attempts near a major port also happens to be the species in involved here.

Trying to use natural history logic to explain vagrant records (or escapee records) x-post-facto is perilous. In August 2000, a Red-cockaded Woodpecker was documented in the Chicago area, something like 600+ km N of nearest known breeders (and I think Doug saw that bird). There are probably hundreds of similar anomalous records (of non-migratory species dispersing hundred, sometimes 1000+km, from nearest source, crossing expanses of unsuitable habitat and often seemingly bypassing more suitable habitat. Go figure. It is only natural to try to interpret each case as having human transport as an explanation, because the record defies everything we think we know about natural patterns of distribution. That was my position for decades. But with accumulating N of anomalous records of sedentary species, many of which are highly unlikely to have been in cages etc., these anomalies themselves could be considered a pattern, and I have modified my views on this accordingly.

For almost every anomalous record, one can invent a somewhat plausible scenario, an ex post facto just-so story, to "explain" the anomaly. So, in this case, *Amazilia amazilia*, being a bird of dry forest, almost certainly makes some seasonal local movements, perhaps more so during years with extreme weather. "Individual One", our Panamanian bird, is programmed to disperse and sets off to the N following edges and disturbed habitat. Even though this trajectory brings it to the wettest area of the W. Hemisphere, the Chocó, it keeps on going because these areas may have the requisite edge habitats but aren't really what it is programmed to look for. And so it just keeps going. And defying probability, gets detected in Panama. The inference from the incredibly low probability that "Individual One" would ever be detected and photographed is that there must be hundreds of such individuals that never get detected.

Have we dealt with the first US records of Sungrebe and Rufous-necked Wood-Rail both from Bosque del Apache? I can't remember*. Has ABA?

3. All true enough, but there is still reasonable doubt in this case, so it seems better for now in the Appendix. If that's what the vote leads to, perhaps there will be follow-up records of this or

other Peruvian dry-zone species after other ENSO events that will lead NACC to re-evaluate in future...—

4. ABA dealt with both the wood-rail (57th suppl.) and sungrebe (52nd suppl.).

ABA-CLCL report for

Sungrebe: https://nam02.safelinks.protection.outlook.com/?url=https%3A%2F%2Fwww.aba.org%2Fbirding_archive_files%2Fv43n6p26.pdf&data=02%7C01%7CCHESERT%40si.edu%7Cc1640c595d274943405b08d7db1c4d44%7C989b5e2a14e44efe93b78cdd5fc5d11c%7C0%7C1%7C637218786918143252&sd=5pYPtNDIFCnHz09e1FIGafiD8aA8oTXze8r8PGRjy8%3D&reserved=0

ABA-CLC report for RN Wood-

Rail: https://nam02.safelinks.protection.outlook.com/?url=https%3A%2F%2Fwww.aba.org%2Fwp-content%2Fuploads%2F2020%2F03%2F2015_CLC_Report.pdf&data=02%7C01%7CCHESERT%40si.edu%7Cc1640c595d274943405b08d7db1c4d44%7C989b5e2a14e44efe93b78cdd5fc5d11c%7C0%7C1%7C637218786918143252&sd=pNhqBcg7Vvns4U9Z%2FBWrH%2FMGnzSLOKbmcSZ3K4wi3Vg%3D&reserved=0

This was when I was off the Committee, so I can't add more.

I don't think vagrancy in the *Amazilia* is similar to either of these (particularly the wood-rail). Both of the of those are waterbirds, and must move if conditions dry up. I just cannot imagine an *Amazilia* Hummingbird moving very far to find better conditions.

5. What about the original BC Xantus's Hummingbird in 1998, before the first CA record. How did ABA deal with that one? Roughly 2500 km N of nearest Xantus's population.

I can't imagine an Amethyst-throated Sunangel moving 4000 km from the mountains of Mexico to Quebec, yet I think this is treated as a natural vagrant.

A Buff-bellied Hummingbird showed up in Wisconsin in JUNE 2017, 2000 km from nearest breeding population and 3+ months before the onset of its normal NE dispersal pattern to SE TX and S LA.

A Green-breasted Mango also showed up in Wisconsin, in Sept. 2007, also at least 2000 km from nearest breeding population. Another one showed up near Charlotte NC in Nov. 2000.

And there are many other such nonsensical records in hummingbirds. Grasping desperately for a sensible pattern, my interpretation is that hummingbirds in general are amazing dispersers that generate anomalous records. A biogeographic tribute to this is Juan Fernandez Firecrown (*Sephanoides fernandensis*), derived from a colonization event crossing 600+ km of open ocean, an absolute minimum of 2 times in within a hummingbird's reproductive lifespan.

Go figure!

6. FWIW, we treat the record of Amethyst-throated Mountain-gem/Hummingbird in Quebec as a natural occurrence, published in the 59th supplement along with a first US record from south Texas.

Here's what Pyle et al. (2017) said about these records:

Amethyst-throated Hummingbird (*Lampornis amethystinus*)—ABA CLC Record #2017–11. Amethyst-throated Hummingbird has been considered a non-migratory hummingbird that resides in central Mexico through Honduras (Howell and Webb 1995). First-cycle males of this species were photographed in Saguenay County, Quebec, July 30–31, 2016 (Denault et al. 2017) and in the Davis Mountains, Jeff Davis County, Texas, October 14– 15, 2016. Based on both records, the CLC accepted the species to the *ABA Checklist* in September 2017, by a vote of 8–0. These records fit the remarkable pattern of northward vagrancy to the ABA Area by other supposedly resident Mexican hummingbirds, and the CLC saw no reason to believe that either bird was transported to these locations. We follow Chesser et al. (2017) in placing it between Plain-capped Starthroat and Blue-throated Hummingbird on the *ABA Checklist*.

7. I am inclined to vote for the Amazilia Hummingbird in Panama as a natural vagrant. Like others, I immediately thought of several of the ridiculous records of hummingbirds in the US, hundreds or more kilometers from where they are supposed to be found. Amazilia Hummingbird is very common, widespread, and adaptable in its range and as noted by Van that although it is a dry forest species, it is perfectly happy in towns throughout Peru and I can imagine a bird like this hopping to town, even through otherwise inappropriate habitat. Much of that habitat is inappropriate for *Amazilia tzacatl* as well, which nonetheless is scattered through the lowlands of western Colombia. I would also note that there is a photo in e-bird of an Amazilia Hummingbird from the east slope of Ecuador near Sumaco. Not as far out of range but requiring a bird to have crossed the Andes and found a tourist place at mid-elevation in humid montane forest.

Thinking about this being an escape from a ship going through the Panama canal just feels very unlikely to me. As George Angehr notes the location is about 100 km from the Panama Canal. Further, would you really export hummingbirds by ship? I know Ruschi from Brazil, who did import non-Brazilian hummingbirds to eastern Brazil had a system for keeping them alive for trips on airplanes. Also the example of captive breeding program in Peru would presumably be nominate amazilia, not this subspecies. I actually think that the listing of all hummingbirds on CITES2 was due to a petition by Ecuadorian ornithologists who talked about a market for hummingbirds. We might get a better sense of this if we contacted some Ecuadorians. It would be the right subspecies too.

As I write this, I am thinking that we should postpone a vote until we have a better sense of what the scale of hummingbirds in captivity is in the range of this subspecies. If this record isn't deal with in time for this supplement, I think that is okay. It will be 5 years since the record rather than 4.

8. Good additional points.

My only add-ons:

1. Because there's a published photo, doesn't the record automatically go in Appendix, and thus the vote would only be whether to upgrade it to main list? Thus we could add it to Appendix in Supplement and then have more extensive proposal and time to consider it for main list?

2. I don't think a sophisticated bird shipment was being proposed but rather something along lines of lonely-sailor-buys-novelty-item-in-port.

3. I'm also certain that the original impetus for CITES status for hummingbirds came from Ecuador.

.....

And one other trivial thing, for SACC to consider first, is the English name. A change to "Amazilis" Hummingbird might be worth the slight, 1-letter sacrifice of stability given that it is NOT an *Amazilia*, sensu stricto, which is misleading. Doug — give me your read on this and whether it's worthy of consideration, minimally.

9. If not accepted for the main list, it would go in the Appendix. Options at this point would be:

(1) Postpone the vote until next year, which would allow more time to gather information on *A. amazilia* in captivity.

(2) Add this species to the Appendix now (provided that it doesn't receive the votes to add it to the main list) and then re-consider it next year for the main list.

I have a slight preference for postponing and dealing with this record all at once, but the other option is also reasonable.

As to the English name, my guess is that it is called *Amazilia* Hummingbird because of the species name rather than the genus name (if it were for the genus, one might expect the type species to have this English name) and the species name is still *amazilia*, so my first reaction would be to keep the English name as is.

10. This has become an interesting discussion. One of the reasons I voted for Garnet-throated Mountain-gem is that it resides in the northern Mexican highlands, where other hummingbirds have a history of long-distance vagrancy (e.g., White-eared, Blue-throated, Rivoli's, Broad-billed, Mexican Violetear). I don't think the suite of hummingbirds in NW Peru includes any prone to vagrancy, but the east side record of *Amazilis* in Ecuador opens my eyes a bit. My original idea about the Panama record was a one-off occurrence from a passing boat. If you have ever looked at the Gulf of Panama, it is littered with cargo ships as far the eye can see.

11. The only problem I have with this is the difference in sampling effort, namely comparing USA with its hummingbird feeder cult to NW South America with many fewer feeders and observers would predict far more vagrant records from the former. Without checking each record individually, I'm pretty sure that most of our outrageous records were from homeowners with feeders, but who weren't serious birders, who noticed a "different" hummingbird and either figured it out themselves or sought help. So, one prediction would be that as sampling intensifies in NW South America as use of feeders lodges becomes more widespread, then we'll see more data on long-D dispersal of hummers there, at least those species that live in habitats where flowering has a strong seasonal component.

Treat Cinereous Owl *Strix sartorii* as a separate species from Barred Owl *S. varia***Background:**

In 1873, Robert Ridgway described an owl from high-elevation pine forests in the mountains of Veracruz as *Syrnium nebulosum* var. *sartorii* (Baird & Ridgway 1873), *Syrnium nebulosum* Audubon, 1839, being a synonym of Barred Owl *Strix varia* Barton, 1799, rather than Great Gray Owl *Strix nebulosa* Forster, 1772. Ever since, most authors have continued to consider this taxon conspecific with the Barred Owl (*Strix varia*), naming it *Strix varia sartorii*, despite differences from Barred Owl in plumage (Baird & Ridgway 1873), habitat (e.g., Binford 1989), and genetics (Barrowclough et al. 2011). Indeed, in many respects, *sartorii* is far more similar to Fulvous Owl (*Strix fulvescens*) than it is to Barred Owl. Both occur in roughly similar habitats and elevations, and their vocalizations (discussed in depth under “New Information”) bear very little resemblance to the songs and calls of Barred Owl. However, *sartorii* is notably distinct from *fulvescens* in size, plumage coloration, and even in particulars of the feathering on the toes (fully feathered in *sartorii* and most populations of *varia*, only partially feathered in *fulvescens*; Ridgway 1914), as well as in certain specifics of the vocal repertoire.

The persistence in treating *sartorii* as subspecies of *varia* likely stems from the dearth of information available on the taxon. As recently as 2015, no photographs of *sartorii* had been published, and its voice remained formally undescribed. However, Barrowclough et al. (2011) advocated for raising *sartorii* to species rank, based on genetic (mtDNA) analyses that suggested that the Fulvous Owl is more closely related to nominate *Strix varia* than is *sartorii* (see their Figures 1 and 2 on the next page). They wrote:

One could lump the Fulvous Owl with the Barred Owl to create a monophyletic species, as has been done in the past by some authors (e.g., Peters 1940), but this seems unwarranted to us because the vocalizations of the Fulvous Owl, the Mexican Barred Owl, and the Barred Owls of the United States and Canada all differ substantially from each other (S. Howell pers. comm.). The Barred Owl of Mexico, the Barred Owl of the United States and Canada, and the Fulvous Owl of Mexico and Central America are each monophyletic and diagnosable on the basis of many mtDNA characters and vocalizations. They are weakly diagnosable on the basis of plumage (these are owls, after all). Thus, they certainly comprise three phylogenetic species and probably represent three biological species, given their allopatry, known vocal differences, and the understandable reluctance to recognize paraphyletic taxa (Johnson et al. 1999). The genetic divergences of 4–5% among the three suggest isolation over perhaps a couple of million years. We recognize three species: the Northern Barred Owl (*S. varia*), the Mexican Barred Owl (*S. sartorii*), and the Fulvous Owl (*S. fulvescens*).

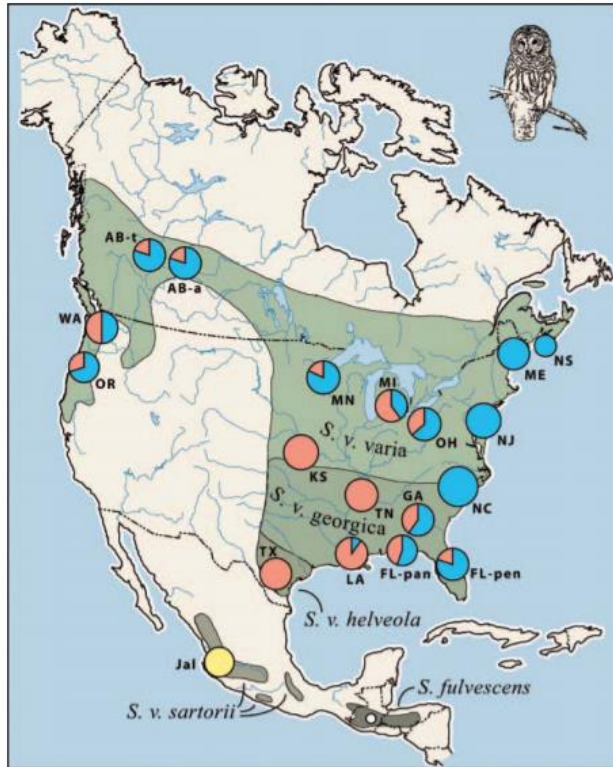


FIG. 1. Distribution, taxonomy, and phylogeography of Barred Owls across their range. Approximate distributions of four generally recognized (AOU 1957) subspecies are indicated by different shades of green; distribution of Fulvous Owl is also indicated. Approximate geographic locations of 19 population samples are indicated by pie-diagrams and locality abbreviations (Table 1). Observed proportions of sampled individuals in each of two major haplotype clades (Fig. 3) are indicated by different colors; area of each pie-diagram is proportional to sample size.

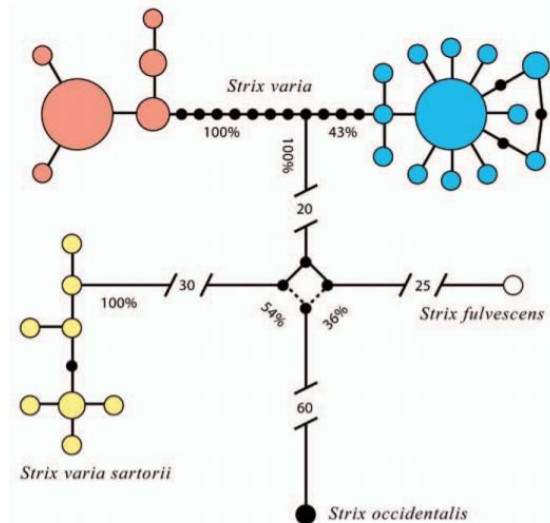


FIG. 2. Minimum-spanning network for 28 haplotypes (open circles) observed among U.S. and Mexican populations of Barred Owls, plus a Fulvous Owl, for 1,115 bp of ND6 plus CO3 mitochondrial sequence. Areas of circles are proportional to numbers of individuals that have that haplotype. Branch lengths within taxa are indicated by single steps; unobserved haplotypes within taxa are indicated by dots. Branch lengths between taxa, not drawn to scale, are indicated by numbers along branches. Bootstrap support values for some major nodes are shown below branches.

New Information:

The discovery in 2015 of a population of *sartorii* on Cerro San Juan in Nayarit, Mexico (Pieplow and Spencer 2015) has finally made audio recordings and photographs of this elusive taxon available. An analysis of the voices of *sartorii*, *varia*, and *fulvescens* (Pieplow and Spencer 2020) shows clear vocal differences.

Many owls in the genus *Strix*, including the Barred Owl (Mazur and James 2000, Odom and Mennill 2010) and the Spotted Owl (*S. occidentalis*; Gutiérrez et al. 1995), have two song types: a “rhythmic song” with primary and secondary notes arranged in a species-specific syncopated rhythm, and a “series song” with mostly primary notes in a steadier but still distinctive rhythm.

Pieplow and Spencer (2020) found both the rhythmic and series songs of *sartorii* to differ strikingly from the corresponding songs of Barred Owl in both rhythmic pattern and number of notes (see their Figures 1 and 2 below). The rhythmic song of *sartorii* consists of seven primary notes and three secondary notes, whereas the analogous song of the Barred Owl consists of six primary notes and two secondary notes, arranged in a different pattern. The rhythmic song of *sartorii* more closely resembles that of Fulvous Owl, but the single analyzed example of *sartorii*

rhythmic song fell outside the range of variation of Fulvous Owl both in frequency and in number of notes, being lower in pitch and having seven primary notes, versus five or occasionally six in the Fulvous Owl.

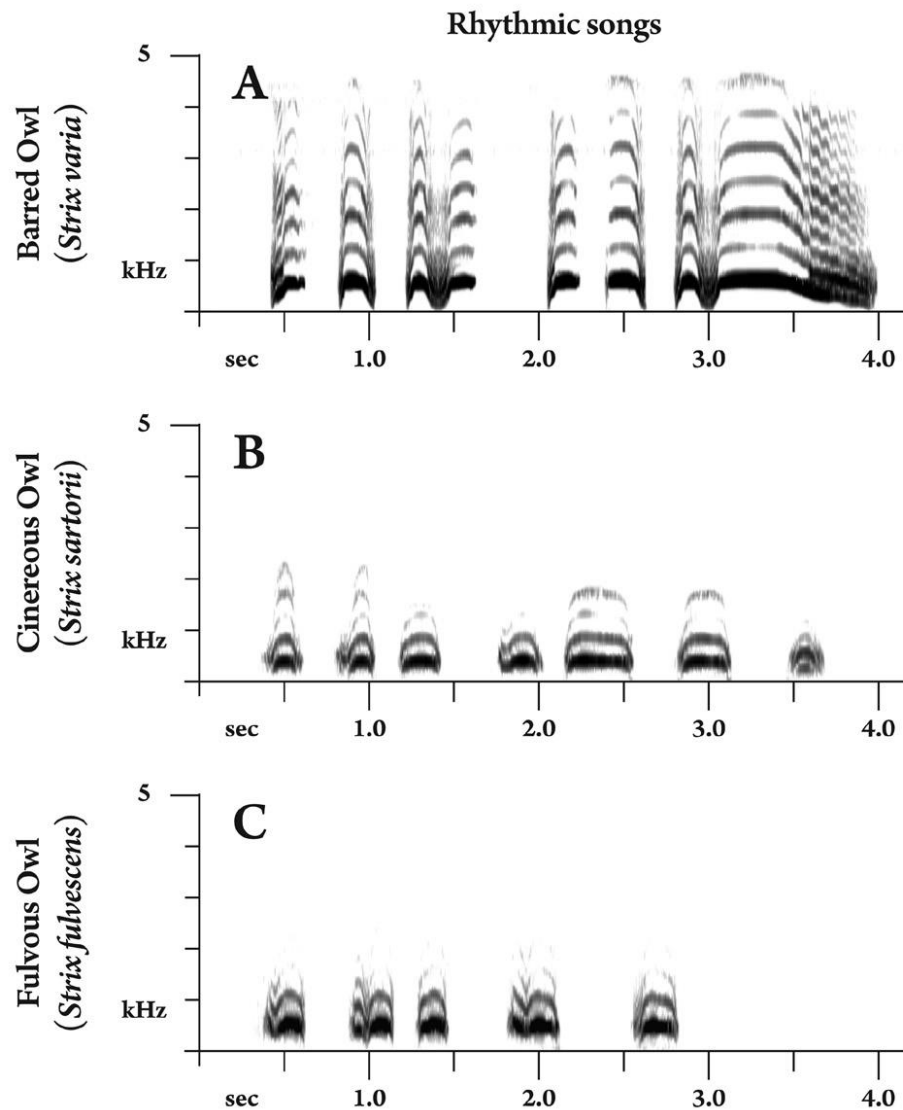


FIGURE 1. (A) Rhythmic song of a Barred Owl (*Strix varia*), Arkansas, 20 March 2005 (Gerrit Vyn and Benjamin Clock, ML 128926). (B) Rhythmic song of a Cinereous Owl (*S. sartorii*), Rancho La Noria, Nayarit, Mexico, 4 June 2015 (Nathan Pieplow, ML 21681321). (C) Rhythmic song of a Fulvous Owl (*S. fulvescens*), Finca Las Nubes, Guatemala, 8 March 2013 (Mike Nelson, XC 125759). Spectrograms have been graphically edited to remove echo and insect noise. Note that the number of visible harmonics depends greatly on the distance from the microphone to the bird.

Unlike the Fulvous Owl but like the Barred Owl, *sartorii* also has a distinctive and frequently deployed series song. Pieplow and Spencer found no evidence for a series song in their review of Fulvous Owl recordings (n=88). The absence or rarity of a series song in Fulvous Owl marks a striking difference in vocal repertoire between it and its congeners. The series song of *sartorii*

differs from that of Barred Owl in its syncopated beginning, its uniformity in pitch, and its lack of a drawn-out “hoo-wah” note at the end. In the Barred Owl’s series song, the highest and loudest notes are at the end, while in that of *sartorii*, the highest and loudest notes are in the middle.

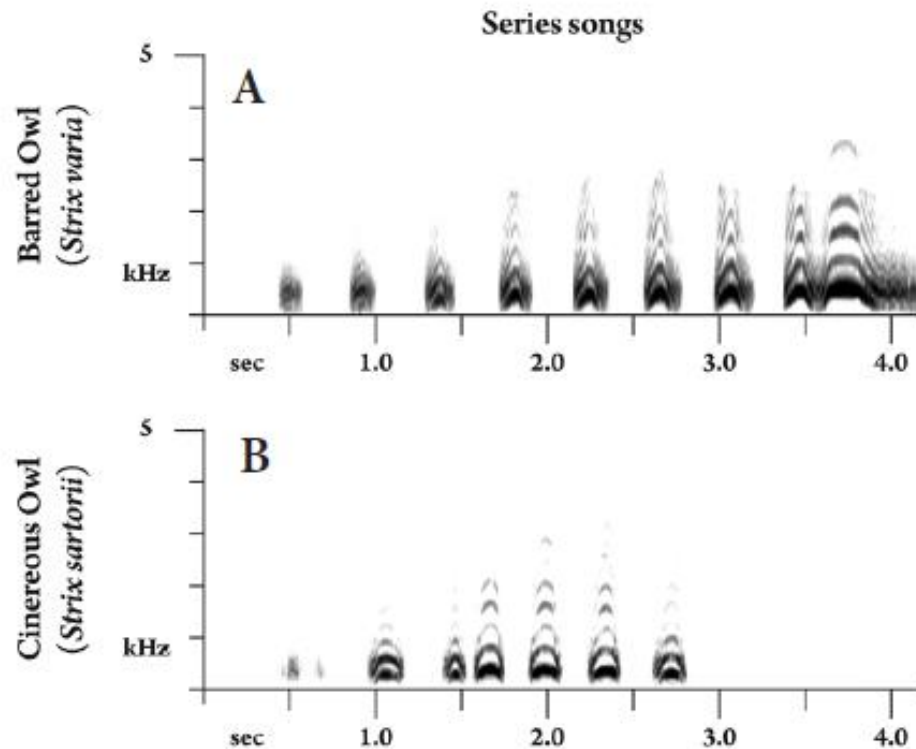


FIGURE 2. (A) Series song of a Barred Owl, West Virginia, 3 May 2010 (Andrew Spencer, XC 48645). (B) Series song of a Cinereous Owl, Rancho La Noria, Nayarit, Mexico, 5 June 2015 (Nathan Pieplow).

Although our analysis contained songs from only a single individual, subsequent observers in 2016, 2019, and 2020 made additional recordings and videos from the general area of Cerro San Juan, Nayarit, that can be heard on xeno-canto.org and in the Macaulay Library (ebird.org/media). It is likely that these recordings cumulatively record a minimum of three additional individuals, and possibly more. All these recordings contain series songs very similar to the one illustrated above in Fig. 2b.

Vocalizations in owls are presumed to be innate (e.g., Gahr 2000), are typically species-specific, and discriminate closely related species (Wiens et al. 2001). The vocal distinctiveness of *sartorii*, combined with previously documented differences in plumage, habitat, and genetics, make an extremely strong case for considering *Strix sartorii* a species separate from *Strix varia*.

Recommendation:

We recommend that *Strix sartorii* be split from *Strix varia*, and we recommend for it the English name of “Cinereous Owl.”

Beginning with Ridgway (1914), most authors have used the English name “Mexican Barred Owl” for *sartorii*, and this is the name that Barrowclough et al. (2011) used in proposing the split. However, “Mexican Barred Owl” is inappropriate if *sartorii* and *varia* are not sister taxa, and Barrowclough’s suggested English name of “Northern Barred Owl” for *Strix varia* seems to us unnecessary. In light of NACC guideline 1.1.a on relative range size, since *sartorii* is a rare and relatively little-known taxon occupying a much smaller geographic range, its split need not affect the English name of *Strix varia*.

Although “Cinereous Owl” was one of the names historically applied to the Great Gray Owl (*Strix nebulosa*, Audubon 1840, Allen 1867), it is an appropriate name for *sartorii* because the ash-gray coloration of that taxon is a key difference separating it from the Fulvous Owl. “Cinereous Owl” is the name currently in use in the IOC taxonomy (Gill et al. 2021), and “Barred Owl (Cinereous)” is the name given in the eBird/Clements checklist (Clements et al. 2019). Thus, we recommend “Cinereous Owl” to the NACC as well.

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doi.org/10.1002/jwmg.82.

Submitted by: Nathan Pieplow, University of Colorado Boulder, and Andrew Spencer, Cornell Laboratory of Ornithology

Date of Proposal: 23 February 2021

Treat *Euphonia godmani* as a separate species from Scrub *Euphonia* *E. affinis***Effect on NACC:**

Acceptance of this proposal would split *Euphonia affinis* to recognize *Euphonia godmani* as a separate species, which would add one species to the NACC area.

Background:

Euphonia affinis is a member of the morphologically conserved subfamily Euphoniinae of the true finches family Fringillidae, formerly included within the family Thraupidae (Isler and Isler 1987, Zuccon et al. 2012). *Euphonia affinis* occurs in the tropical lowlands and mid elevations of northern Mexico south into Costa Rica (Clements et al. 2019). Two distinctive subspecies are widely recognized, *E. a. affinis* Lesson 1842 and *E. a. godmani* Brewster 1889, with a proposed third subspecies *olmecorum* being closely aligned with *affinis* (Dickerman 1981, Hilty 2020). The two subspecies groups *godmani* and *affinis/olmecorum* are readily identifiable, differing in the subcaudal covert feathers (undertail coverts) being white in both sexes of *godmani* and yellow in *affinis/olmecorum*. The two groups are believed to be allopatric with *godmani* being a west Mexican endemic occurring from southern Sonora to central Guerrero and *affinis/olmecorum* occurring from eastern San Luis Potosí, southern Tamaulipas, and western Oaxaca south to Honduras and on the Pacific Coast south to northwestern Costa Rica (Clements et al. 2019). Neither taxon is believed to occur in a roughly ~80-mile gap in southeastern Guerrero.

Past taxonomic authorities have recognized *godmani* and *affinis* as separate species, including Hellmayr (1936), van Rossem (1945), Eisenmann (1955), and Navarro-Sigüenza and Peterson (2004). In contrast, others have suggested they should be maintained as a single species (Blake 1950, Miller et al. 1957, Storer 1970). Dickerman (1981) noted a novel difference between *godmani* and *affinis* (the outer rectrix of *affinis* is entirely black whereas in *godmani* the white of the inner web reaches the posterior edge), but retained the two as a single species. Unlike several recent splits of Mexican species, *E. affinis* was not mentioned as a potential split in Howell and Webb (1995), but *E. a. godmani* was considered to possibly be a valid species in Howell (1998). Other recent treatments have also retained *godmani* within *affinis* (i.e., Howard and Moore 2003, Clements et al. 2019, Hilty 2020). Thus, past treatments are contentious, but new data merit revisiting species limits within this complex.

New information:

A recent study by Vázquez-López et al. (2020) has provided new insight into phenotypic and genetic differentiation within the *E. affinis* complex. This integrative study examined phylogeographic patterns among multiple loci in combination with variation in plumage, morphology, song, and environmental niche models to assess species limits within the group.

Methods of Vázquez-López et al. (2020):

To assess phenotypic variation, Vázquez-López et al. (2020) used six morphometric measurements from 355 specimens (233 males and 122 females), including bill length, bill width, bill depth, wing chord, tarsus length, and tail length, which were then incorporated into a principal component analysis (PCA). The authors also analyzed 19 recordings of *E. affinis* calls, from which they extracted minimum frequency, maximum frequency, bandwidth, call duration, note count, and the note rate. The song variables were then incorporated into a separate PCA analysis. Finally, the authors also generated ecological niche models using all 19 BioClim variables, which were incorporated into Maxent. These niche models were projected to the last glacial maximum under the MIROC-ESM and CCSM models. The authors evaluated niche overlap (Broennimann et al. 2012) and calculated Schoener's *D* and Hellinger's *I* to compare niche equivalency between the two groups (Warren et al. 2008).

For their genetic analyses, Vázquez-López et al. (2020) sequenced the mitochondrial gene ND2 and four introns, ODC (Ornithine Decarboxylase) intron 7, MUSK (Muscle, skeletal receptor tyrosine-protein kinase) intron 3, GAPDH (Glyceraldehyde-3-phosphate dehydrogenase) intron 11 and BRM (BRM transcription regulatory protein) intron 15. All loci were sequenced for four individuals of *E. a. godmani*, twelve of *E. a. affinis*, and seven of *E. a. olmecorum* (Fig. 1).

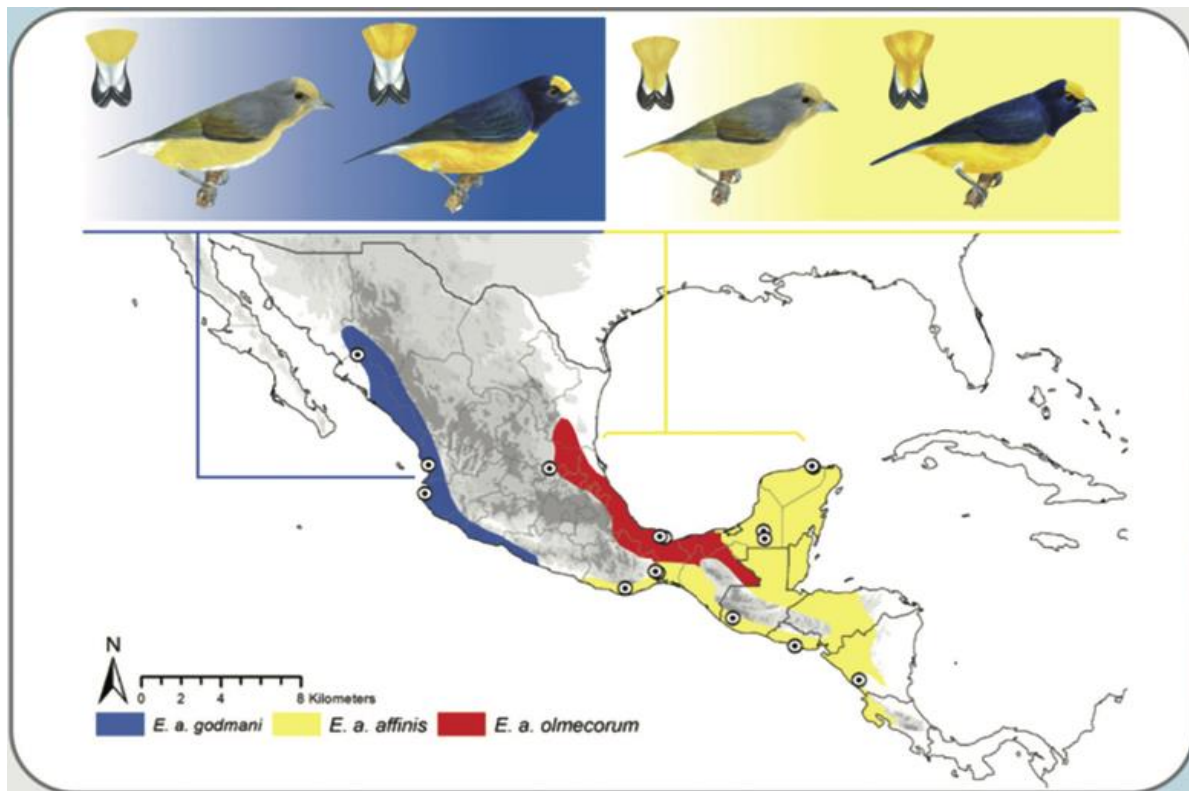


Figure 1: Above, phenotypic differences between the *godmani* group and the *affinis* group within the *E. affinis* complex. Below, a map showing subspecies distributions and collecting localities for the genetic samples, including 4 *E. a. godmani*, 12 *E. a. affinis*, and 7 *E. a. olmecorum*.

These data were combined with outgroup taxa from GenBank from other studies. These loci were subsequently aligned, and the authors calculated heterozygosity, nucleotide diversity, F_{st} , and haplotype networks for the ingroup taxa. A Bayesian phylogeny was inferred with MrBayes. A time-calibrated phylogeny was inferred using BEAST, using the molecular clock rates from Lerner et al. (2011) and with the divergence between Fringillidae and New World nine-primaried oscines of 17.1 mya as calculated by Oliveros et al. (2019).

Phenotypic variation:

The authors highlighted divergence in the undertail coverts, which are white in *E. a. godmani* and yellow in *E. a. affinis* and *E. a. olmecorum* (Fig. 1). This is a diagnosable, fixed plumage difference between the *godmani* and *affinis* groups, whereas the genus *Euphonia* exhibits plumage conservatism more broadly. In other words, the difference in undertail coverts between the *godmani* and *affinis* groups is commensurate with interspecific differences among other *Euphonia* species.

Vázquez-López et al. (2020) found broad overlap in each of the morphological characters examined (Fig. 2). This is perhaps unsurprising given the intraspecific morphological conservatism within the Euphoniinae generally.

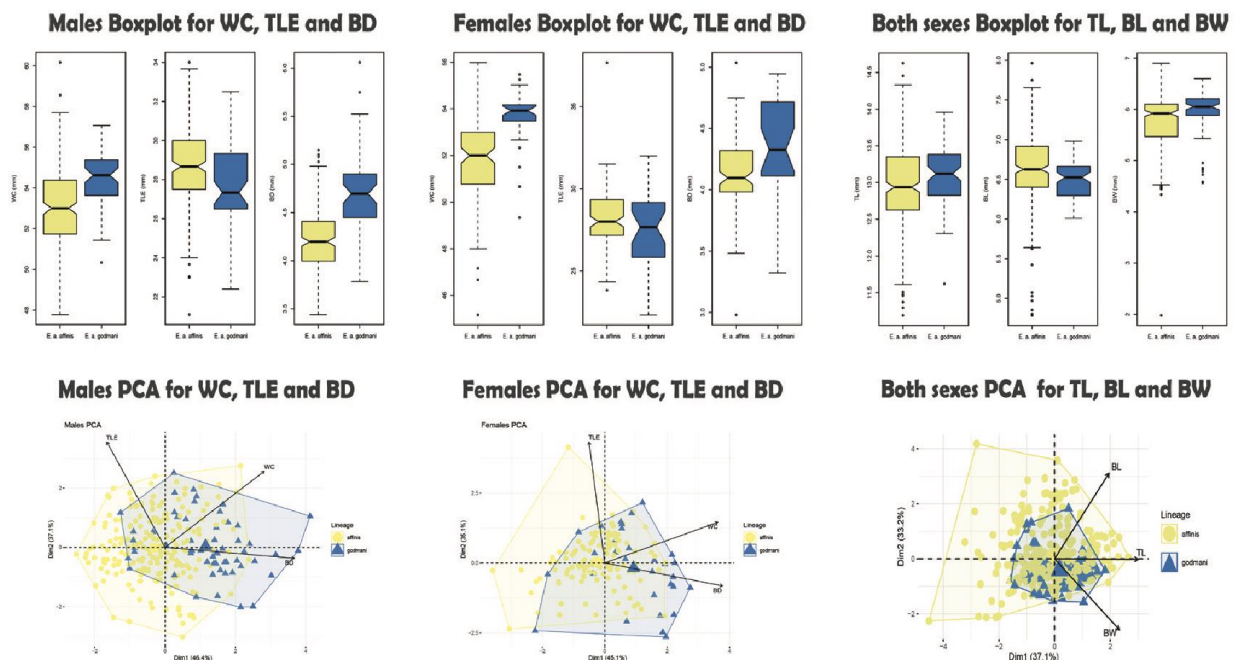


Figure 2: Variation in morphometric measurements between [*affinis*] (yellow) and [*godmani*] (blue) groups within the *E. affinis* complex.

Vázquez-López et al. (2020) found that calls of *E. a. affinis* had significantly fewer notes per second (mean = 2.9 notes/sec) compared to those of *E. a. godmani* (5.9 notes/sec).

Additionally, the first principal component axis of vocal variation did not overlap between the two groups, suggesting further vocal divergence (Fig. 3).

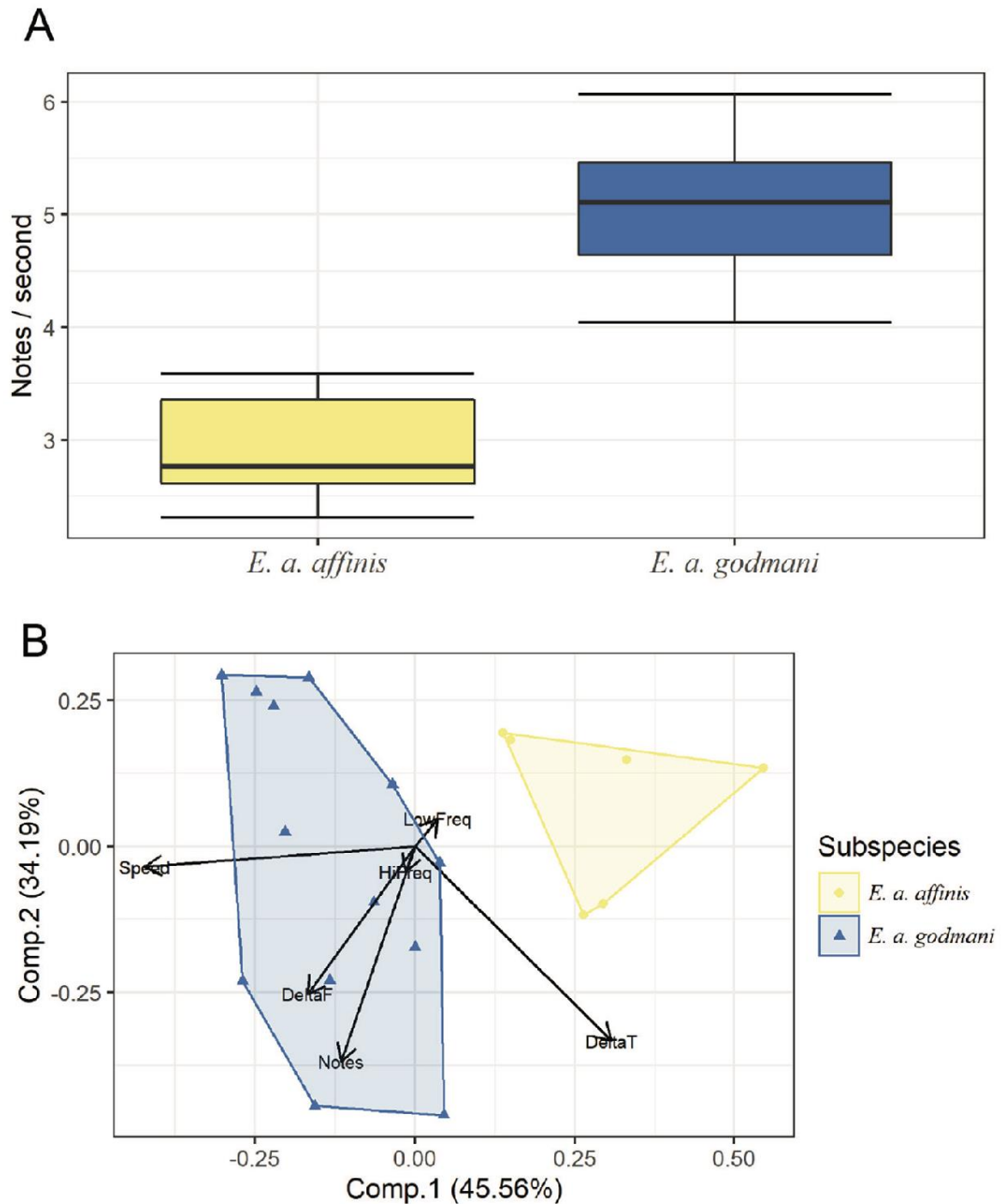


Figure 3: Vocal variation between *E. a. affinis* group (yellow) and *E. a. godmani* group (blue). Panel A shows variation in notes per second, while Panel B shows non-overlapping multivariate distributions of calls. PCA loadings shown with arrows.

Ecological niche modeling revealed niche divergence between the *affinis* and *godmani* groups, specifically that contemporary niches had observed Schoener's $D = 0.01$ and Hellinger's $I = 0.06$ values that fall outside of the distribution of expected values from simulations, thereby rejecting the niche conservatism hypothesis. However, examining niche models revealed that both lineages have suitable niche space that co-occurs geographically during modern times, the last glacial maximum, and the last interglacial period (Fig. 4). Overall, this suggests that the *affinis* and *godmani* groups are largely similar in terms of the abiotic niches that they currently occupy and have occupied over recent evolutionary time.

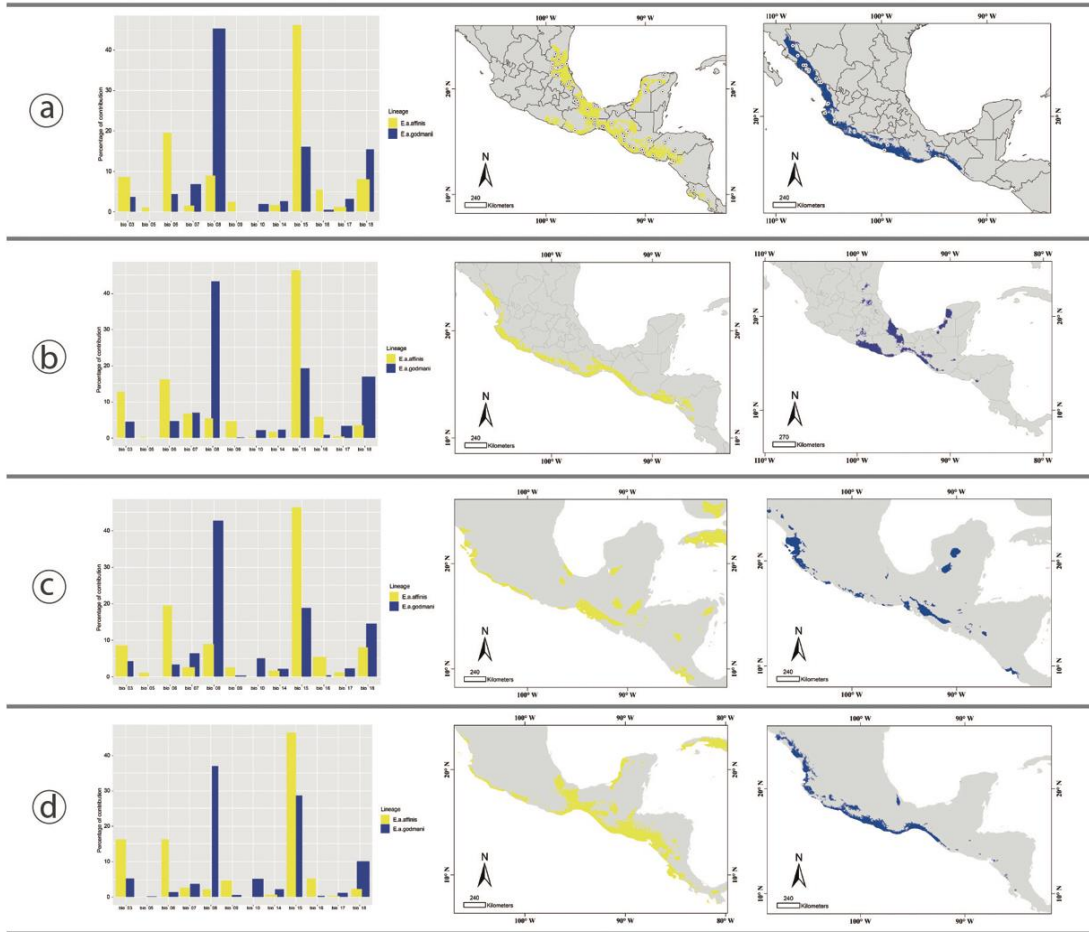


Figure 4: Results from ecological niche models generated for [*affinis*] in yellow and [*godmani*] in blue. First column for each panel A-D shows response scores for 12 BioClim variables. 2nd column shows pixels of suitable habitat for [*affinis*], while 3rd column shows pixels of suitable habitat for [*godmani*].

Phylogeographic and phylogenetic patterns:

The phylogenetic analyses recovered reciprocal monophyly for ND2, ODC, MUSK, and BRM (Fig. 5). In contrast, GAPDH did not exhibit reciprocal monophyly. The concatenated phylogeny showed substantial divergence between the *affinis* and *godmani* groups, with an estimated divergence time of 2.6 mya (1.5–4.0 mya, 95% HPD). Furthermore, Vázquez-López et al.

(2020) inferred the *E. affinis* complex as sister to a clade containing *E. chlorotica*, *E. finschi*, and *E. luteicapilla* with strong support (1.0 PP). Importantly, the estimates of divergence times and the inferred topology differ considerably from what was recently reported by Imfeld et al. (2020), which was based on UCE data; they found that *E. affinis* is sister to *E. luteicapilla* alone with a divergence estimate of 0.68 mya between these two species. Imfeld et al. (2020) did not sample all three described subspecies of *E. a. affinis*, but the maximum crown age of *E. affinis* estimated by Imfeld et al. (2020) of 0.68 is dramatically more recent than the 2.6 mya (1.5–4.0 mya, 95% HPD) between *godmani* and *affinis/olmecorum* as estimated by Vázquez-López et al. (2020).

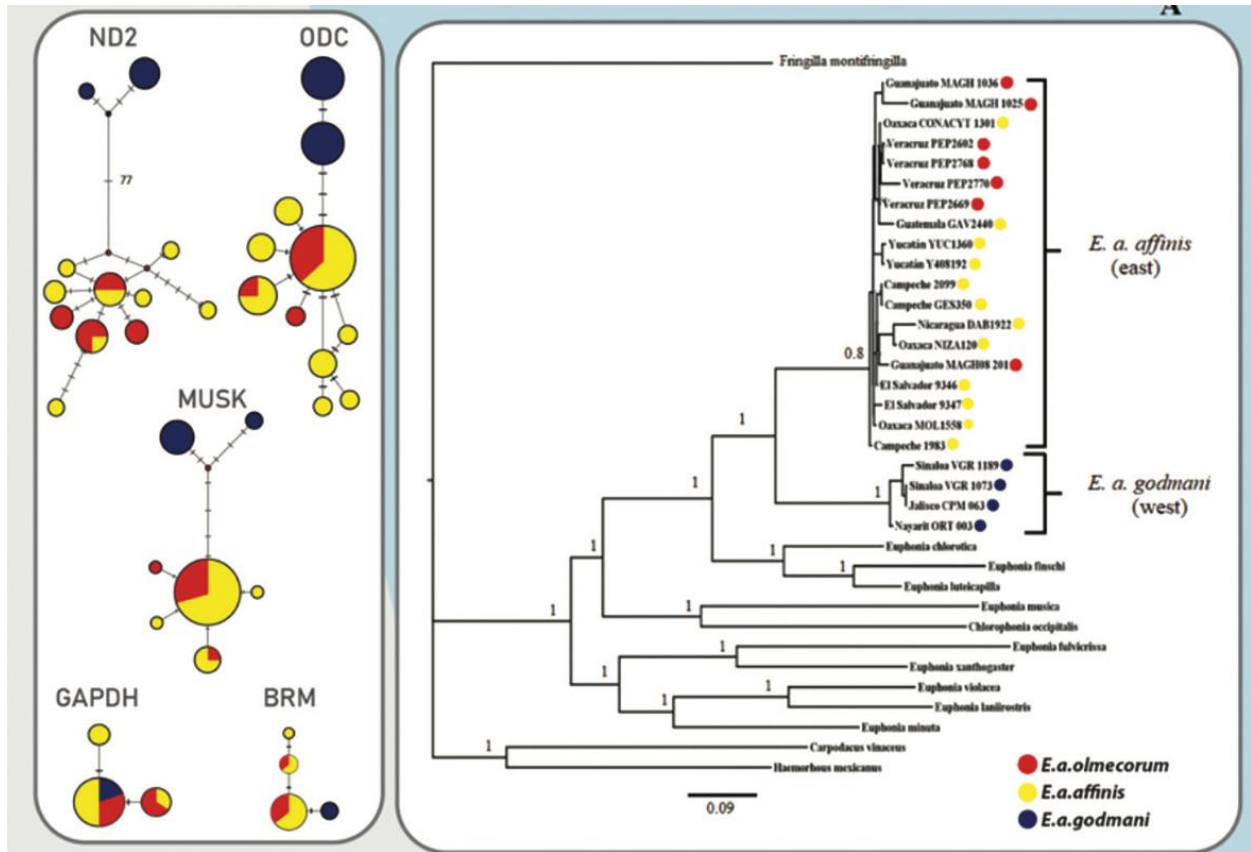


Figure 5: Results of haplotype networks and Bayesian inference of the concatenated alignment. *E. a. olmecorum* is shown in red, *E. a. affinis* is in yellow, and *E. a. godmani* is in blue.

The divergence times estimated by Vázquez-López et al. (2020) suggest the *affinis* and *godmani* groups diverged between the Pliocene and Pleistocene epochs, following completion of the orogeny of the Sierra Madre Occidental and the Transmexican Volcanic Belt. These events were important for the establishment and spread of the tropical dry forest and corresponding forest edges that characterize much of the Pacific slope of Mexico and the distribution of the *godmani* group. The Pacific slope of Mexico is an area of high endemism, with numerous Mexican land birds restricted to distributions similar to those of the *godmani* group (Bertelli et al. 2017). Thus, the splitting of *godmani* from *affinis* makes sense in light of the broader biogeography of Mexico and other codistributed taxa.

Summary and contextualization of new findings:

Notwithstanding discrepancies in interspecific topology and divergence timing estimates between Imfeld et al. (2020) and Vázquez-López et al. (2020), there is evidence for reciprocal monophyly between *affinis* and *godmani* in multiple loci. This suggests a considerable period of independent evolution between these lineages. Furthermore, these putative taxa correspond to geographically cohesive units that are diagnosable in plumage and also in song. Finally, the Pacific slope of Mexico is an area of high endemism, and the distribution of *godmani* corresponds with many other species that only occur in those ecoregions of western Mexico.

The two groups are allopatric, thus there is no direct test of reproductive isolation. However, there are multiple phenotypic characters (song + plumage), phylogeographic evidence, and biogeographic support to recognize *godmani* as a separate species from *affinis* under the Biological Species Concept.

Recommendation:

We recommend splitting the *godmani* and *affinis* groups to recognize two species within the *E. affinis* complex. This is based on phylogeographic evidence and multiple phenotypes that are differentiated and diagnosable between the two groups.

English names:

Godman's Euphonia has long been used for *godmani* (Ridgway 1902), but an alternative name might be West Mexican Euphonia, as it is endemic to west Mexico and that prefix been used for other species in the region. Scrub Euphonia could be retained for *affinis* as the two taxa are allopatric although it has also been known as Lesson's Euphonia (Ridgway 1902).

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Submitted by: Nicholas A. Mason, David Vander Pluym, Melisa Vázquez-López, and Blanca E. Hernández-Baños

Date of proposal: 25 February 2021

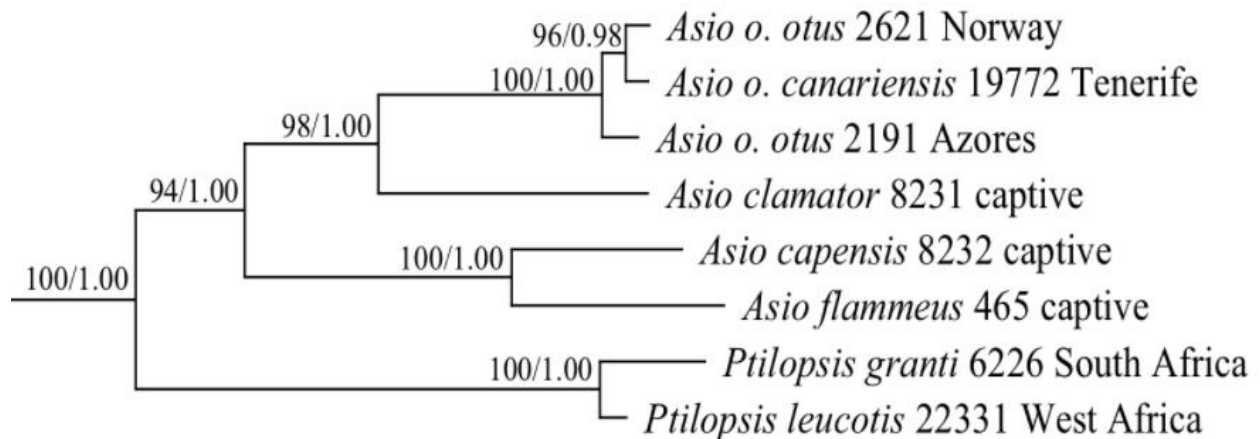
Subsume *Pseudoscops* into *Asio*, transferring Jamaican Owl *P. grammicus* and Striped Owl *P. clamator*

Background:

Kaup described *Pseudoscops* as a subgenus of *Otus* in 1848. The subgenus consisted of the single species *Ephialtes grammicus*, a Jamaican endemic described by Gosse the previous year, and Ridgway (1914), Cory (1918), and Peters (1940) all treated the genus as monotypic. *Pseudoscops* has long been considered to be closely related to *Asio*, however, and Ford (1967, *vide* Olson 1995)) united these two genera, along with the monotypic genera *Rhinoptynx* and *Nesasio*, in the subfamily Asioninae and suggested that they all be placed in *Asio*. Olson (1995), in a study of the osteology of owls in this subfamily, proposed that *grammicus* and *Asio clamator*, the species sometimes placed in the monotypic genus *Rhinoptynx*, were sister species and suggested that they be merged into *Pseudoscops*. In the sixth edition of the checklist (AOU 1983), *clamator* had been placed in *Asio* and *grammicus* in a monotypic *Pseudoscops*, but AOU (1998), following Olson (1995), placed both species in *Pseudoscops*.

New Information:

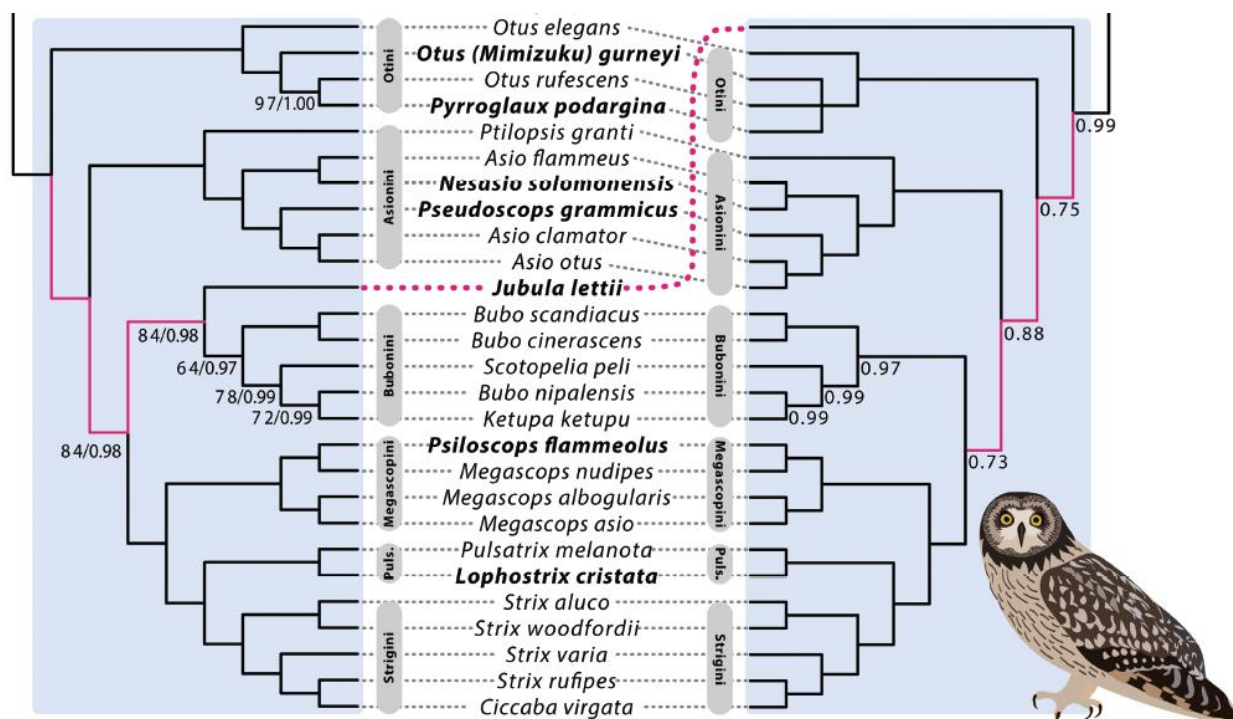
The first molecular phylogeny to include one of these species was that of Wink et al. (2009), who gathered cytochrome-b and RAG-1 sequences for 97 taxa of typical owls, including *Pseudoscops clamator* (as *Asio clamator*), from 15 of the larger genera as well as some (but not all) smaller genera. They found *clamator* to be part of a clade of four species of *Asio*, the other three species being *otus*, *capensis*, and *flammeus*, and found that *Asio* was sister to *Ptilopsis*. Within the *Asio* clade, *clamator* was sister to *otus*, and *clamator*+*otus* was sister to *capensis*+*flammeus*:



Support for this result was strong, although note that the individuals sampled for three of their four species of *Asio* were captive birds. Also, the other species of *Pseudoscops* (*P. grammicus*) was not sampled, and neither was *Nesasio solomonensis*, another species thought to be closely

related to *Asio*. Based on this study, SACC transferred *P. clamator* to *Asio* (see SACC Proposal 713: <https://www.museum.lsu.edu/~Remsen/SACCprop713.htm>).

More recently, Salter et al. (2020) sequenced UCEs and near-complete mitochondrial genomes for 43 species of owls, including representatives of 27 of the 28 genera, including 6 not included in previous molecular studies. Of note to this proposal, their sampling included both *P. grammicus* and *P. clamator* (as *Asio clamator*), and they also sampled two additional species of *Asio* (*otus* and *flammeus*) as well as the extralimital species *N. solomonensis*. Their phylogenetic results (see the relevant part of their UCE tree below) indicated that these five species form a well-supported clade, sister to *Ptilopsis*, in which *P. grammicus* is sister to a clade consisting of *clamator* and *otus*, and that this clade is sister to a clade consisting of *A. flammeus* and *N. solomonensis*. Thus, the three species of questionable placement, *grammicus*, *clamator*, and *solomonensis*, are interspersed with *Asio* as represented by *otus* and *flammeus*. Their mitochondrial phylogeny differed slightly because *P. grammicus* was sister to *otus* (rather than *clamator*+*otus*) and *grammicus*+*otus* was sister to *clamator*.



Part of Figure 2 from Salter et al. (2020), showing trees resulting from Maximum Likelihood and Bayesian analyses (on the left) and SVDquartets analysis (on the right). All nodes received 100% bootstrap support and 1.0 Bayesian posterior probability unless noted otherwise. Pink branches and dotted lines indicate conflicting relationships, neither of which applies to the *Asio* clade.

Recommendation:

We recommend that the committee transfer *grammicus* and *clamator* from *Pseudoscops* to *Asio*, to form part of an expanded monophyletic *Asio* that also includes the extralimital species

Nesasio solomonensis. We don't see a reasonable alternative to this. Other options consistent with the phylogeny would involve (1) restricting *Asio* to *otus* (the type species), *clamator*, and *grammicus*; (2) restricting *Pseudoscops* to *grammicus* and restricting *Asio* to *otus* and *clamator*, *contra* the mtDNA phylogeny; or (3) restricting *Pseudoscops* to *grammicus* and restricting *Asio* solely to *otus*, with *clamator* being placed once again in *Rhinoptynx*. However, all of these options would require that *A. flammeus* be removed from *Asio* and that guesswork be applied to the unsampled species of *Asio*. Moreover, the nodes uniting the *Asio* clade (*otus-clamator-capensis-flammeus*) in Wink et al. (2009) and in the supplementary trees of Salter et al. (2020) are similar in depth to other nodes uniting genera in the Strigidae, suggesting that the phylogenetic diversity in the proposed expanded *Asio* is typical of genera in this family.

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Submitted by: Terry Chessser and Max T. Kirsch

Date of Proposal: 1 March 2021

Transfer Spruce Grouse *Falcapennis canadensis* to *Canachites***Background:**

The Spruce Grouse *Falcapennis canadensis* was described by Linnaeus (1758). Initially placed in the genus *Tetrao* with all other grouse (and partridges, quails, etc.), it was moved to the newly erected *Canace* (of which it was made the type species) by Reichenbach (1852). Stejneger (1885) found that *Canace* Reichenbach, 1852, was preoccupied by a genus of flies (Diptera) of the same name, so he created the substitute name *Canachites* (type by original designation *Tetrao canadensis* Linnaeus, 1758). The following year, the first edition of the AOU Check-list (1886) placed Spruce and Franklin's Grouse (treated as separate species at the time) in the genus *Dendragapus* alongside Blue Grouse, where they remained until the third edition (AOU 1910) transferred them to *Canachites*, based primarily on differences in the number of rectrices and in overall plumage pattern between Spruce+Franklin's Grouse and Blue Grouse, and a lack of cervical vocal sacs in Spruce Grouse and Franklin's Grouse (Short 1967, Schroeder et al. 2020).

Yamashina (1939), taking into account many close similarities in appearance and behavior between Spruce (and Franklin's) and Siberian Grouse *Falcapennis falcapennis*, concluded that they were best treated as congeneric, and accordingly recommended merging *Canachites* into *Falcapennis* (which has priority).

The fifth edition of the Check-list (AOU 1957) lumped Spruce and Franklin's Grouse into a single species, Spruce Grouse *Canachites canadensis*. [The common name Spruce Grouse and scientific name *Canachites/Dendragapus/Falcapennis canadensis* refer to the combined species for the remainder of the proposal. Franklin's Grouse could merit re-recognition as a separate species from Spruce Grouse, but that's an issue for a different proposal.]

In his monographic review of grouse generic limits, Short (1967) merged *Canachites* back into *Dendragapus*, his rationale being that the previous reasons for separating them were either erroneous or lacked taxonomic utility and were outweighed by similarities. (He also merged *Falcapennis* into *Dendragapus* for the first time, following and building upon the reasoning of Yamashina [1939] that Spruce and Siberian Grouse should be considered congeneric.) The sixth edition of the Check-list (AOU 1983) followed suit, subsuming *Canachites* into *Dendragapus*.

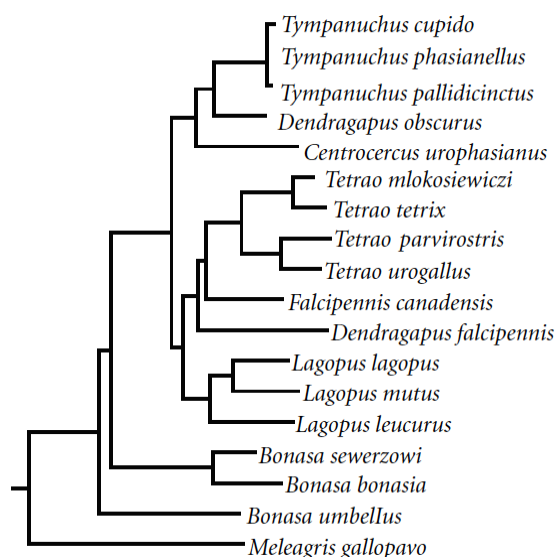
Ellsworth et al. (1996), based on restriction enzyme analysis of mitochondrial DNA of all North American grouse species recognized at the time (plus Western Capercaillie *Tetrao urogallus*), determined that Spruce and Blue Grouse were not sister taxa, and accordingly recommended removing Spruce Grouse from *Dendragapus*; in their trees, Spruce Grouse was sister to Ruffed Grouse, whereas Blue Grouse formed a clade with ptarmigan and Western Capercaillie. Dickerman and Gustafson (1996) affirmed previous suggestions that Spruce and Siberian

Grouse were close relatives, and accordingly, the seventh edition of the Check-list (AOU 1998) placed Spruce Grouse in *Falcapennis*, where it remains to this day.

New Information:

The first molecular phylogenetic study to include both Spruce and Siberian Grouse was Gutiérrez et al. (2000), who sequenced 5 mitochondrial regions from all grouse species (apart from Gunnison Sage-Grouse, only just described at the time), as well as a few distinctive subspecific forms sometimes afforded species status, including both Franklin's and nominate-group Spruce Grouse. In none of their trees was there support for a sister relationship between Spruce (plus Franklin's) and Siberian Grouse, and accordingly they recommended returning the former to *Canachites*. In contrast, Lucchini et al. (2001), also sequencing 5 mitochondrial regions (2 of which were the same as in the previous study) from all grouse species, recovered a sister relationship between Spruce and Siberian Grouse with strong support, and the two together sister to *Tetrao* (including *Lyrurus*); however, their cyt-b sequence of Siberian Grouse appears to be a chimeric sequence, half of which is identical to that of Spruce Grouse (L. Raty, <https://www.birdforum.net/threads/spruce-grouse.165442/#post-3177131>), making their conclusion in this regard suspect. Drovetski (2002) sequenced four loci (one mitochondrial, one autosomal, two W-linked) from all grouse species (and a few distinctive subspecific forms), and recovered Spruce and Siberian Grouse as sister taxa, albeit with relatively low support.

Kimball et al. (2011) produced a supermatrix phylogeny of 170 galliform taxa using two mitochondrial regions and four nuclear introns. Almost all grouse species were represented, including both Spruce and Siberian Grouse (as *Dendragapus falcapennis*). *Falcapennis* was paraphyletic in their tree, with Siberian Grouse sister to a combined Spruce Grouse + *Tetrao*.



Part of figure 1 from Kimball et al. (2011), showing phylogenetic relationships among the grouse (and turkeys).

The most comprehensive molecular phylogenetic study of grouse to date is that of Persons et al. (2016), who reconstructed a phylogeny of all grouse species using eight autosomal loci (seven newly sequenced), two W-linked loci, four mitochondrial regions, and UCE loci. They found no support for a sister relationship between Spruce and Siberian grouse in the majority of their analyses, although the topology of the *Falcapennis-Tetrao* clade varied between trees, with Siberian Grouse sister to *Tetrao* + *Lyrurus* and Spruce Grouse sister to the previous clade in the nuclear phylogeny, and the positions of Spruce and Siberian Grouse reversed in the combined nuclear and mitochondrial phylogeny and the UCE phylogenies. Depending on the dataset (maternal or autosomal), the estimated divergence times between Spruce Grouse, Siberian Grouse, and *Tetrao* + *Lyrurus* were similar to or slightly older than the divergence times among the genera *Tympanuchus*, *Dendragapus*, and *Centrocercus*, or between White-tailed Ptarmigan and the other two ptarmigan species.

Figures 2-5 from Persons et al. are below:

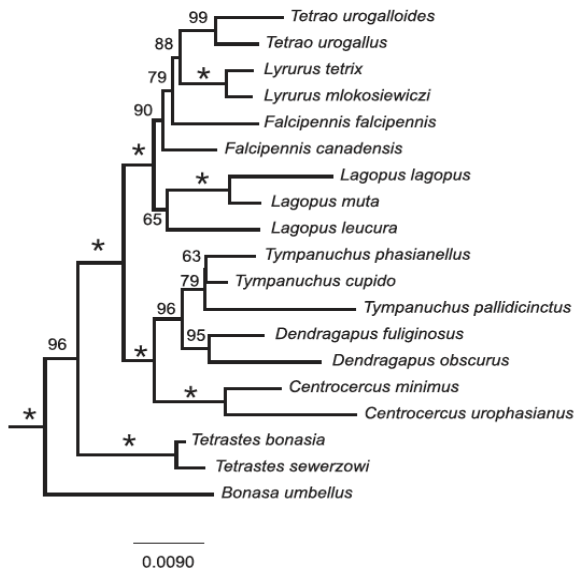


Fig. 2. ML phylogeny using the seven newly sequenced introns. Values above nodes are bootstrap percentages from 1000 bootstrap replicates. *Indicates 100% bootstrap support.

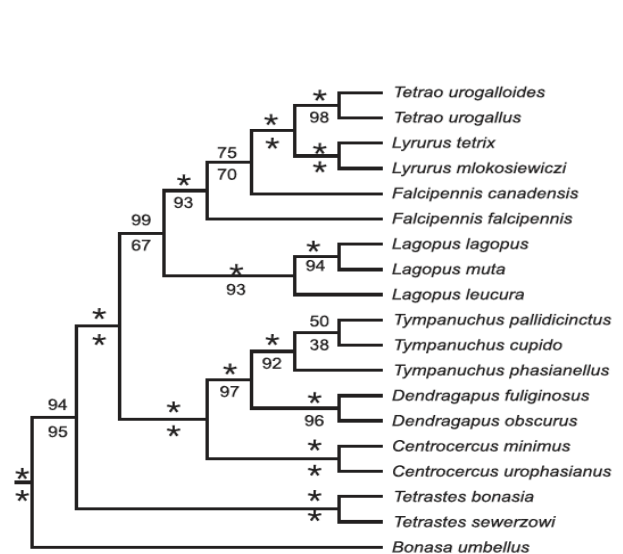


Fig. 3. ML bootstrap consensus tree of the combined intron and mitochondrial data. Values above nodes are bootstrap percentages from 1000 bootstrap replicates from RAXML; values below nodes are bootstrap percentages from ASTRAL. *Indicates 100% bootstrap support.

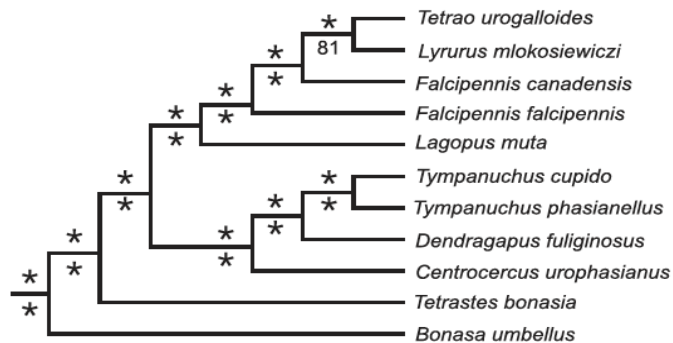


Fig. 4. ML bootstrap consensus tree of the UCEs. Values above nodes are bootstrap percentages from 1000 bootstrap replicates from RAXML; values below nodes are bootstrap percentages from ASTRAL. *Indicates 100% bootstrap support.

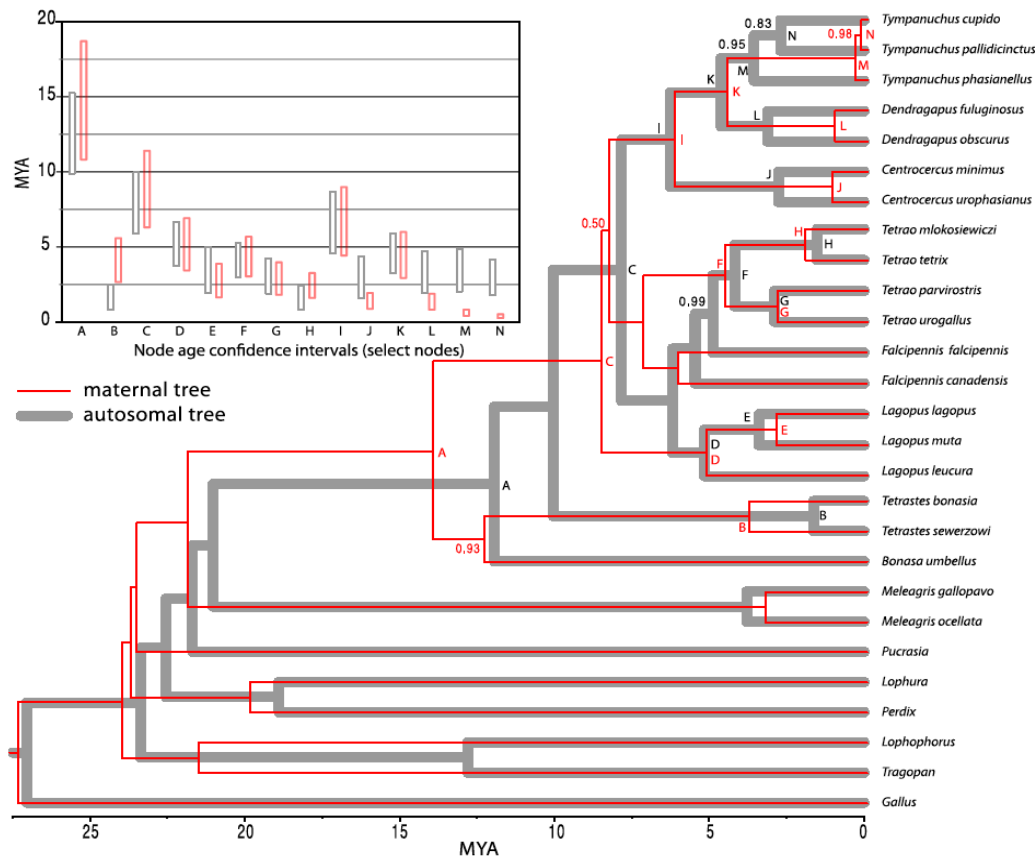


Fig. 5. Branch lengths from maternal and autosomal markers. Graph in upper left indicates the confidence intervals around each time estimate for the two datasets.

Recommendation:

Two potential solutions to the paraphyly of *Falcapennis* are as follows:

1. Merge both species of *Falcapennis* into an expanded *Tetrao* (also including *Lyrurus*). Although this would keep the morphologically and ecologically similar Spruce and Siberian Grouse in the same genus, and although there are, for example, certain details of plumage pattern shared between Siberian+Spruce Grouse and Black-billed Capercaillie *Tetrao urogalloides*, this option is difficult to reconcile with the extreme variation in size (the largest Western Capercaillies *T. urogallus* are several times heavier than Spruce or Siberian Grouse), morphology, ecology, and breeding display behavior that would be contained within a *Tetrao* so defined (Potapov and Sale 2013), seemingly much more than within any other grouse genus.
2. Restrict *Falcapennis* to Siberian Grouse, moving Spruce Grouse back to a (for now, pending a split of Franklin's Grouse) monospecific *Canachites*. Given how dissimilar Spruce and Siberian Grouse are to the capercaillies and black grouse, this seems like the better option, and it perhaps emphasizes that Spruce and Siberian Grouse aren't as closely related as they look. This treatment also has historical precedent, unlike *Tetrao sensu* option 1—Spruce Grouse was placed in *Canachites* in the AOU Check-list, and

accordingly much of the other literature dealing with the species, for most of the 20th century.

Given how heterogeneous an expanded *Tetrao* would be in morphology and behavior, as well as the historical precedent for recognizing *Canachites*, I recommend option 2.

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Submitted by: Max T. Kirsch

Date of Proposal: 2 March 2021

Transfer Five-striped Sparrow *Amphispiza quinquestriata* to *Amphispizopsis***Background:**

The generic allocation of the Five-striped Sparrow *Amphispiza quinquestriata* has long been controversial. Originally described in the genus *Zonotrichia*, various authors have transferred it back and forth between *Aimophila* and *Amphispiza* over the past century and a half. In his monographic study of relationships in the genus *Aimophila*, Wolf (1977) concluded that the Five-striped Sparrow was likely not closely related to any other members of that genus or to the superficially similar-looking Black-throated Sparrow *Amphispiza bilineata*; he further proposed that Five-striped Sparrow was perhaps most closely related to the ground-sparrows (*Melospiza*) instead but refrained from making any taxonomic recommendations pending further study of relationships among New World sparrows. Wolters (1980) described a new genus, *Amphispizopsis*—type by original designation *Zonotrichia quinquestriata* Sclater & Salvin, 1868—and also included in the new genus two other species at the time placed in *Aimophila* (Bridled Sparrow *Peucaea mystacalis* and Black-chested Sparrow *P. humeralis*). However, this treatment was not followed by subsequent authors. Sibley and Monroe's (1990) global classification is one of few to have subsequently cited *Amphispizopsis*, as an alternate genus merged into *Aimophila*.

Five-striped Sparrow was first added to the AOU Check-list in the 34th supplement (AOU 1982); it was placed in the genus *Amphispiza*, and it remained in *Amphispiza* through the 40th supplement (AOU 1995). It was moved to *Aimophila* in the 41st supplement (AOU 1997); in the seventh edition (AOU 1998), it was noted that its former inclusion in *Amphispiza* was based on unpublished data and that an alternative view was to be found in Phillips and Phillips Farfán (1993). Based on DaCosta et al. (2009), proposal 2009-A-12b recommended that Five-striped Sparrow be transferred from *Aimophila* back to *Amphispiza*. Some committee members proposed that it be placed in *Amphispizopsis* instead, however, resulting in proposal 2009-E-3, in which a majority of the committee voted to transfer Five-striped Sparrow to *Amphispiza*, where the species currently remains. Comments in favor of recognizing *Amphispizopsis* for Five-striped Sparrow emphasized morphological, behavioral, and genetic differences between Five-striped and Black-throated Sparrows on par with other sparrows placed in separate genera, whereas comments in favor of merging Five-striped Sparrow into *Amphispiza* placed more weight on minimizing the number of monotypic genera.

Although similar to Black-throated Sparrow *Amphispiza bilineata* in some aspects of overall coloration (e.g., some aspects of face pattern), Five-striped Sparrow is quite different in structure and behavior: it is a relatively large sparrow with a long bill, long and rounded tail, strong tarsi, and skulking habits. Except when singing, Five-striped is typically secretive and hard to observe, foraging alone or in pairs on the ground or low in shrubs, and when pursued it tends to run along the ground rather than flush (Groschupf 2020, JLD pers. obs.). In its structure and behavior, it more closely recalls some of its former congeners (now in *Aimophila* and

Peucaea) than it does the smaller, more delicate, and much tamer and bolder Black-throated Sparrow, which in winter tends to forage in small groups in more open habitats, often with other sparrow species, and readily flies and perches up in vegetation (Storer 1955, JLD pers. obs.). Juvenile Five-striped Sparrows are similar to adults in their general pattern of light and dark coloration, but are duller overall and have a less distinct head pattern; in addition, they have a distinctive yellowish wash on the belly, and (unlike most juvenile sparrows) only faint and difficult-to-see streaking on the breast (Phillips and Phillips Farfán 1993, Groschupf 2020). In contrast, juvenile Black-throated Sparrows have a bold and contrasting head pattern, similar to that of adults but with a white throat, and instead of the adult's black throat and breast patch they have fine but distinct streaks across the breast (Johnson et al. 2020). The call notes of Five-striped are quite unlike the tinkling call notes of Black-throated, and are more reminiscent of the calls of, e.g., Canyon Towhee *Melospiza fusca*; the two species' songs also show little resemblance to each other: forced-sounding, brief, and unmusical in Five-striped (with singing birds often beginning with a series of sputtering call notes before finally transitioning to a series of brief songs) vs. sweet, melodic, and structurally more complex in Black-throated (Groschupf 2020, Johnson et al. 2020, JLD pers. obs.).

New information:

Klicka et al. (2014) produced a comprehensive mitochondrial DNA phylogeny of the family Passerellidae (see Figure 1 below). In it, Five-striped and Black-throated Sparrow are sister taxa, although with only moderate support (Bayesian posterior probability of 0.96; bootstrap value of 73%). The node uniting the two species is relatively deep—deeper than the nodes uniting most other congeneric sparrows, and somewhat deeper than the node uniting the two species in the sister clade to *Amphispiza*, Lark Sparrow *Chondestes grammacus* and Lark Bunting *Calamospiza melanocorys*—suggesting that Five-striped and Black-throated Sparrows have relatively long independent evolutionary histories.

Barker et al. (2015) again recovered a sister relationship between Five-striped and Black-throated Sparrows, with a posterior probability of 0.93 (see Figure 2 below). The estimated age of the split between the two is around 6 mya, older than some sparrow genera and younger than others; relevant in this case is that it's older than the split between the two species in the sister clade to *Amphispiza*, Lark Sparrow *Chondestes grammacus* and Lark Bunting *Calamospiza melanocorys*, which are universally placed in separate genera. Our proposal would mean that all four taxa in this clade, both pairs long-diverged, would become monotypic genera.

Cicero et al. (2020) independently sequenced 4 mitochondrial and 3 nuclear genes from 43 New World sparrow species, including all species formerly placed in *Aimophila*. The two species of *Amphispiza* are sister taxa in the maximum clade credibility tree for the concatenated analysis (but with only 0.72 posterior probability and separated by long branches), and together the two are sister to *Chondestes grammacus* (*Calamospiza melanocorys* was not sampled). However, the relationships among these three species differ in Cicero et al.'s species tree (Supplementary figure S2), in which *Amphispiza* is paraphyletic: *A. quinquestriata* is sister to *C. grammacus* (albeit with posterior probability below 0.70), with the two together sister to *A. bilineata*.

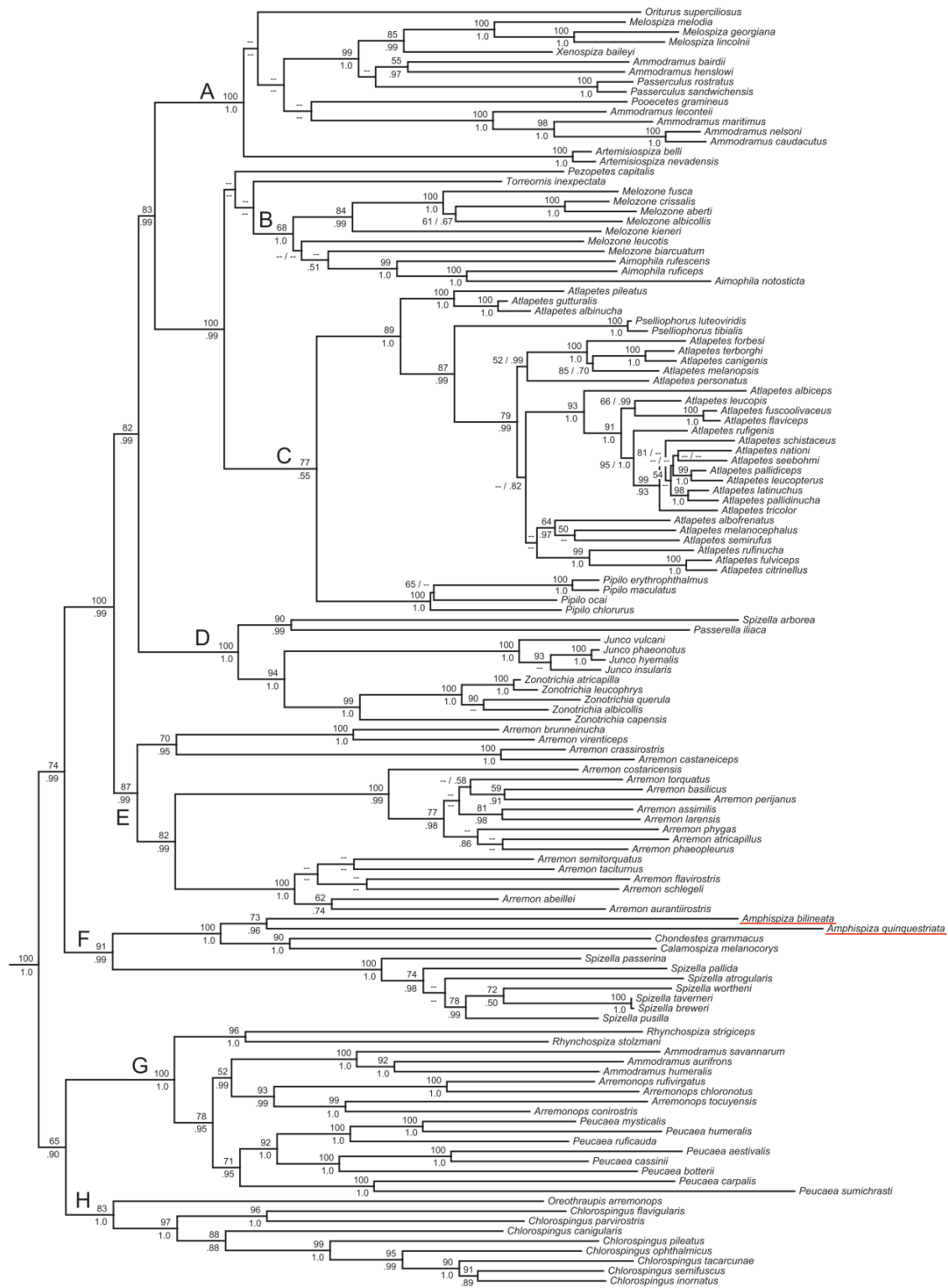


Figure 1. Maximum likelihood phylogenetic tree from Klicka et al. (2014), inferred from mitochondrial DNA, with bootstrap support above and Bayesian posterior probability below each node (and nodes with bootstrap support below 70% or posterior probability below 0.50 marked with dashes). The two species of *Amphispiza* are underlined in red.

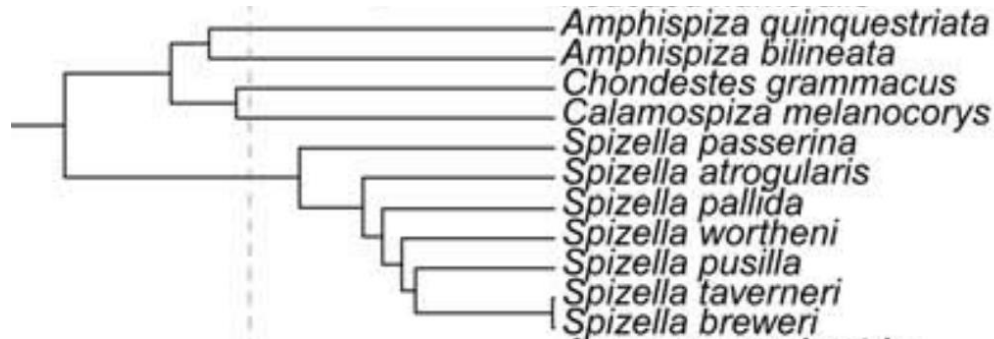


Figure 2. The clade comprising *Amphispiza* and its close relatives (“Clade D” of Klicka et al. 2014) from figure 1 of Barker et al. (2014), a time-scaled phylogeny of Emberizoidea; note the relative ages of the *Amphispiza quinquestriata*-*A. bilineata* split and the *Chondestes grammacus*-*Calamospiza melanocorys* split. The dashed line marks 5 mya.

Two other more recent NACC proposals revising generic limits in New World sparrows are perhaps worth mentioning: 2015-A-6 (Transfer American Tree Sparrow *Spizella arborea* to *Spizelloides*) and 2018-C-15c (Revise generic assignments of New World “grassland” sparrows).

To summarize proposal 2015-A-6: American Tree Sparrow was found to be sister to Fox Sparrow in the mitochondrial tree of Klicka et al. (2014), although a sister relationship between the two was not supported by their nuclear tree. As such, also taking into account the striking morphological differences between the two species (and among them and the related genera *Zonotrichia* and *Junco*), Slager & Klicka (2014), and accordingly 2015-A-6, recommended transferring American Tree Sparrow to a monospecific *Spizelloides*, retaining a monospecific *Passerella* for Fox Sparrow, rather than merging American Tree Sparrow into *Passerella* (or merging all species in Klicka et al. 2014’s Clade D into a single genus). From Slager & Klicka (2014):

“The long branches subtending *S. arborea* and *Passerella iliaca* on the mtDNA tree indicate that these two lineages are relatively ancient. Merging both into *Passerella* (see Rising 2011) overlooks the morphological and genetic distinctiveness and long independent histories of these two taxa.”

The node uniting *S. arborea* and *Passerella iliaca* in the mtDNA tree in Klicka et al. (2014) is similar in depth to—even slightly shallower than—that uniting *Amphispiza bilineata* and *A. quinquestriata*, which similarly show notable morphological (and behavioral) differences (and similarly may not be sister taxa, per Cicero et al. 2020). However, in contrast to the 2009 Five-striped Sparrow proposals, comments on 2015-A-6 showed unanimous support for recognizing

Spizelloides, with none proposing to instead merge American Tree Sparrow into *Passerella* in order to avoid creating another monotypic sparrow genus.

Summarizing proposal 2018-C-15c: *Passerculus*, *Melospiza*, *Xenospiza*, *Ammodramus bairdii*, and *A. henslowii* form a well-supported clade, but the precise relationships among the five are less than certain, differing from dataset to dataset (with the two former *Ammodramus* species sister in, e.g., the mitochondrial tree of Klicka et al. 2014, but not in their nuclear or species trees or in Barker et al. 2015). Accordingly, given the options to (1) merge the two former *Ammodramus* into *Passerculus*, (2) place the two former *Ammodramus* in a resurrected genus *Centronyx*, or (3) merge all of the above genera and species into an expanded *Passerculus*, the authors of the proposal recommended option 3. However, the committee voted for option 2, emphasizing the morphological and behavioral cohesiveness of each currently recognized genus and the morphological and behavioral differences between genera in this clade (option 2 also provided the least destabilization to prior generic limits). Note that the splits between genera in this clade are somewhat more recent than the split between *Amphispiza bilineata* and *A. quinquestriata*, per Barker et al. 2015.

Recommendation:

Five-striped Sparrow and Black-throated Sparrow differ strongly in various aspects of morphology and behavior (perhaps obscured in the past by their superficially similar plumage patterns and Five-striped Sparrow's relative unfamiliarity), and are on relatively old independent evolutionary trajectories. In more recent revisions of sparrow generic limits, the committee voted to recognize more, rather than fewer, genera, placing an emphasis on morphological and behavioral cohesiveness within genera.

Does it make sense to recognize four monotypic genera in this part of the tree (*Amphispiza*, *Amphispizopsis*, *Chondestes*, and *Calamospiza*)? We would argue that yes, it does - each species is highly distinct from the others in morphology and behavior, and the four species diverged relatively long ago. It makes much more sense to our eye than the current arrangement, treating the morphologically and behaviorally quite different Black-throated and Five-striped Sparrows as congeneric when Lark Sparrow and Lark Bunting are not—or a hypothetical alternative involving merging Lark Sparrow and Lark Bunting, or all four species in this clade, into a single morphologically and behaviorally highly heterogeneous genus.

Accordingly, because of the morphological, behavioral, and genetic differences between Five-striped and Black-throated Sparrows, as well as to make generic limits more morphologically and behaviorally consistent within Passerellidae, we recommend a YES vote to transfer Five-striped Sparrow from *Amphispiza* to *Amphispizopsis* (as *Amphispizopsis quinquestriata*).

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Submitted by: Max T. Kirsch, Jon Dunn, Carla Cicero, and Louis Bevier

Date of Proposal: 2 March 2021

Elevate *Melopyrrha portoricensis grandis* to species status**Effect on the *Check-list*:**

Currently Puerto Rican Bullfinch *Melopyrrha portoricensis* is treated as polytypic, with nominate *portoricensis* on Puerto Rico and a second subspecies, *grandis*, on St. Kitts. If adopted, this proposal would recognize *grandis* as a species, and *Melopyrrha portoricensis* would become monotypic.

Note that until recently (Burns et al. 2014), these taxa were classified in *Loxigilla*, and are now placed in the genus *Melopyrrha* along with Cuban Bullfinch and Greater Antillean Bullfinch (Chesser et al. 2018). Most previous literature on their taxonomy placed them in *Loxigilla*.

Background:

The population of bullfinches on St. Kitts originally was described as a subspecies, *Loxigilla portoricensis grandis*, by Lawrence (1881: [204](#)) on the basis of nine specimens collected in 1880. As noted by Garrido and Wiley (2003), "In the nineteenth century, most authors had the tendency to describe new taxa as species. An exception was Lawrence's (1882) description of *L. portoricensis grandis* as a subspecies. Three factors may have contributed to his decision: (1) a lack of material for comparison, (2) poor knowledge of the genus (Lawrence had to consult Juan Gundlach by correspondence regarding the plumage), and (3) Lawrence's inability to assemble Ober's nine topotypes to write his description. In fact, two contemporary authors, Cory (1892) and Ridgway (1901), considered the taxa as distinct species."

Hellmayr (1938: [page 160](#)) again treated *grandis* as a subspecies; we don't know whether this was a change that he instigated, but this seems possible because his synonymy does not list authors later than Cory (1892) and Ridgway (1901). Hellmayr did not specifically note this, however; for that matter, there is no indication that Hellmayr was personally familiar with specimens of this taxon.

Adults of both recognized populations of *L. portoricensis* share a similar overall coloration and pattern, they are black birds with a reddish-orange crown, throat, and undertail coverts. Juveniles are olive-brown overall in color, paler underneath with reddish-orange undertail coverts, paler than in adults. This basic adult color pattern of black with reddish undertail coverts, throat and at least some reddish coloration on the head is also seen in the Greater Antillean Bullfinch as well as the more distantly related Lesser Antillean Bullfinch.

Whether to split *grandis* was considered earlier by NACC (Proposal 2005-A-07, submitted by the late Jim Rising), which was based largely on Garrido and Wiley (2003). At that time, the proposal did not pass.

New information:

There isn't any, and indeed new information is unlikely to be forthcoming, as *grandis* has not been reported in over 90 years (Olson 1984) and is presumed to be extinct. That said, the case of *grandis* merits a fresh reappraisal, as the 2005 proposal perhaps did not fully delineate just how different *grandis* is from nominate *portoricensis*.

Garrido and Wiley (2003) found sexual dimorphism in linear measurements (lengths of the wing, tail, culmen, and tarsus) in nominate *portoricensis*, but no such dimorphism was apparent in *grandis*. This may be a valid distinction between the two taxa, but given the small sample size for *grandis*, they interpreted this result with caution.

More apparent was that these linear measurements show little or no overlap between the two taxa. Table 1 from Garrido and Wiley (2003) is shown below:

TABLE 1. Mean, standard deviation, range, and sample size (parentheses) for wing, tail, culmen, and tarsus for *Loxigilla portoricensis* populations in Puerto Rico (*L. p. portoricensis*) and St. Kitts (*L. p. grandis*). Statistical analyses are within-sex comparisons (two-sample t-test; equal variances not assumed) between Puerto Rican and St. Kitts specimens.

Sex	Locality	Statistic	Measurements (mm)			
			Wing	Tail	Culmen	Tarsus
Males	Puerto Rico		89.7 ± 3.9	73.6 ± 3.3	15.1 ± 1.9	22.6 ± 1.2
			80.0–99.0	66.0–80.0	12.0–18.0	18.4–25.9
			(55)	(52)	(53)	(55)
	St. Kitts		102.3 ± 3.4	78.5 ± 23.4	19.9 ± 1.1	27.3 ± 2.5
			95.0–107.0	71.0–81.0	17.7–20.9	23.2–31.7
			(8)	(8)	(8)	(8)
		t	-9.50	-3.84	-10.25	-5.20
		df	9	9	14	7
		P (2-tailed)	< 0.001	0.004	< 0.001	0.001
Females	Puerto Rico		84.1 ± 2.9	69.4 ± 3.7	15.5 ± 1.2	22.3 ± 1.2
			80.5–92.5	64.0–77.0	11.4–16.1	19.6–25.4
			(36)	(35)	(35)	(32)
	St. Kitts		101.7 ± 4.0	75.5 ± 2.2	19.7 ± 1.9	26.5 ± 0.8
			97.0–104.0	83.0–76.5	17.6–20.6	26.2–27.4
			(3)	(3)	(3)	(3)
		t	-7.37	-4.32	-5.68	-8.59
		df	2	3	2	3
		P (2-tailed)	0.018	0.023	0.030	0.003

Unfortunately, there are no data on the mass of *grandis*, but a side by side comparison of specimens of *grandis* and nominate *portoricensis* (Figure 1 in Garrido and Wiley 2003; see photo on next page) allows for some appreciation of what these linear differences might mean in terms of overall size.

Plumage differences between *grandis* and *portoricensis* were classified by Garrido and Wiley as being "substantially greater than those defining subspecies within the other *Loxigilla* species". Ridgway (1901) provided a good description of the differences between adults:



FIG. 1. *Loxigilla portoricensis* specimen from St. Kitts (*grandis*) (above: ANSP #128168; male) compared with specimen from Puerto Rico (*portoricensis*) (below: ANSP #84804; female), showing the substantial difference in body and culmen size. Photograph by Douglas Wechsler of VIREO, Academy of Natural Sciences of Philadelphia. [from Garrido and Wiley 2003]

"Similar to *P. portoricensis* but much larger and with the rufous markings darker (intermediate between ferruginous and vinaceous-rufous); that of the throat more restricted, scarcely extending to the chest, and that of the under tail-coverts mixed with black". In terms of plumage, these differences are comparable in magnitude to the differences between nominate *portoricensis* and Greater Antillean Bullfinch *Melopyrrha violacea*.

Garrido and Wiley also compared specimens of immatures of both taxa, and again found distinct differences: "*grandis* is darker and more brownish, with less greenish-olive on the underparts. The color of the undertail coverts is the same in both forms, as is the white of the axillars. Upperparts also differ: olive in *portoricensis* and reddish-brown in *grandis*. The head of *grandis* is grayer than in *portoricensis*."

Additionally, there is some evidence of habitat differences, also noted in Garrido and Wiley (2003). Nominate *portoricensis* occurs throughout the island of Puerto Rico, from lowlands to the highlands, whereas *grandis* was restricted to the highest slopes of Mount Misery. It's

unknown why *grandis* did not occur in more habitats on St. Kitts, but it may have been due to differences in habitat preference.

Recommendation:

The extinct population on St. Kitts differs in every possible way from nominate *portoricensis*: the plumage is different between the two in both adults and juveniles; *grandis* is markedly larger than *portoricensis*; and there is some evidence (based on a small sample size) that it lacked the sexual size dimorphism of *portoricensis*, therefore we recommend that the subspecies *grandis* be split from *portoricensis* and be elevated to species rank with the name *Melopyrrha grandis*.

Because *grandis* has not been recognized as a species for such a long time, it does not have an accepted English name. Ridgway (1901) and Hellmayr (1938) referred to it as "St. Christopher Bullfinch". If split, we recommend the English name St. Kitts Bullfinch following the current name widely in use for the island, including usage by the government of St Kitts and Nevis

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Submitted by: Jeff Gerbracht and Tom Schulenberg, Cornell Lab of Ornithology

Date of Proposal: 2 March 2021

Treat Bahama Nuthatch *Sitta insularis* as a separate species from Brown-headed Nuthatch *S. pusilla*

Effect on the Checklist:

The approval of this proposal would split *Sitta pusilla* into two species, both of which occur in the NACC area: (1) *S. pusilla* (mainland southeastern United States) and (2) *S. insularis* (Grand Bahama Island in the Bahamas). It would therefore add a species to the checklist. If the committee votes to split *S. pusilla* into two species, then English names for the two daughter species also should be considered. Thus, this proposal consists of two sub-proposals: (A) split *S. insularis* from *S. pusilla*, and (B) if (A) passes, use the English names Bahama Nuthatch and Brown-headed Nuthatch, respectively.

Background:

Sitta pusilla, Latham, 1790, is endemic to pine forests of the southeastern United States and Grand Bahama Island in the Bahamas. It represents one of the cooperative-breeding species that are native to North America. Two subspecies are recognized:

- *S. p. pusilla*, Latham, 1790: mainland southeastern United States (west to SE Oklahoma and E Texas and north to S Delaware)
- *S. p. insularis*, Bond, 1931: Grand Bahama Island in the Bahamas

The two subspecies are morphologically similar, although individuals on Grand Bahama have a longer and more slender bill (2 mm longer) and shorter wings than mainland birds. Additionally, insular birds have darker lores and auriculars, which are medium gray in the mainland populations (Bond 1931, Slater *et al.* 2020).

The subspecific rank of continental and insular forms was not debated until differences in morphological (plumage and morphometrics) and behavioral (voice) characters were reported by Hayes *et al.* (2004). Plumage differences were not considered to distinguish the two subspecies, because the authors found character overlap between taxa, and the poor quality of most study skins did not allow for accurate descriptions. Seven morphometric measurements were taken from museum specimens: bill length, bill width, bill depth, wing length, tail length, tarsus length, and middle toe length. The sample size for the mainland population consisted of 106 adults and 8 juveniles and for the insular population, 11 adults and 7 juveniles. Juveniles were excluded from further analyses because they presented variation associated with age. Consistent with the initial description of the Grand Bahama population, the bill-wing ratio was greater for the insular population (mean = 0.20 ± 0.02 SE) than for the continental form (0.17 ± 0.001), although one of the insular birds overlapped with the continental measurements. Discriminant function analyses using bill-wing ratio and tarsus length assigned correctly 100% of the continental specimens but only 91% of the insular ones.

Vocal analyses performed by Hayes *et al.* (2004) included recordings from 10 individuals of the continental population and 12 individuals of the insular population. At least three calls were identified in the Grand Bahama birds, and the most distinctive vocalization, a rapid, high-pitched call, did not resemble any call of the mainland population. Non-standardized playbacks were reported, with Grand Bahama birds responding more vigorously to this high-pitched call than to a continental call.

The NACC considered a proposal to split the Bahama Nuthatch from the Brown-headed Nuthatch based on these findings, but decided against the taxonomic change because of insufficient or conflicting information (Banks et al. 2006).

New information:

Recent genetic studies and a more detailed vocal study have added to the argument for splitting these taxa. Lloyd et al. (2008) sequenced two mitochondrial DNA markers (ND6: 447 bp, and control region: 511 bp, total: 958 bp) for 33 individuals, including 30 samples from the mainland (North Carolina, Georgia, Alabama, Florida, Louisiana, and Texas) and three samples from the insular population (Grand Bahama); however, just two of the three Bahamian samples were included in the analyses due to sequencing issues. The two Bahamian samples each represented a unique haplotype when the two markers were combined. A Bayesian phylogenetic analysis recovered a polytomy that included all the samples of the Brown-headed Nuthatch, even the two insular samples (Figure 1). The authors highlighted that the two insular samples showed a clearly distinct clade. They also mentioned that the mainland and island haplotypes differed by 1.37% mean sequence divergence, thus showing significant and relatively long-term genetic differentiation (which they estimated as 685,000 years based on 2% sequence divergence per million years). The authors discussed that the low levels of genetic variation are consistent with other passerines at the intraspecific level. They proposed that the unique mitochondrial genetic makeup and long-term isolation from the mainland of the Bahamian population suggest that it should be considered a distinct taxon, and that research regarding its specific status should be prioritized.

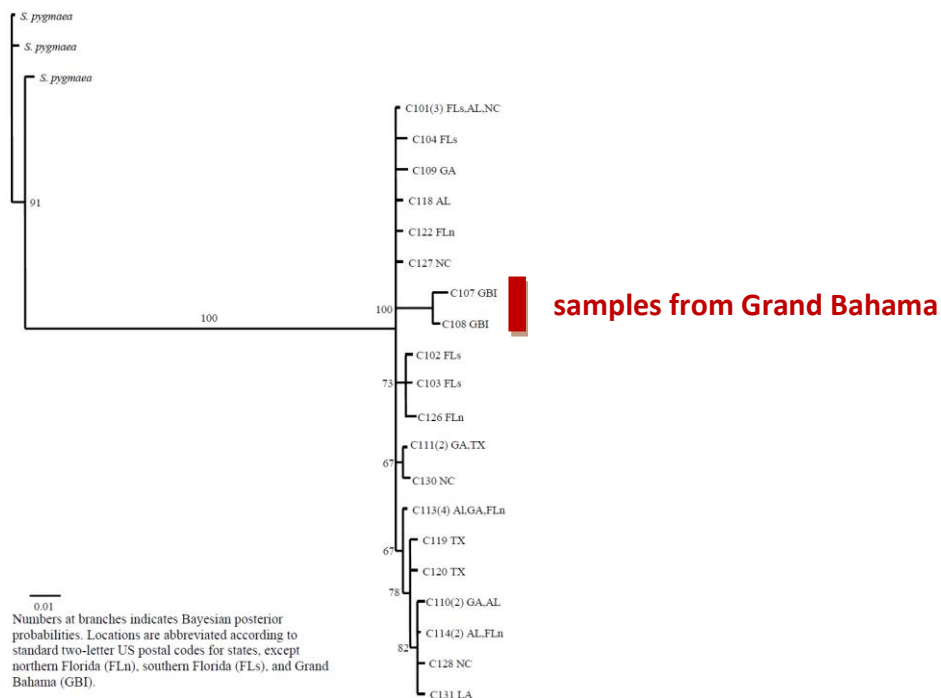


Figure 1. Rooted phylogram of concatenated haplotypes.

Figure 1. From Lloyd et al. (2008).

Han et al. (2019) examined the population genetic structure of the Brown-headed Nuthatch using nine microsatellite markers designed for this species. That study included 14 populations, 13 from Florida (389 individuals) and one from Grand Bahama (4 individuals). The authors reported that the insular population showed moderate to high differentiation from all Florida populations (pairwise F_{ST} from 0.134 to 0.223); within the mainland, pairwise F_{ST} among populations varied from 0.001 to 0.085. Additionally, the samples from the Bahama population exhibited low heterozygosity, suggesting a severe loss of genetic diversity. Because the Bahama population was represented only by four samples, it was excluded from other population genetic structure analyses in the paper.

More compelling evidence in support of this split comes from two recent studies of vocalizations. Levy and Cox (2020) used recordings from both the Bahama and Florida populations to compare playback responses, specifically to assess whether the Brown-headed Nuthatch from Grand Bahama Island represents a different species from mainland populations. In Grand Bahama Island, the researchers located seven birds, one juvenile, two females, and four males. They captured and banded the four males. Afterwards, the researchers returned to the localities where they banded the males to conduct playback of songs of the mainland and island populations; they recorded whether they could detect the birds when playing the different vocalizations. The authors found that “males were three times more likely to respond when calls of a Bahama male were used versus calls of males in Florida”. In this case, the ‘response’ means if the bird was detected or not while playing a particular vocalization.

Levy and Cox (2020) followed a different protocol on the mainland, where they conducted trials at 20 stations in Florida using vocalizations from four different taxa: continental *S. pusilla*, insular *S. pusilla*, Pygmy Nuthatch (*S. pygmaea*), and House Wren (*Troglodytes aedon*). The authors did not capture and band the birds; instead, they recorded whether the birds approached the speaker in response to the different vocalizations, but without identification of individuals (see Figure 2 on next page). The researchers estimated detection probabilities with single-season occupancy models. They found that on the mainland the “nuthatches were detected at 0.72 (± 0.02 ; mean \pm standard deviation) of trials where conspecific vocalizations were used, but were detected much less frequently 0.27–0.30 (± 0.04) when Bahama Nuthatch and Pygmy Nuthatch vocalizations were used.”

As a proxy for aggression, Levy and Cox (2020) used a score to register the distance that the birds approached to the speaker: “(1) the individual remained ≥ 8 m from the speaker; (2) the individual approached within 8 m of the speaker; (3) the individual descended the bole of the tree and approached within 3 m of the speaker; and (4) the individual flew directly over or landed within 1 m of the speaker.” Using a non-parametric Kruskal-Wallis test and post-hoc non-parametric Dunn’s multiple comparison test, the authors found that the continental Brown-headed Nuthatch significantly responded most aggressively toward vocalizations of the same subspecies ($\chi^2 = 16.7$, $df = 3$, $P < 0.001$; Figure 3).

Additionally, Levy and Cox (2020) examined 10 call spectrograms from mainland males and one from Grand Bahama. The Bahama call had a higher peak frequency (6.1 vs. 4.8 kHz ± 0.6 ; Figure 4). The authors conclude that the vocalizations of the mainland and insular populations have diverged significantly and might affect interactions in the case of coming into contact.

Percent of Brown-headed Nuthatch responses to vocalizations of four taxa ($N = 62$ total detections for all taxa). Vocalizations of each taxon were broadcast 54 times, and bars represent the percentage of positive detections (\pm standard error) elicited by the taxon-specific vocalization. Taxa are arranged on the x-axis based on their relatedness to *Sitta pusilla* (close to more distant).

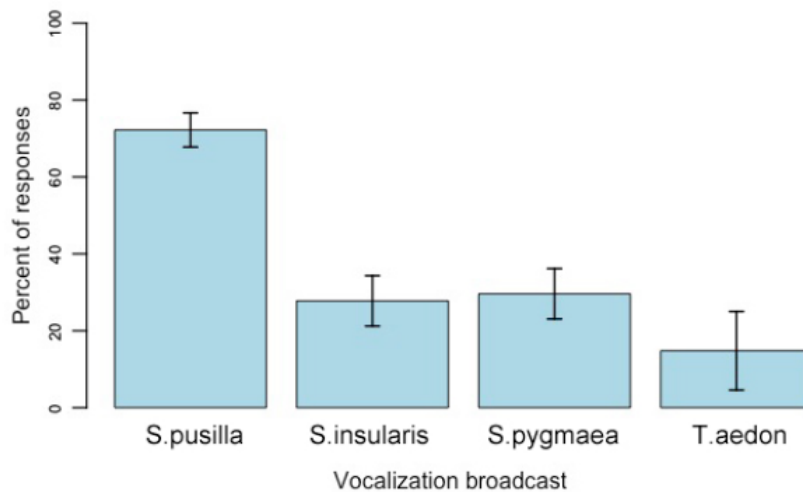


Figure 2. From Levy and Cox 2020.

Boxplot of approach scores for all positive detections of Brown-headed Nuthatch individuals to taxon-specific vocalizations ($N = 62$ responses). The midline represents the median approach score; lower and upper lines represent the first and third quartiles, respectively. Vertical lines represent the maximum and minimum values, and the dots indicate outliers.

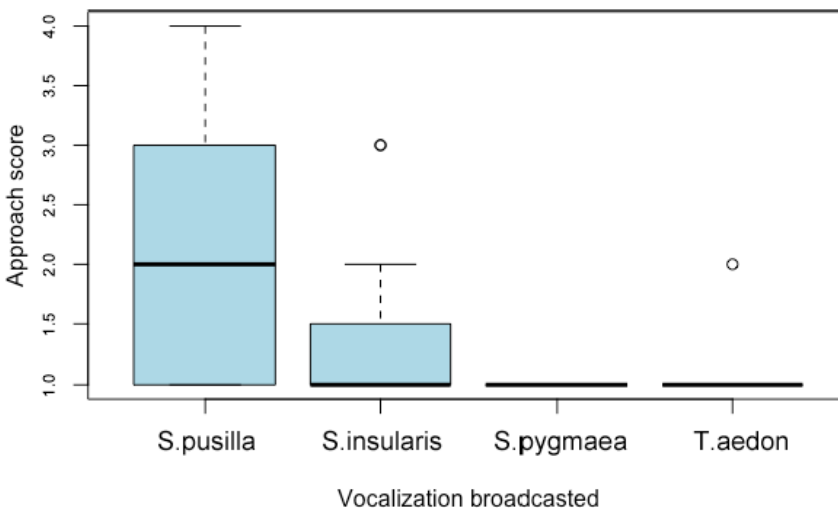


Figure 3. From Levy and Cox 2020.

Spectrograms of the disyllabic vocalizations of the Brown-headed Nuthatch produced by a male on Grand Bahama Island (A) and a male in east central Florida (B).

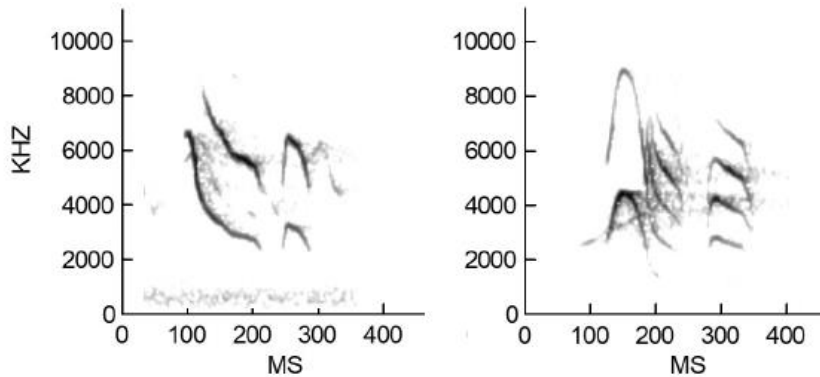


Figure 4. From Levy and Cox 2020.

Boesman and Collar (2020) analyzed 45 sound recordings of the Bahama Nuthatch, gathered from 2005 to 2018, and compared them to publicly available recordings of the mainland populations. They mentioned that the insular vocalizations possess homologous counterparts to the mainland vocalizations, although most of the insular vocalizations are much higher pitched (Table 1 and Figure 5).

TABLE 1

Max. (fundamental) frequency in kHz for five of six homologous vocalisations in the repertoire of Brown-headed Nuthatch *Sitta pusilla* and Bahama Nuthatch *S. insularis* (mean values), and their calculated difference (Δ). Missing in this list is the ‘twitter’ call (vocalisation 3), which proved too variable in frequency to be worth measuring and testing. With the exception of the commonly heard *skew-doo* call (see Table 2) and high-pitched *pit* calls, sound-recordings of other vocalisations are rare even for *pusilla*, and measurements are based on just 1–2 available recordings, as detailed in the text. * = an estimate, as the fundamental frequency is not fully visible on the sonogram for the available recordings.

	<i>Sitta pusilla</i>	<i>Sitta insularis</i>	Δ
<i>Skew-doo</i> call	4.3	6.3	2.0
High-pitched chitter	5.0	8.0	3.0
High-pitched <i>pit</i>	3.8	6.2	2.4
High-pitched <i>tink</i>	5.0	7.2	2.2
Begging call	3.0*	8.0	5.0*

Boesman and Collar (2020) reported that the Grand Bahama population has almost its entire vocabulary 2.0–3.0 kHz higher in frequency than the mainland population. The authors stated that “The vocabulary of *S. insularis* was found to be as extensive as that of *S. pusilla*, and most of its vocalizations possess homologous counterparts in the mainland taxon, including the ‘warble’ call that Hayes et al. (2004) considered unique to *insularis*. Five out of six of the counterpart vocalizations were nevertheless found to be much higher pitched in *S. insularis* vs. *S. pusilla*.” They further argued that the Bahama Nuthatch vocalizations should not

be considered a dialect within the Brown-headed Nuthatch because dialects are not present within the entire mainland population, and they were “unaware of any case where the term ‘dialect’ has been applied to an entire vocabulary that occupies a completely different frequency range to that of a conspecific.”

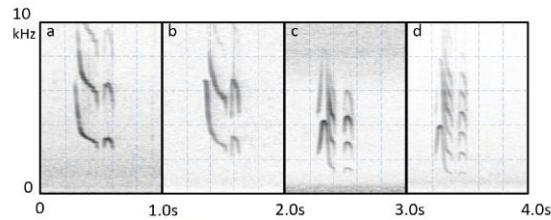


Figure 1. Sonogram of vocalisation 1. Typical skew-dee call. Bahama Nuthatch *Sitta insularis* (a-b) and Brown-headed Nuthatch *S. pusilla* (c-d). Extracts from recordings (a) P. Merritt; (b) M. Oberle; (c) ML172477891 (Florida; J. Graham); (d) ML50234281 (Georgia; E. Cormier).

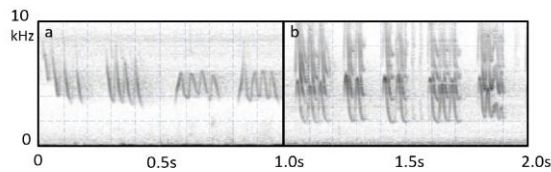


Figure 2. Sonogram of vocalisation 2. (a) High-pitched chitters (first two calls) and warble (second two calls) of Bahama Nuthatch *Sitta insularis* (extract from ML 163289, J. Gerbracht); (b) rarely given, structurally similar vocalisation of Brown-headed Nuthatch *S. pusilla*: ML 196494 (Florida; B. McGuire).

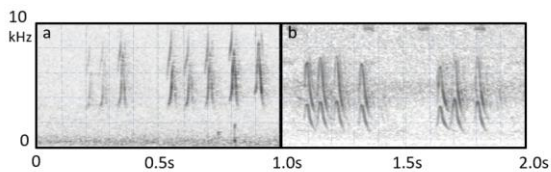


Figure 3. Sonogram of vocalisation 2. Short chattering bursts (a) Bahama Nuthatch *Sitta insularis* (M. Gardner); (b) Brown-headed Nuthatch *S. pusilla* (extract from ML 14767, South Carolina; C. Sutherland).

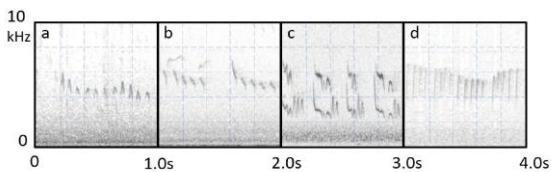


Figure 4. Sonogram of vocalisations 3 and 7, all of Bahama Nuthatch *Sitta insularis*. (a-b) Twitters (M. Oberle); (c) twitters (P. Merritt); (d) high-pitched trill (M. Gardner).

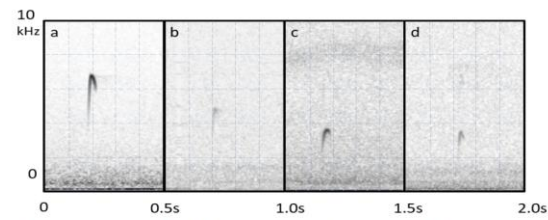


Figure 5. Sonogram of vocalisation 4. Single high-pitched pit note. Bahama Nuthatch *Sitta insularis* (a) high-pitched example (M. Oberle); (b) lower pitched example (M. Gardner); Brown-headed Nuthatch *S. pusilla* (c) extract from XC 130526 (Florida; M. Nelson); (d) extract from ML 87147361 (Florida; T. Auer).

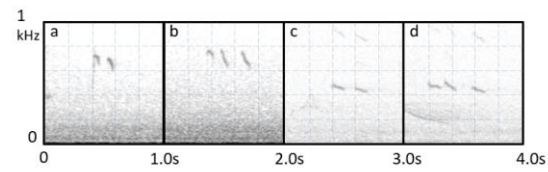


Figure 6. Sonogram of vocalisation 5. High-pitched tink calls: (a-b) Bahama Nuthatch *Sitta insularis* (M. Oberle); (c-d) Brown-headed Nuthatch *S. pusilla* extract from XC 112506 (Georgia; L. Wolff).

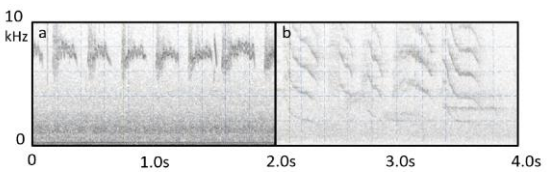


Figure 7. Sonograms of vocalisation 6. (a) Begging calls at the nest of Bahama Nuthatch *Sitta insularis* (M. Oberle); (b) Brown-headed Nuthatch *S. pusilla* juvenile begging calls, extract from ML 164533561 (North Carolina; L. Beegle).

Figure 5. From Boesman and Collar 2020.

Currently, only del Hoyo and Collar (2016) consider *S. insularis* (Bahama Nuthatch) to be a different species from *S. pusilla* (Brown-headed Nuthatch). Their split is based on plumage coloration, morphological measurements, and vocalizations. The other three world lists (Dickinson and Christidis 2014, Clements et al. 2019, Gill et al. 2021) recognize *S. pusilla* as a single species with two subspecies, *S. p. pusilla* and *S. p. insularis*.

Recommendation:

The combination of morphometric differences outlined by Hayes et al. (2004), genetic differences from both Loyd et al. (2008) and Han et al. (2019), and the strong vocal evidence provided by Levy and Cox (2020) and Boesman and Collar (2020), argue for a species level split between the Bahama and mainland populations of Brown-headed Nuthatch. Although the genetic data are based on a relatively small number of individuals of the Bahama Nuthatch, the high *Fst* distinguishing island from mainland populations based on microsatellites (Han et al.

2019) suggests relatively strong divergence. The plumage and morphological data are consistent but insufficient by themselves to support species rank. The vocal data are the most convincing, with notable differences in maximum frequency of calls as well as clear differences in playback responses. Taken together, we recommend splitting *S. insularis* from *S. pusilla*. Banks (2006) indicated that there was insufficient or conflicting information. Now we have additional data detailing vocal differences between the groups (Levy and Cox 2020, Boesman and Collar 2020), differential response to the different vocalizations, and congruence of vocal differences with genetic and phenotypic differences. If the committee votes to split *Sitta insularis* from *Sitta pusilla*, we recommend the English names Bahama Nuthatch (*Sitta insularis*) and Brown-headed Nuthatch (*Sitta pusilla*). These names have been used commonly in the literature to differentiate the two taxa currently recognized as subspecies. Please vote on each of these two sub-proposals:

- A. Split *S. insularis* from *S. pusilla*.
- B. If A passes, use the English names Bahama Nuthatch and Brown-headed Nuthatch, respectively.

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Submitted by: Rosa Alicia Jiménez and Carla Cicero, Museum of Vertebrate Zoology, and Jeff Gerbracht, Cornell Laboratory of Ornithology

Proposal Date: 5 Mar 2021

Add Common Wood-Pigeon *Columba palumbus* to the Main List**Background:**

This widespread Western Palearctic species is one of the more common pigeons in the world. Although some populations (e.g., from Great Britain) are mostly resident, northern and eastern populations are highly migratory, migrating south and west after the breeding season. Its range has been expanding northwards over the last 120 years. It has bred in the Faeroes as well as southeastern Iceland, and the *Icelandic Birding Pages* website lists some 622 records through 2011.

New AOS Record:

From 5-13 May 2019, a Common Wood-Pigeon was recorded at La Romaine, Quebec. It was photographed (published photo in Pyle et al. 2020). The record was accepted by the Quebec Bird Records Committee in October 2019 (Pyle et al. 2020) and was accepted unanimously by the ABA-CLC in 2020 (Pyle et al. 2020).

Discussion:

The photos clearly document the record. Pyle et al. (2020) indicated that the photos are not detailed enough to determine the age or to ascertain whether there were signs of captivity. They proposed that the record likely pertains to the widespread mainland nominate European subspecies. It is perhaps more likely that the Quebec bird originated from the more easterly or northerly part of the range as the birds there are much more migratory (Gibbs et al. 2001). Pyle et al. (2020) mentioned a May 1935 record by Alan Brooks off Newfoundland on board a ship crossing the Atlantic in a westerly direction (Gosselin 1992). The position of the ship when the bird was recorded is not known.

Recommendation:

I recommend that we add Common Wood-Pigeon to the Main List. Given the hundreds of records in Iceland, I see little that is controversial with this record.

Position on Check-list:

From Dickinson and Remsen (2013) and Clements et al. (2019), the species would follow Rock Dove *Columba livia*. Dickinson and Remsen (2013) placed it after Somali Pigeon *C. oliviae* in the linear sequence of *Columba*.

English name:

Dickinson and Remsen (2013) referred to *C. palumbus* as simply Wood Pigeon. Gibbs et al. (2001) used Common Wood Pigeon for the English name, as did Clements et al. (2019), but with the hyphen, so Common Wood-Pigeon. I favor the name Common Wood-Pigeon as some 8-10 species of Asian pigeons are known by the group name “wood-pigeon”, and our standard practice is to use a modifier when a species name would potentially be the same as a group name.

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Submitted by: Jon L. Dunn

Date of Proposal: 7 March 2021

Add Pallas's Gull *Ichthyaetus ichthyaeus* to the Main List**Background:**

From 2-4 May 2019, an adult Pallas's Gull *Ichthyaeus ichthyaeus* in alternate plumage was present on Shemya Island (western Aleutian Islands), Alaska. On the last day it was found dead and is now preserved as a specimen at the University of Alaska Museum, Fairbanks (UAM 43000). It was sexed as a female and showed no signs of captivity or having been aboard a ship. This specimen record was accepted by the Alaska Checklist Committee in November 2019 and unanimously approved by the ABA Checklist Committee in 2020 (Pyle et al. 2020; photo).

Discussion:

The occurrence of this primarily central Asia species is surprising, but perhaps not shocking. It breeds east to northwestern Mongolia and winters primarily around the Indian Subcontinent and Persian Gulf with some west to the eastern Mediterranean and east to Thailand. It is casual to coastal East Asia but is nearly annual in Japan (Brazil 2018).

Recommendation:

I recommend that we add Pallas's Gull to the Main List. I see nothing controversial about this record.

English name:

Historically this species was known as Great Black-headed Gull, but most now use the English name of Pallas's Gull, including the main active global lists (IOC, Clements, BirdLife). Dickinson and Remsen (2013) listed both names (as Pallas's/Great Black-headed) in their update of the Howard & Moore list. Rasmussen and Anderton (2005) used Great Black-headed Gull, which previously was the widely used English name. It is a great name as they are indeed huge and the jet black head is the major field mark with alternate plumaged adults, although use of this name necessitates use of the lengthy name Common Black-headed Gull for *Chroicocephalus ridibundus*, rather than simply Black-headed Gull (apparently a key reason for the adoption of Pallas's Gull for *I. ichthyaeus* was to be able to return to Black-headed Gull for *C. ridibundus*). Following widespread and currently accepted usage in the Old World, I recommend that we follow suit with Pallas's Gull, but in the notes say that Great Black-headed Gull is an alternative English name.

Position on the Checklist:

Dickinson and Remsen (2013) listed it last in the genus *Ichthyaeus*, a genus of five species, none of the others having been recorded in North America. In our linear sequence it would follow Franklin's Gull (*Leucophaeus pipixcan*).

Literature Cited:

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Submitted by: Jon L. Dunn

Date of Proposal: 7 March 2021

Add Pallas's Grasshopper-Warbler *Helopsaltes certhiola* to the Main List**Background:**

From 9-12 September a Pallas's Grasshopper-Warbler was present at Gambell, St. Lawrence Island, Alaska. The bird was well-photographed. It was accepted by the Alaska Checklist Committee in April 2020 and the ABA Checklist Committee later in 2020 (Pyle et al. 2020; photo). The bird was identified as in first fall (formative) plumage.

Discussion:

Birds in this genus, as well as other related genera, are notoriously difficult to see, let alone identify, except when singing. The photos of this individual are sharp and show extensive detail, enough for expert reviewers Peter Kennerley and Chris Goodie to endorse the identification. Pallas's and Middendorff's (*H. ochotensis*) grasshopper-warblers present identification problems, the latter species having a more obscurely streaked back. Photos of this bird show bold streaking down the back. Middendorff's and Pallas's meet and interbreed extensively along the coastal plain of the lower Primorskiy region, in particular along the lower Amur River. At this location and on Sakhalin, up to 70% of the breeding birds are reported to be hybrids. One wonders if the two are even valid species. The hybridization was reported by Kalyakin et al. (1993) and summarized in English by Kennerley and Pearson (2010). Despite these issues, Kennerley and Goodie had no reservations about endorsing the Gambell bird as Pallas's, although they refrained from identifying it to subspecies.

Recommendation:

I recommend that we add Pallas's Grasshopper-Warbler to the Main List. With the extensive hybridization in the lower Primorskiy region and Sakhalin, I'm uneasy about accepting a non-specimen record. Despite this, Kennerley and Goodie strongly supported the record, and with their expertise, I find this compelling. The Alaska Checklist Committee and ABA-CLC reached the same conclusion.

English name:

Most call this species Pallas's Grasshopper-Warbler, and this name is used in the main active global lists (IOC, Clements, and BirdLife), although Rasmussen and Anderton (2005), Dickinson and Christidis (2014), and a few others used Rusty-rumped Warbler. Given that this species and Pallas's Gull are Old World species (not ours), I recommend that we don't invent a new name or use one that is not widely used, especially in current treatments. Birders from the U.K. often use the English name of P. G. Tips, a reference to the pale tips to the outer tail feathers. The name Rusty-rumped Warbler denotes a small patch on the lower back/rump which is unmarked warm brown, perhaps "rusty." It is normally covered up by the tertials on the folded wing. This field mark is very difficult to see under most field circumstances. If one does see a Pallas's, the black streaking on the back and upper tail coverts is what stands out, and it is the best separating feature from Middendorff's Grasshopper Warbler (*H. ochotensis*). These two are presumably sister species as they hybridize commonly in the lower Primorskiy region and on Sakhalin (Kennerley and Pearson 2010). Another taxon, Styan's Grasshopper-Warbler (*H. pleskei*), was once considered a subspecies of Middendorff's. Together the three form a superspecies (Kennerley and Pearson 2010), so for symmetry and to imply the relationships having

“grasshopper” in the name is helpful. Rusty-rumped Warbler doesn’t convey this. Frederick William Styan was an English tea merchant who spent many years in China and collected many specimens for the British Museum. Alexander Theodor von Middendorff was a zoologist and explorer of Baltic German and Estonian descent (1815-1894). Pallas was one of the giants of Old World ornithology who explored well into Russia. Under Notes, I recommend that we mention that Rusty-rumped Warbler is an alternative English name.

Position on Check-list:

Kennerley and Pearson (2010) and Clements et al. (2019) listed this species prior to Middendorff’s Grasshopper-Warbler (*H. ochotensis*).

Literature Cited:

- Clements, J. F., T. S. Schulenberg, M. Iliff, D. Roberson, T. A. Fredericks, B. L. Sullivan, and C. L. Wood. 2019. The eBird-Clements Checklist of Birds of the World (tinyurl.com/eBird-Clements). Cornell Lab of Ornithology.
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Submitted by: Jon L. Dunn

Date of Proposal: 7 March 2021

Add Tricolored Munia *Lonchura malacca* to the U.S. List**Background:**

This Indian species is sometimes treated as conspecific with *L. atricapilla* (Black-headed or Chestnut Munia), with which it interbreeds. There is a hybrid zone in eastern India between the Madras area and Sambalpur, Orissa (Rasmussen and Anderton 2005). The AOU split the two species in the 42nd supplement (AOU 2000). Tricolored Munia is established on Puerto Rico and Jamaica and has been reported elsewhere in the West Indies.

In Florida there have been at least six records of Tricolored Munia, with five records from the Dry Tortugas alone, between 1999 and 2015. The ABA-CLC, following acceptance by the Florida Ornithological Society Records Committee (FOSRC) in 2014 (Greenlaw 2016) and ascertaining its establishment in Cuba, accepted the species to the ABA list (Pyle et al 2020; includes a photo of one of the Dry Tortugas birds).

Discussion:

Our current distributional statement for this species (updated when split in AOU 2000) treats it as “reportedly introduced or observed in Cuba ... but in the absence of voucher specimens some of these reports may be of *L. atricapilla*.” Recent information, however, confirms the identification and indicates that *L. malacca* is now established in Cuba. This species was listed and illustrated in Garrido and Kirkconnell (2000), who gave the status as “widespread but locally common. First specimen collected near Aguada de Pasajeros, in summer 1990. Abundant in rice fields at Zapata Peninsula.” They called this species Chestnut Mannikin *Lonchura malacca*, but this is before the split. The plate clearly refers to the taxon with extensive white underparts, which is *malacca* rather than *atricapilla*. Given its presence in Cuba for some three decades and its local abundance, it surely meets our criterion for acceptance of an established introduced population. Pyle et al. (2020) referred to it as abundant in parts of Cuba, but I have yet to see the species there in nine trips, although I hardly take time to look in the rice fields where it thrives.

Recommendation:

I recommend that we add Tricolored Munia to the U.S. list. The FOSRC and the ABA-CLC added the species, and I see no reason not to follow their decisions. The records from the remote Dry Tortugas are particularly compelling for me. Given the proximal established population on Cuba, it seems likely that the five records on the Dry Tortugas originated from there rather than from released cage birds from the mainland of Florida.

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- American Ornithologists' Union (AOU). 2000. Forty-second supplement to the American Ornithologists' Union *Check-list of North American Birds*. Auk 117:847-858.
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Rasmussen, P. C., and J. C. Anderton. 2005. *Birds of South Asia. The Ripley Guide*. Vols. 1 and 2. Smithsonian Institution and Lynx Edicions.

Submitted by: Jon L. Dunn

Date of Proposal: 7 March 2021

Treat *Catharus swainsoni* as a separate species from *C. ustulatus*

Background:

We currently consider Swainson's Thrush *Catharus ustulatus* to consist of two groups: the olive-backed (and gray-backed) *swainsoni* group, which breeds in forests and woodlands across much of Canada and northern and more mountainous regions of the US and winters primarily in South America, and the russet-backed *ustulatus* group, which breeds along the Pacific coast from southeastern Alaska and Canada south to California and winters in Mexico and Central America (AOU 1998; Fig. 1).

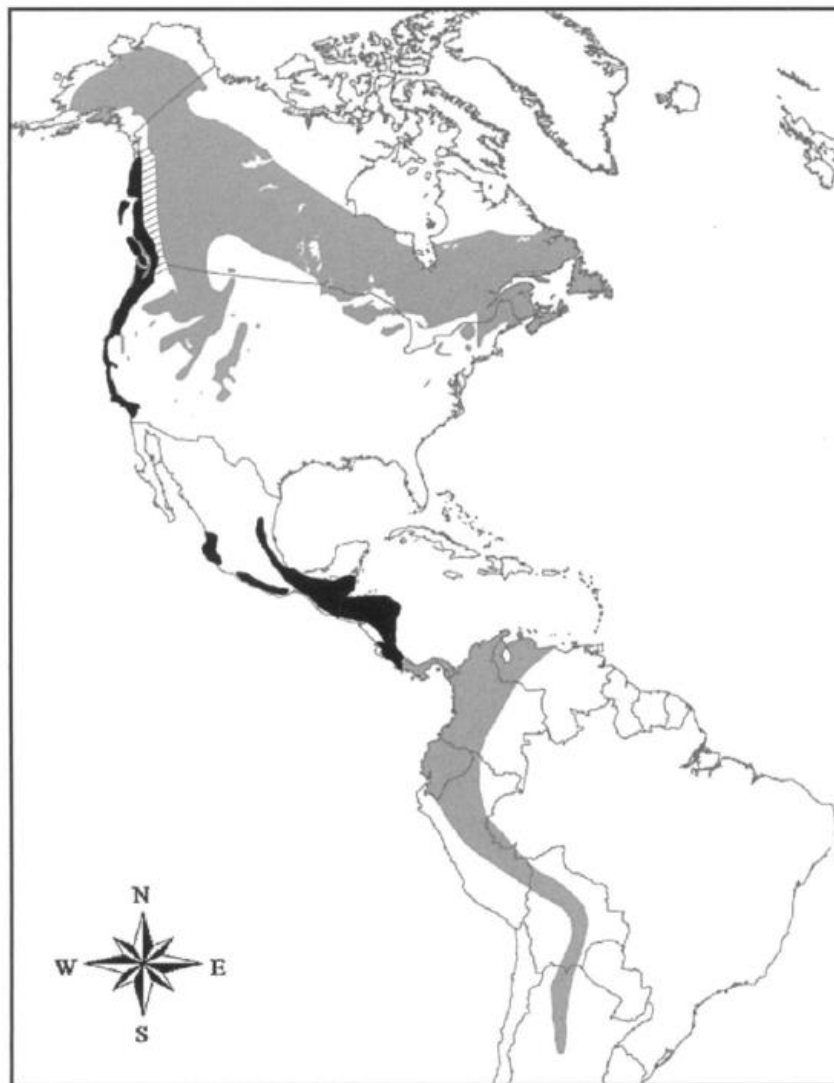


Figure 1. Breeding and wintering ranges of the coastal *ustulatus* (black) and inland *swainsoni* (gray) groups. Potential contact zones are indicated by the black and white stripes. From Ruegg (2007).

The early nomenclatural history of these forms is tortured. Although *ustulatus sensu lato* was illustrated by Wilson as early as 1812 (under the preoccupied name *Turdus solitarius*), the first valid name for the species (*ustulatus*) was provided by Nuttall in 1840 for a russet-backed bird from the “forests of the Oregon”, a type locality now accepted as Fort Vancouver, Washington. Similarly, although Swainson provided a description of a specimen of *swainsoni* in 1832, he believed it to be an exemplar of *Merula Wilsoni* Bonaparte, leaving Cabanis (*in* Tschudi 1845) to propose the first valid name (*swainsoni*) for the olive-backed form that occupies most of North America.

Both taxa were described as species, as was standard practice at the time, and both were listed as species by Baird (1864, *fide* Bond 1963). However, they were treated as conspecific by standard authorities in the twentieth century (e.g., Ridgway 1907, Hellmayr 1934, Mayr and Greenway 1964) and have typically been treated as a single species to the present (e.g., Dickinson and Christidis 2014, Clements 2019, IOC 2020). English names used by Ridgway and Hellmayr for subspecies *ustulatus* and *swainsoni* were Russet-backed Thrush and Olive-backed Thrush, respectively, and the same names have been used for the groups (AOU 1998).

In addition to the differences in the color of the back noted above (olive, or gray in Rocky Mountain populations, in *swainsoni* vs. russet in *ustulatus*), *ustulatus* differs most noticeably in the less conspicuous spotting on its chest. The two forms differ in habitat through much of their breeding ranges: *ustulatus* is found in riparian woodlands, whereas *swainsoni* occurs in mixed hardwood or spruce-fir forests in the eastern and northern parts of its range (Bent 1949). Western *swainsoni*, however, occupy riparian habitats in at least some areas (Evans Mack and Yong 2020).

New Information:

Kristen Ruegg and colleagues have published a series of papers on Swainson’s Thrush over the past 20 years, beginning with studies of migration and continuing into many other areas, including genomics, and Kira Delmore and colleagues have also published recent studies of migration and genomics in this species. Their landmark papers have established the following:

(1) Banding and genetic data indicate that there is almost no overlap in the migration routes and wintering grounds of the *ustulatus* and *swainsoni* groups (Ruegg and Smith 2002). The coastal *ustulatus* group migrates along the Pacific coast to winter in Mexico and Central America, whereas the interior *swainsoni* group uses more easterly routes to migrate to and from its wintering grounds in South America and Panama. The winter ranges of the two groups are essentially parapatric rather than widely separated. Mitochondrial genetic data showed that these groups diverged in the late Pleistocene (they show a 0.7% divergence using the control region) and have undergone recent demographic expansions.

(2) Climate differs substantially between the ranges of *ustulatus* and *swainsoni*, and areas of secondary contact between the two groups occur in the boundary regions where the climate shifts from the wetter coniferous forests of the coastal region to drier forests of the interior west (Ruegg et al. 2006).

(3) Advertising songs of Swainson's Thrush are characterized by much individual variation, and each individual has songs that differ in the types and order of syllables (Ruegg et al. 2006). However, the most common song types appear to vary geographically, those of *ustulatus* being longer and having lower initial frequencies than those of *swainsoni* (Fig. 2). These differences in songs have been characterized as similar to differences in dialects in other species that learn their songs (Ruegg 2007). Songs from a mixed population that included both genetic types, but was more coastal genetically, tended to be more similar to those of the inland group *swainsoni*. Ruegg et al. (2006) proposed that the differing acoustical characteristics of typical *ustulatus* and *swainsoni* songs may be the result of differing transmission dynamics in the two forest types. Calls were apparently not studied.

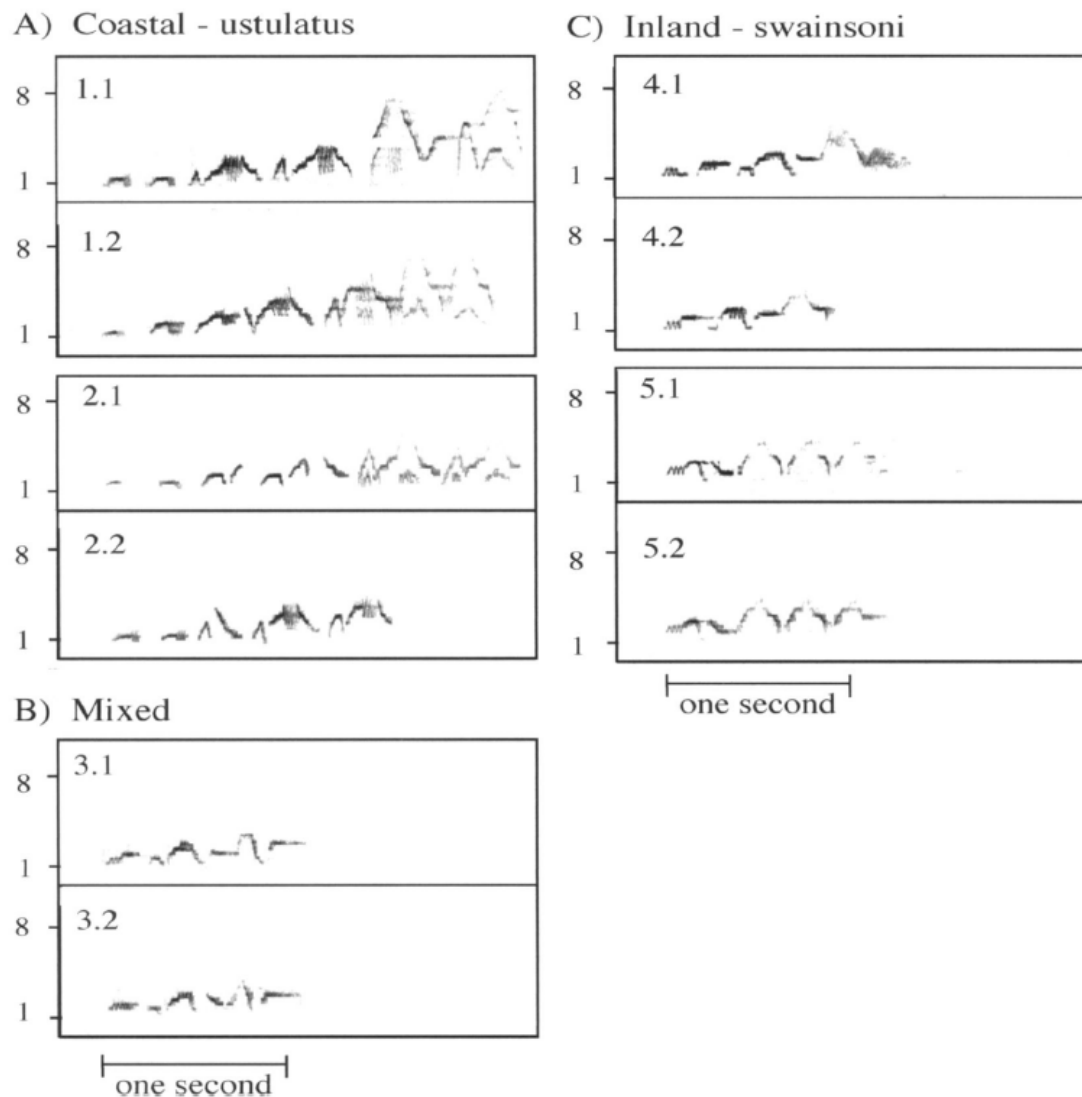


Figure 2. Sonograms of the most common song types in the *ustulatus* and *swainsoni* groups, as well as two examples from a mixed population. Note that each individual sings several song types. From Ruegg et al. (2006).

Subsequent investigation of vocalizations determined that these differences in song are not consistent across the ranges of *ustulatus* and *swainsoni* (Mlodinow et al. 2013, Pieplow 2013). These same authors found average differences in contact calls and alarm calls but emphasized that these were not diagnostic, although they noted that they could prove useful for identification in conjunction with other characters. More recently, Boesman (2016) concluded that the difference in the alarm call was consistent and diagnostic between the *ustulatus* and *swainsoni* groups, and he also found a subtle difference in songs that appeared to be consistent: songs of *ustulatus* begin with 2-3 similar notes with an inverted “U” shape, whereas those of *swainsoni* begin with notes of different shape that rise in pitch (Fig. 3). He noted that this is a small detail in the song and of unknown significance in species recognition.

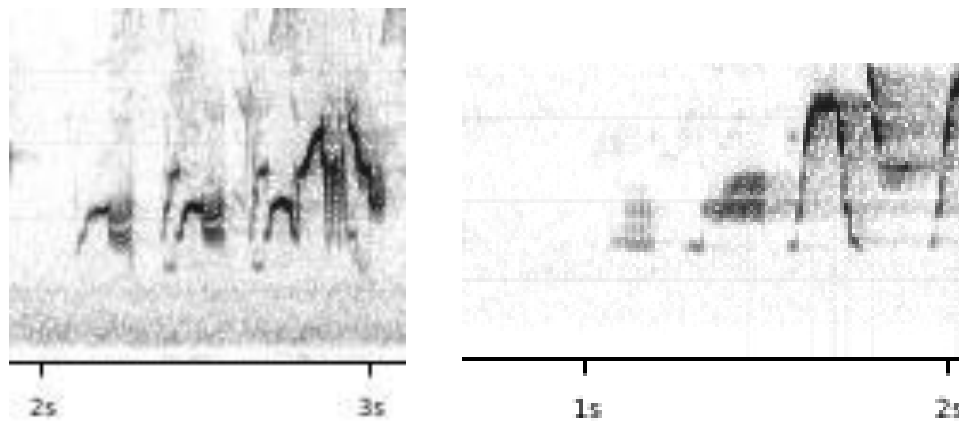


Figure 3. Initial notes of typical songs of *ustulatus* (left) and *swainsoni* (right). From Boesman (2016).

(4) A transect through a hybrid zone in southwestern British Columbia showed that the transition from *ustulatus* to *swainsoni* phenotypes and genotypes occurred in an 80-km area that marked the transition from the coastal to the interior climatic zone (Ruegg 2007, 2008). Blood samples, measurements, and plumage assessment were taken from live birds (specimens were not collected). Character clines were mapped for body size, plumage color, wing:tarsus ratio, mitochondrial DNA, and AFLPs, as shown below (Fig. 4). The clines for the three phenotypic characters and the AFLPs were largely concordant, whereas the mtDNA cline was shifted slightly southwestward. The width of the hybrid zone was roughly half of the estimated dispersal distance of this species of 150 km, suggesting that barriers to gene flow may be keeping the zone narrower than expected, although the dispersal estimate was heavily influenced by a single data point. The estimate was based on 10 recoveries of banded birds in subsequent years, six of which were recovered from within the 10-minute lat-long blocks in which they were banded and were treated as dispersal of 0 km, the other four of which were at distances of 8 km, 11 km, 11 km, and 476 km (Ruegg 2008).

The center of the contact zone included recent hybrids, back-crosses, and pure individuals of both groups, and population density in this area was low (of 15 individuals, 27% were parentals, 40% hybrids, 33% of uncertain assignment). Data on pairings was apparently not gathered. Ruegg (2008) concluded that characteristics of this zone were consistent with those of a tension zone that balanced dispersal into the zone with pre- or post-mating barriers to gene flow. She

hypothesized that differences in molt, migration, or the timing of breeding may help to maintain the hybrid zone, as has been proposed for Baltimore and Bullock's orioles and Northern Flickers.

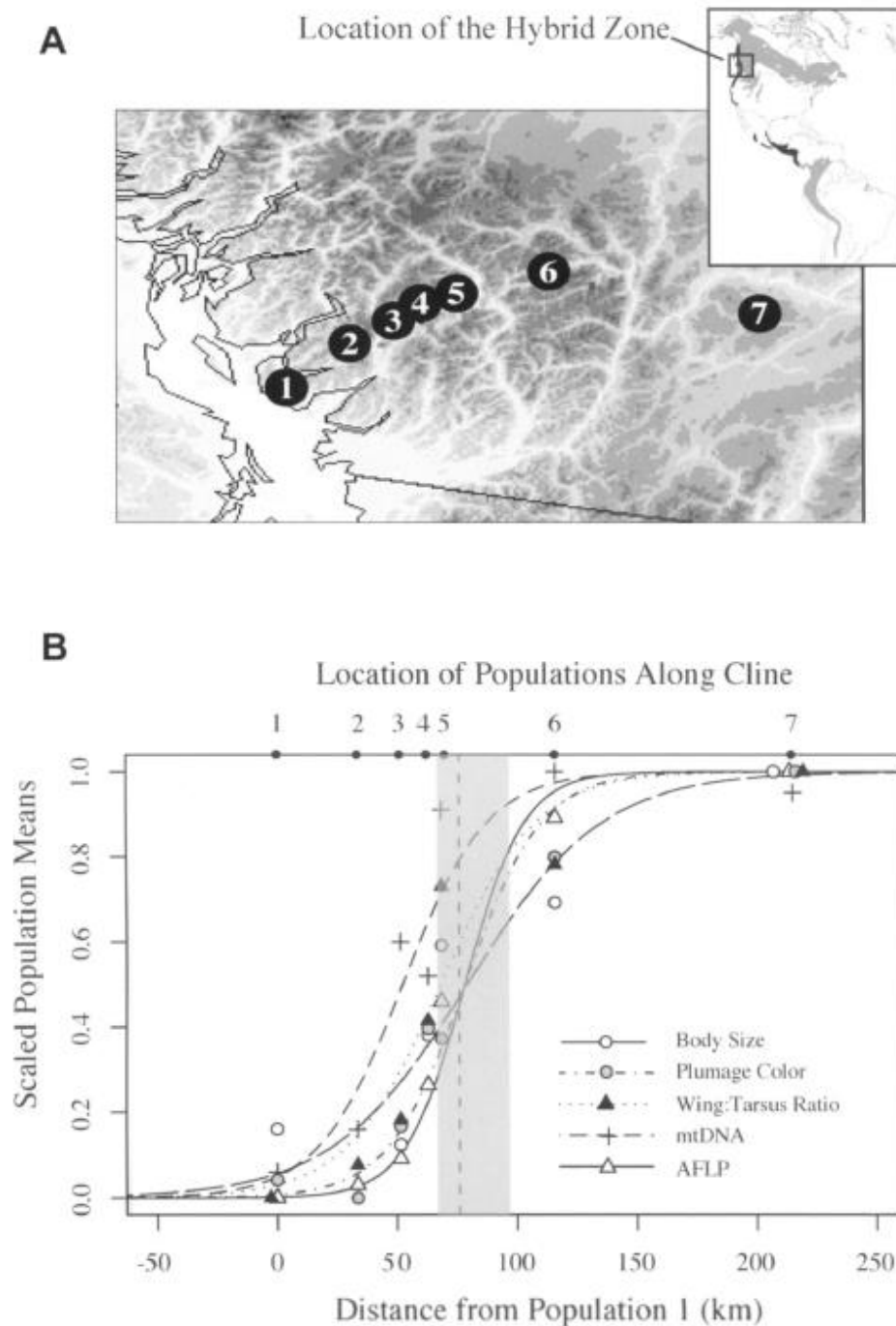


Figure 4. (A) Map of sampling locations in British Columbia. (B) Shape and width of various character clines through the hybrid zone. From Ruegg (2007).

(5) Working in the same hybrid zone as Ruegg (2008), Delmore et al. (2014) used geolocators to track migration routes of individuals of *ustulatus* and *swainsoni*, as well as hybrid individuals. Hybrids were more variable than pure parental forms in their migratory routes. Some hybrid individuals used the same route as one parental group on fall migration and the other on spring migration, whereas other hybrid individuals used intermediate routes over relatively inhospitable arid or mountainous areas (Fig. 5). Based on these results, Delmore et al. (2014) suggested that migratory behavior might be a source of selection against hybrids. They also estimated the strength of selection against hybrids in this area and determined it to be moderately strong.

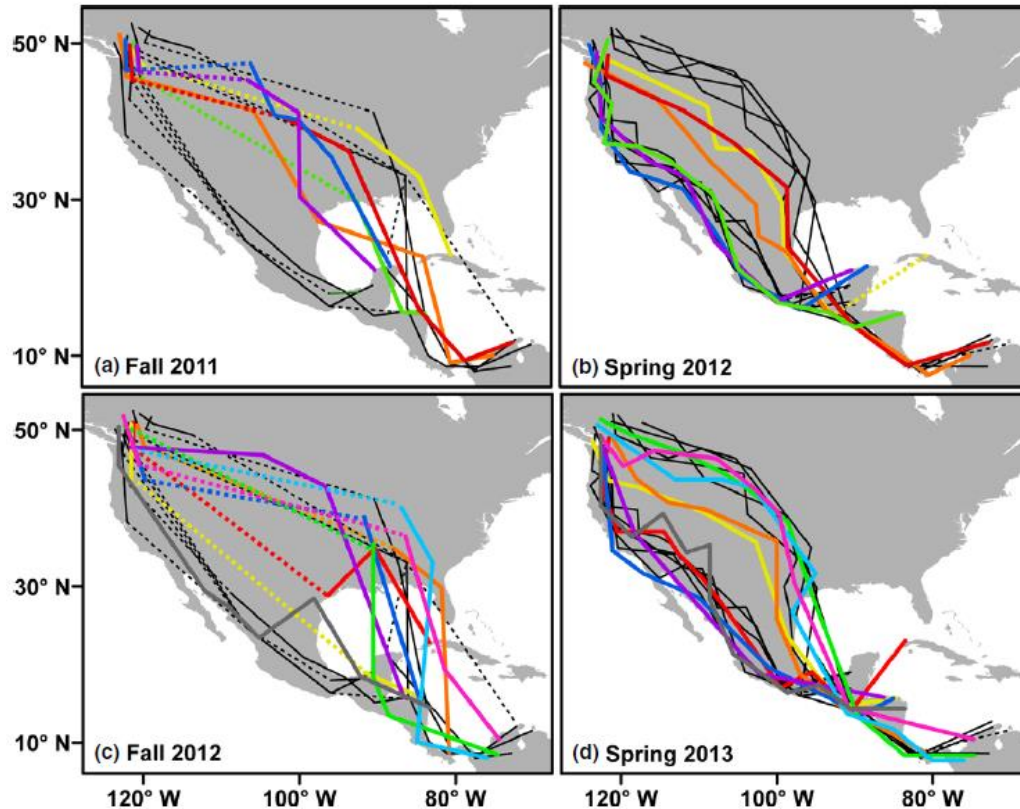


Figure 5. Migration routes of pure parental and hybrid individuals in 2011-2012 and 2012-2013. Routes of pure parentals (four *ustulatus* and five *swainsoni*) are shown in black, and those of hybrids are in color. From Delmore et al. (2014). Dashed lines indicate periods near the equinox, when latitude could not be estimated accurately.

(6) Ruegg et al. (2014) conducted genomic studies on 15 “pure” individuals of *swainsoni* (five each from New Hampshire, New Mexico, and Fairbanks, AK), and 10 “pure” individuals of *ustulatus* (five each from coastal California and British Columbia) using RAD-PE sequencing and focusing on migration. They found “genomic islands of divergence” on 15 of 23 chromosomes and an accelerated rate of divergence on the Z chromosome. Genes known to be linked to migration were significantly more differentiated than expected by chance, but these genes were typically not located within the islands of divergence. Thus, they concluded that genes linked to migration were related to divergence, but that the genomic islands were not

facilitating adaptive divergence in migratory behavior. In contrast, Delmore et al. (2015), who sampled in southern British Columbia and used whole genome shotgun resequencing, found that “genes linked to migratory traits were concentrated in islands of differentiation” and concluded that migration is under divergent selection in these islands. They found the median F_{ST} between *ustulatus* and *swainsoni* to be 0.08 (mean 0.10).

Bay and Ruegg (2017) suggested that the differing conclusions of Ruegg et al. (2014) and Delmore et al. (2015) resulted from differing parameters used to define the genomic islands, and they used demographic modelling to dig more deeply into the data. They found high levels of introgression from inland to coastal populations, which were not restricted to areas proposed to be under selection. Their “observations are most consistent with a model of selective sweeps in the inland population followed by neutral introgression into the coastal subspecies,” but they also concluded that other processes have likely influenced the observed genetic patterns. Based on SNPs, they estimated the divergence time between *ustulatus* and *swainsoni* to be only 48,000-64,000 years.

Recommendation:

This is a classic “gray area” situation in which different conclusions regarding species status can be reached depending on which data are considered more important and how those data are interpreted. The overview provided above indicates the following (with comparisons, when available, to the species that provided the most recent split within this genus, Bicknell’s Thrush *C. bicknelli* and Gray-cheeked Thrush *C. minimus*):

(1) Plumage variation between *ustulatus* and *swainsoni* is comparable to that between subspecies, and differences in song are subtle. No playback trials have been conducted, making the significance of the variation in song unclear. In the Bicknell’s and Gray-cheeked split, playback results (Ouellet 1993) indicated that *bicknelli* does not respond to the quite similar songs of *minimus*, although little detail was provided on these experiments. I don’t have access to committee records at the moment, owing to the pandemic, but this was probably important in the recognition of *bicknelli* as a species.

(2) The two groups are genetically distinct but show relatively low levels of divergence in mtDNA (0.7%), a level of divergence roughly comparable to that between *bicknelli* and *minimus* (as extrapolated from the time divergence estimate of 0.4 million years in Voelker et al. 2013).

(3) A transect of the hybrid zone in southwestern British Columbia revealed that the zone was relatively narrow with largely concordant character clines, that the center of the zone contained parental forms as well as recent hybrids and backcrosses, and that selection against hybrids was moderately strong. Selection against hybrids has been hypothesized to be mediated through migration, molt, timing of breeding, or climate. However, studies of contact zones in other areas have not been conducted for this species, and the population of breeding adults at Hyder, Alaska appears to be a hybrid swarm, in phenotype and mtDNA (Pruett et al. 2013; Gibson and Withrow 2015; K. Winker, pers. comm.).

(4) The genomic studies found quite a bit of introgression as well as genomic islands of divergence. F_{ST} was relatively low (median value 0.08), considerably lower than for typical

species but also not as low as for most subspecies, at least compared to a study using UCEs (McLaughlin et al. 2020), in which values for subspecies pairs ranged from 0.01-0.02, with one outlier, whereas values for species pairs ranged from 0.33-0.59, with one outlier (it was proposed that the outliers probably represent errors in taxonomic rank). Everson et al. (2019) contrasted the three-species clade of *C. fuscescens-minimus-bicknelli*, determining that F_{ST} values between species in this group were remarkably similar: *fuscescens-minimus* (0.161), *minimus-bicknelli* (0.176), and *fuscescens-bicknelli* (0.188). The F_{ST} for *C. bicknelli* vs *C. minimus* was 0.234-0.354 in a genotyping-by-sequencing (GBS) study (Fitzgerald et al. 2020), and introgression between these species was low (3/37 individuals were >2% admixed based on the GBS SNP analysis). Whether F_{ST} values from UCEs or GBS are comparable to those from whole genome resequencing or other genomic methods is a good question, but F_{ST} is a proportional measure so theoretically they should be roughly comparable, although likely with some variation. Divergence estimates, based on SNPs, were 48,000-64,000 years ago for *ustulatus-swainsoni* (Bay and Ruegg 2017) compared to 417,000-423,000 years ago for *bicknelli-minimus* (Fitzgerald et al. 2020).

Taking all of this into consideration, I recommend a NO vote on this proposal. Phenotypic variation (both morphological and vocal) is minor, and genetic differentiation, although seemingly occupying a gray area between subspecies and species, seems to me more typical of well-defined subspecies than of species. In my view, the data from the hybrid zone provide better support for species status. Even here, however, the results are undermined by small sample sizes and the fact that all the data come from a single hybrid transect in southwestern British Columbia, whereas the potential contact zone stretches from northwestern Washington to Alaska. Hybrid zones can vary in width, and interactions along a contact zone can vary. The genetically mixed population in Hyder, Alaska, for example, appears to be a hybrid swarm, so that the transect through the relatively sharp contact zone in the south, where there is selection against hybrids, may not be typical. It is my understanding that genetic samples were recently gathered in this hybrid zone in Alaska and in other contact zones, and that a range-wide genoscape study on this species is also underway, so we may know more soon.

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