

AOS Classification Committee – North and Middle America
Proposal Set 2022-C
29 March 2022

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Revert to Mew Gull for *Larus brachyrhynchus* (Short-billed Gull)

Background:

The AOS recently voted to separate *Larus brachyrhynchus* from *L. canus*, which triggered a situation in which a new English name might be warranted. The English name approved by the committee was Short-billed Gull (Chesser et al. 2021). However, it is clear that retention of the name Mew Gull for *L. brachyrhynchus* is the more stable and logical choice given the particular situation of English name use within the *Larus canus* complex, specifically that the various subspecies have had an English name already associated with them and in wide usage not only in North America but the English-speaking world.

Argument:

The *Larus canus* complex represents perhaps a unique situation. This species complex is found throughout the temperate region of the Northern Hemisphere, so it is found in Eurasia as well as in North America. This is not unique. What is unique is that the English-speaking communities have used different English names for each population within the complex. Since this change is a two-way split, we will not mention “Kamchatka” Gull (*L.c. kamtschatschensis*) as it remains within *L. canus*, but even at this level that population had a unique English name. In Eurasia, the bird, pre-AOS split, was known as Common Gull. In the Americas it was known as Mew Gull. Mew Gull was not used as an official name for the *Larus canus* complex in the Old World! The basis for my argument is that already having two separate, unique, and widely used names for the two elements of the split (*canus* vs. *brachyrhynchus*), it actually adds confusion and goes against many of the tenets of the AOS Guidelines for English Names to resurrect an old, cumbersome, and for all intents and purposes confusing name (Short-billed Gull) for *brachyrhynchus*. While that name still has little traction, it would be wise to revert to the established and well-known name Mew Gull for *brachyrhynchus* primarily to maintain stability!

From the American Ornithological Society (AOS), 3 June 2020

Guidelines for English bird names:

A. Principles and Procedures

1. *Stability of English names.* The NACC recognizes that there are substantial benefits to nomenclatural stability and that long-established English names should only be changed after careful deliberation and for good cause.

It is clear that Mew Gull is a long-established English name within the region of interest of the AOS; even though Short-billed is older, that name had been largely forgotten except by well-read and history-minded birders and ornithologists. Stability in my opinion is maintained by keeping Mew Gull. The element of confusion is really a moot point in this case, given that the

two entities which were split already had English names in wide circulation. Mew Gull has never been used officially in the Old World for *Larus canus*. It was always Common Gull there. If Mew Gull was in widespread use outside of the Americas, I would understand the need to change the name. But this is not the case. In particular, the multiple books on gulls and gull identification published in recent decades have specifically used Mew Gull and restricted that use to *brachyrhynchus*, or clearly identified that the common name for *canus* is Common Gull, etc. (Howell and Dunn 2007). Olson and Larsson (2004) accepted the taxonomic split of *brachyrhynchus* nearly two decades ago, and they use Mew Gull for *L. brachyrhynchus*. There has never been any confusion in the use of Mew Gull to refer to *brachyrhynchus*. The argument for stability is clear, and strong here. Changing the name is not helping stability, and the Mew Gull name did NOT create confusion. This is a unique situation, and I think one has to take this with the consideration of the “intent of the law” as opposed to “literal meaning of the law.” In other words a split into two species that both have a sizeable range usually automatically means that the old name has to shift, as keeping it for one of the daughter species only creates confusion. In this case, one already had names in wide use to refer to the two daughter species. By reverting to an old name, Short-billed Gull, for *brachyrhynchus* we are in effect adding a third name to this situation, one that most living users of English names have not ever used in their lifetime. This IS confusing. I would add that Mew Gull was not officially used by any Old World bodies as an English name, so this was essentially a name only in use in North America. Seldom have we had a pre-set and stable set of names for a split, such that no name change is necessary – Mew and Common, for the daughter species.

Below I detail how Mew Gull as a name works given the various rules for English Names being followed by the AOS NACC:

B. General Rules for Names

2. Uniqueness. The English name of every species (and of named groups within species) should be unique both within the NACC region and, with occasional exceptions, globally.

Mew Gull is unique for the NACC region, and globally. Retention of this name, even though it previously applied to the entire *canus* complex, is not an issue. The reason is that outside of the NACC region, the name Mew Gull did not have that context. It only referred to *brachyrhynchus*. For all intents and purposes, much of the literature, books, articles, and informal conversation on gulls has separated Mew from Common Gull. Mew Gull does not need a change.

I asked an online group the “Western Palearctic Gulls” forum on Facebook, if the name Mew Gull had ever been used to refer to the *canus* complex in Europe-Asia? The resounding answer was no. So English speakers in the Old World, when they use Mew Gull are referring to *brachyrhynchus*. Mew Gull is therefore unique within the NACC region, and globally.

Here are a few excerpts of what they said:

“Ordinary birders in the UK just call 'our' Common Gulls just that and Mew Gull is unquestionably the American species as it is now. I don't understand the need for inventing Short-billed Gull.” Steve Lister

“For me as an European I, along with others, have never used Mew for Common Gull.” Jan Jorgensen

“I have dipped into the archives (Backhouse 1890) and a few other titles and cannot find any alternative English name other than Common Gull. Witherby (1940) makes reference of a Pennant's Winter Mew Gull *Larus Hybernus* in its treatment of Common Gull and refers to Tunstall's Ornithology of Britain (1771).” Stuart Winter

**** note that *Larus hybernus* was a name given to juvenile Black-legged Kittiwake, not to a member of the *canus* complex **** There might have been more than one taxon called *hybernus*; however, this is old and forgotten, not apt to create any confusion.

3. Length of names. Names may consist of a single word or more than one word.

Mew Gull vs the longer, and cumbersome Short-billed Gull: Mew Gull is shorter, quicker, and well-known. Mew Gull is a well-liked name, the kind of name people remember. It also implies something diminutive and “cute” perhaps, short-billed is literal and true, but somehow it just does not evoke the small, dainty, distinctive look of *brachyrhynchus*. Arguments can be made about how Short-billed is more logical, how it is a literation of the scientific name, and this would all be true. However, the gestalt, the sound, the emotional content of the name Mew Gull has value, particularly so given that retaining it would actually increase name stability!

6. Species marginally distributed in North America. Names generally accepted by global or regional authorities are typically used for species that occur in our area as vagrants, introduced species, or species of otherwise marginal distribution.

This does not apply as this is a split and *brachyrhynchus* is found regularly only in the Americas. However, outside of North America the use of Mew Gull has always been restricted to *brachyrhynchus*, it has not referred to Old World populations.

C. New and modified names based on changes to classification

1. Typical species splits. In the case of true phylogenetic daughter species formerly treated as a single parental species, the usual policy is to create new names for each daughter species. This practice is designed to prevent confusion in the literature as to what taxonomic entity the parental name....

In this case, due to the entrenched nature of the name Mew Gull, and that it has had historical meaning to already separate the New World population from Old World populations, resurrecting an old name (Short-billed Gull) for the species is absolutely creating more confusion. If your goal is to have unique names, retain stability, and decrease confusion – revert to Mew Gull. Let's be clear as well that I understand that Short-billed Gull is an old name for this species, but most of the public is not reading Dwight (1925); to 99.9% of the people, including most academics, Short-billed Gull is a new name entirely without context. The fact that it was an old name does not mean that resurrecting it somehow restores stability, given that its use was so far back in time. Short-billed Gull as a name is forgotten; only ornithological historians know this as a name. As well, as noted above, the fact that it is an English translation of the specific

epithet is nice, clever, and interesting but this does not justify the change, given other features of the name Mew Gull.

1.1 Exceptions. *Strong association of names with particular daughter species may provide exceptions to the above policy.*

Again, with the goal to maximize stability, minimize disruption and confusion. Retention of Mew Gull is the clear answer in this unique case.

1.1.b. Differential usage. *In some cases, a name is much more associated with one daughter species regardless of relative range size. For example, the name Clapper Rail*

Mew Gull has been strongly associated the daughter species *brachyrhynchus*, to the exclusion, in most cases, of the Old World *canus*. It is definitely a unique case that the daughter species already had a well-defined English name that was not in wide usage in the Old World where *canus* is the expected species.

1.1.c. Relative appropriateness. *In some cases, a parental name is much more appropriate for one of the daughter species.*

Again, Mew Gull works, there is no need to resurrect an old name for *brachyrhynchus*. The key is that Mew Gull has not had currency outside of the New World as a name for the *canus* complex; it was widely known to refer to *brachyrhynchus* to the exclusion of *canus*, except in North America. But with the split, this issue becomes moot, and the appropriate solution would be to retain Mew Gull.

Recommendation:

I recommend that NACC revert to Mew Gull before more confusion ensues. I admit this is a very specific and unique situation. A species that had an English name that was not standardized across continents, is split along the lines of that English name dichotomy. I am not sure if this has happened before. Although from a North American perspective it may seem necessary to create or resurrect a new name for the daughter species, *brachyrhynchus*, when you look at it from a worldwide perspective the name Mew Gull is entirely appropriate, retains stability, minimizes confusion, and if you see above with respect to the guidelines on English names, fulfills more of them than resurrection of Short-billed Gull.

I know it is difficult to reverse a decision. However, in this case the decision has not been around for long, and it shows that the committee is willing to re-assess previous work in a new light. While reversing a decision might feel like a negative, I think this is a positive for the committee in the public eye, because special situations sometimes require a second look.

I think that if you value name stability, Mew Gull must be resurrected. If name stability is going to be a factor in various other future situations in which changes may be suggested due to societal norms changing, where stability may be a reason not to make a change, one has to apply the concept logically and evenly. In a much more straightforward situation like this one,

where the arguments are not due to cultural considerations, for nomenclatural stability to have any meaning in future discussions, one should revert to Mew Gull. That is what stability, and several other of the name guidelines highlighted above clarify for *Larus brachyrhynchus*.

References:

- Chesser, R. T., S. M. Billerman, K. J. Burns, C. Cicero, J. L. Dunn, B. E. Hernández-Baños, A. W. Kratter, I. J. Lovette, N. A. Mason, P. C. Rasmussen, J. V. Remsen, Jr., D. F. Stotz, and K. Winker. 2021. Sixty-second supplement to the American Ornithological Society's *Checklist of North American Birds*. *Ornithology* 138 (3): ukab037, pp. 1-18.
- Dwight, J. 1925. The gulls (Laridae) of the world: their plumages, moults, variations, relationships and distribution. *Bulletin of the AMNH* 52 (3): 63-401.
- Howell, S. N. G., and J. Dunn. 2007 *Gulls of the Americas*. Peterson Reference Guides. Houghton Mifflin Company, Boston.
- Olsen, K. M., and H. Larsson. 2004. *Gulls of North America, Europe, and Asia*. Princeton University Press, Princeton.

Submitted by: Alvaro Jaramillo

Date of Proposal: 24 January 2022

Treat *Sturnella lilianae* as a separate species from *S. magna* (Eastern Meadowlark)**Background:**

Eastern Meadowlark (*Sturnella magna*) currently consists of 17 recognized subspecies and ranges from southern Canada to northern Brazil. Three northern subspecies, *S. m. lilianae*, *S. m. auropectoralis*, and *S. m. hippocrepis*, are geographically disjunct from the rest of *S. magna*: *S. m. lilianae* and *S. m. auropectoralis* in the southwestern United States to central Mexico, and *S. m. hippocrepis* in Cuba.

The subspecies *lilianae* (Lilian's Meadowlark) was described by Oberholser (1930) based on longer wings but shorter tail, tarsus, and bill, as well as darker yellow chest and paler upperparts than *S. m. hoopesi*, which occurs in southern Texas. Subspecies *auropectoralis* was described four years later (Saunders 1934) as similar to *lilianae* in some characters (four white outer rectrices, darker yellow chest, and shorter tarsus and tail), but differing from *lilianae* in its darker upperparts and shorter wings, as well as a breeding range south of *lilianae*.

Interestingly, in 1962, Lanyon wrote that bill and tail length were too variable to be used as identifying characteristics in desert meadowlarks. He also noted that *S. m. lilianae* and *Sturnella neglecta* do not share breeding habitat. Their preferred habitat forms a mosaic where *lilianae* occurs in drier grasslands and *neglecta* in wetter irrigated areas. This is, however, climate and agriculture-dependent, and it is important to note that much has probably changed environmentally since 1962. Although no data are available on *neglecta-lilianae* hybrids, it has already been established that *magna* and *neglecta* show hybrid infertility, as demonstrated by both observations in the wild and captive experiments (Lanyon 1957, 1979).

Dickerman and Phillips (1970) described a new subspecies, *saundersi*, based on both plumage and morphological characteristics. However, these birds were collected during the nonbreeding season, possibly represent overwintering birds, and the plumage differences noted may not be maintained in breeding plumage. Additionally, small sample sizes (n = 10-14) and lack of statistical analyses raise questions concerning the validity of this subspecies. Additionally, eBird abundance maps do not show range connectivity between purported *auropectoralis* and *saundersi* populations as suggested by Dickerman and Phillips (Fig. 1; eBird data (2020), eBird Trends data (Fink et al. 2020), Birds of the World profiles for *S. neglecta* and *S. magna* (Davis and Lanyon 2020, Jaster et al. 2020).

More recently, molecular work using two mitochondrial genes (CYTB and ND2) and the sex-linked intron ACO-1-I9 (Barker et al. (2008) showed that *lilianae* and *auropectoralis* were distinct from both *S. neglecta* and the rest of *S. magna*. Importantly, the rest of the subspecies from Mexico and Central/South American grouped with *S. magna* and not with the *lilianae* group.

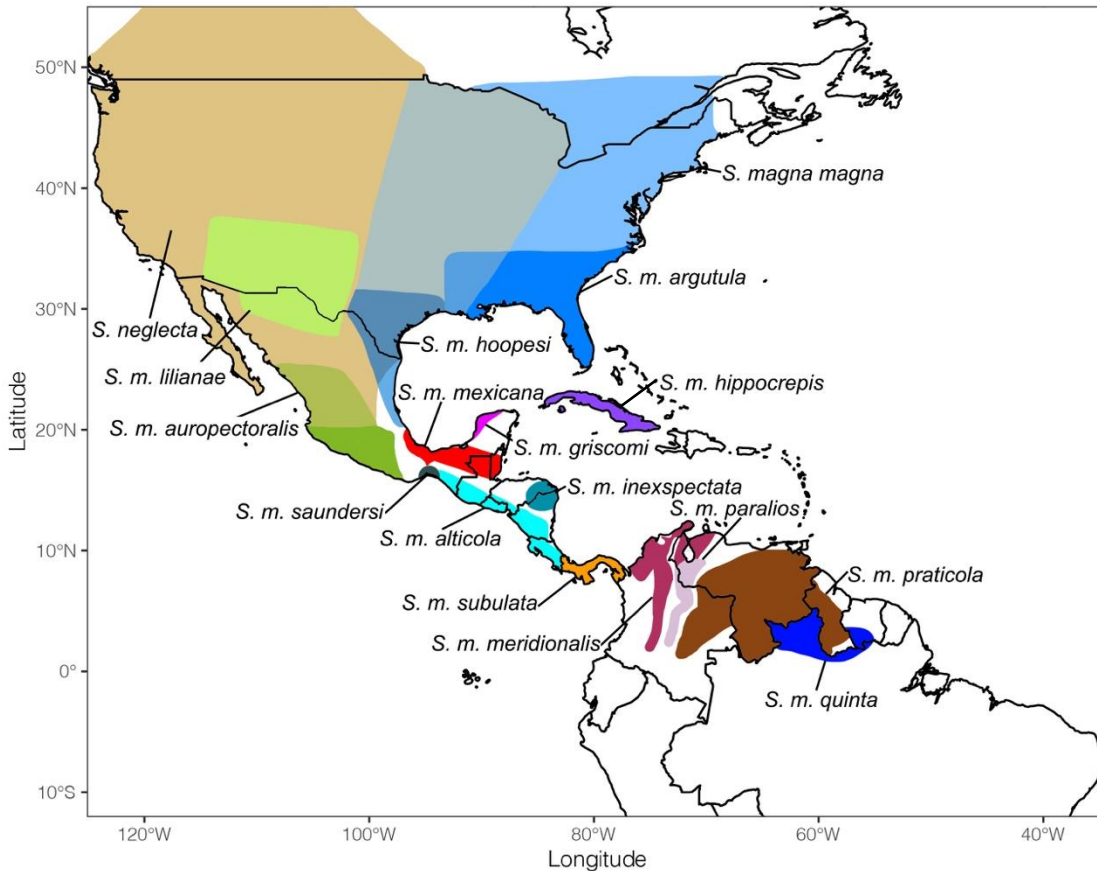


Figure 1: *Sturnella* range map. To our knowledge, this is the first published range map of all subspecies of Eastern Meadowlark. Some of the specimens used to classify subspecies were from the nonbreeding season and in nonbreeding plumage and may not represent valid subspecies. As data used to delineate ranges were taken from multiple sources, range limits are estimates. Intermediate colors between *S. neglecta* and *S. magna* subspecies represent overlap zones between these taxa. Although several sources suggest there are hybrid zones between subspecies in Mexico and Central America, eBird data does not support this. eBird abundance data show gaps in range (visualized above) that correspond to the Sierra Madre Occidental and Oriental, the Llano Estacado, the Isthmus of Tehuantepec, and the Andes. This range map is based on several maps: eBird data (2020), eBird Trends data (Fink et al. 2020), Birds of the World profiles for *S. neglecta* and *S. magna* (Davis and Lanyon 2020, Jaster et al. 2020), and range descriptions from Saunders (1934), Lanyon (1957, 1962), Dickerman and Phillips (1970), Rohwer (1972a, b), Dickerman (1989), Leukering and Pieplow (2009), and Arnold (2020). Taken from Beam et al. 2021.

New Information:

Beam et al. (2021) published new research on meadowlark divergence using whole-genome data and song analysis. They obtained 81 meadowlark songs and 31 whole genomes from throughout the ranges of *S. neglecta*, *S. magna*, and *S. m. lilianae + auropectoralis*. They characterized song variation by measuring song length, minimum and maximum frequencies, starting and ending frequencies, and median frequency. With these data, they ran a Principal Component Analysis (PCA) to test for song similarity, and linear discriminant function analysis (LDA) to see how well these song traits could predict species. The PCA plot (Fig. 2) shows equal separation between *S. magna*, *S. neglecta*, and *S. m. lilianae + auropectoralis* songs.

Importantly, the subspecies *auropectoralis* falls within the broader *lilianae* group. The LDA showed that *S. magna* songs are more likely to be misidentified as *S. m. lilianae* + *auropectoralis* songs, but not vice versa. The rate at which the LDA was able to correctly assign a song to its species was high (90.33%).

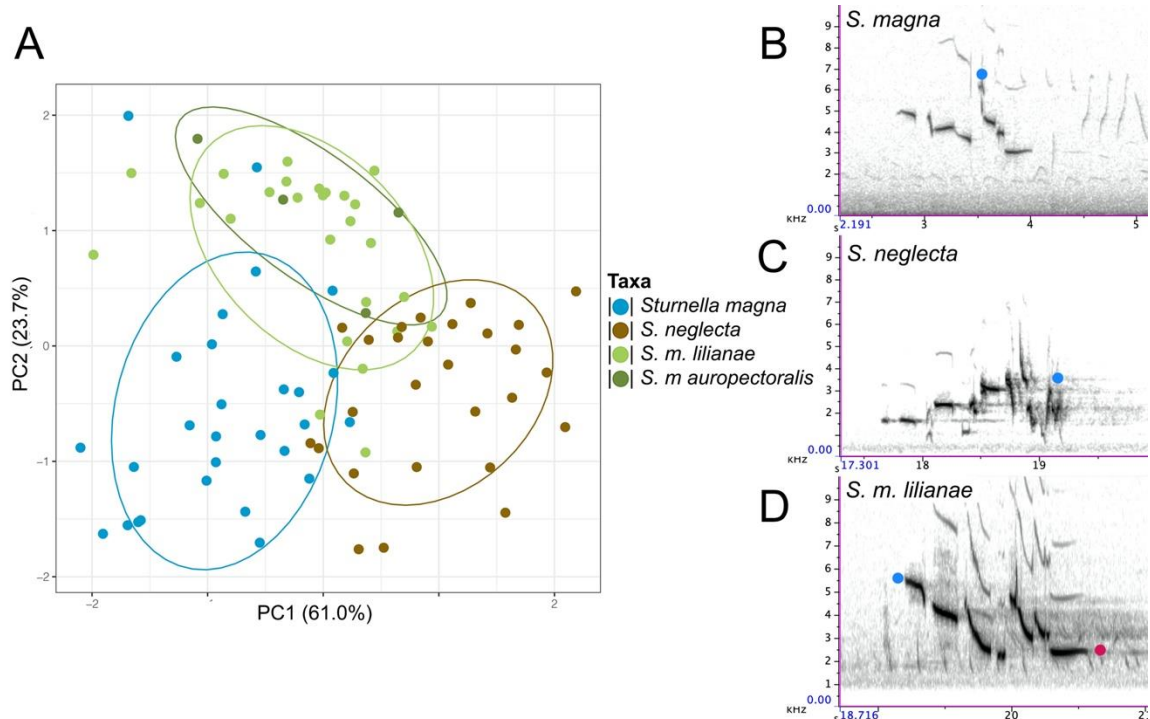


Figure 2. (A) Song PCA plot showing consistent separate clustering of *Sturnella magna lilianae*, *S. neglecta*, and *S. magna*. The subspecies *S. m. auropectoralis* clusters within *S. m. lilianae*. (B) The song spectrogram of *S. magna* showing the maximum frequency occurring in the middle of the song (marked with a blue dot). (C) The song spectrogram of *S. neglecta*. Note the lower overall frequency of the song as well as the quickly descending “gargle” (marked with a blue dot) that occurs just prior to the 19 s mark. (D) The song spectrogram of *S. m. lilianae*. Note the highest frequency occurring at the beginning of the song (marked with a blue dot) and the lowest frequency occurring at the end of the song (marked with a magenta dot). Figure and figure caption taken from Beam et al. 2021.

The PCA of the genomic data shows strong clustering among the 3 taxonomic groups and easily identifiable population structure present between *S. m. lilianae* + *auropectoralis* and *S. m. magna*, as well as between *S. neglecta* and *S. magna* (Fig. 3). Both PC axes explain nearly equal genomic variance, with PC1 explaining 13.91% and PC2 explaining 11.37% of all variance in the dataset. The subspecies *auropectoralis* falls completely within the *lilianae* group, as expected, and, importantly, all other northeastern subspecies (*hoopesi*, *argutula*, and *magna*) form one group. The magnitude of the difference between these groups suggests that *lilianae*, *magna*, and *neglecta* are equally divergent, and that the current designation of *lilianae* as a subspecies does not accurately reflect the true relationship.

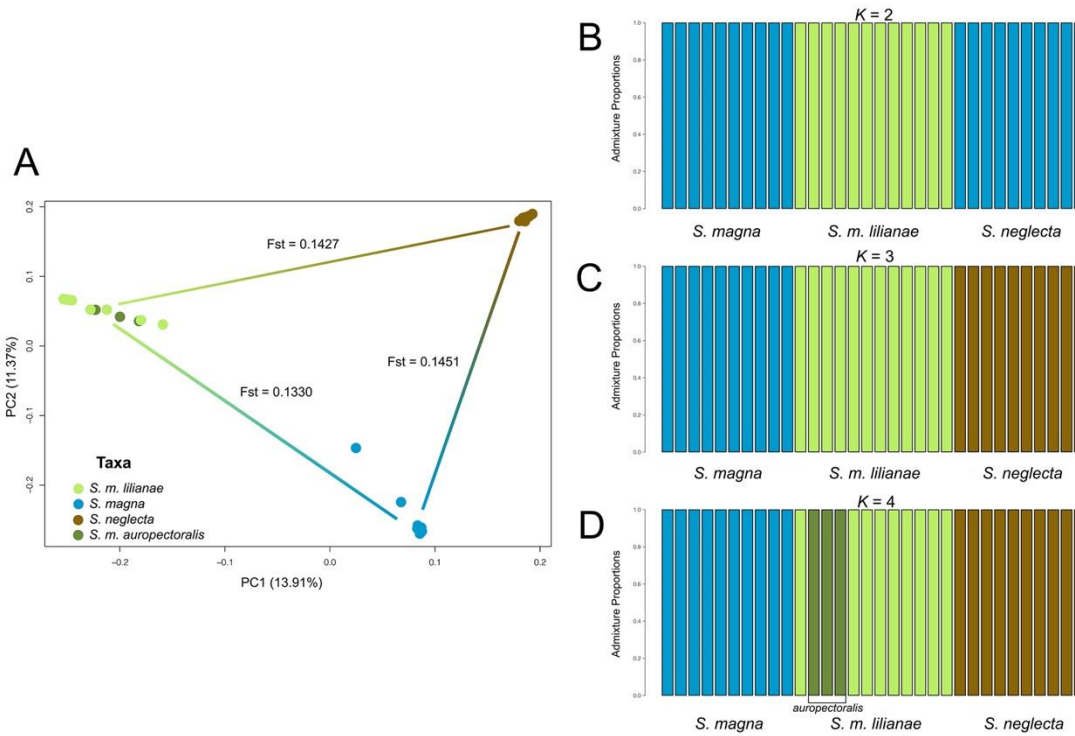


Figure 3. Genomic differentiation between *Sturnella magna*, *S. neglecta*, and *S. m. liliana*. (A) Genetic PCA plot indicating strong population differentiation between *S. m. liliana*, *S. magna*, and *S. neglecta* groups. The subspecies *S. m. auropectoralis* is shown in dark olive and clusters consistently with *S. m. liliana*. Pairwise F_{ST} values are shown next to the lines between groups. (B–D) NGSAdmix plots for K values of 2 (B), 3 (C), and 4 (D). Each bar indicates an individual and bars are grouped together by taxon group. Notably, *S. magna* and *S. neglecta* form a clade separate from *S. m. liliana* when $K = 2$. There is no admixture present within any of the taxa for K values = 2–4. $K = 3$ appears to be the most biologically relevant considering the 3 populations of meadowlarks. The K value of 4 shows additional resolution of *auropectoralis* within *S. m. liliana* (dark olive); however, this group does not appear to be monophyletic (Figure 4). Figure and figure caption taken from Beam et al. 2021.

An ABBA-BABA test—a measure that explicitly estimates the extent of gene flow between groups—using the model of (((A, B), C), O), can be used to examine whether population C shows signatures of introgression with populations A or B, with an outgroup set as population O. Beam et al. (2021) combined the subspecies populations such that 3 groups remained: (1) *S. neglecta* (population A); 2) *S. m. magna*, *S. m. argutula*, and *S. m. hoopesi* (population B); and (3) *S. m. liliana* + *S. m. auropectoralis* (population C). If *liliana* or *auropectoralis* hybridized with either *S. neglecta* or *S. magna* and had fertile offspring, we would expect a significant Z score indicating introgression between the groups. The ABBA-BABA tests showed no evidence of historical or contemporary introgression between *liliana*, *magna* (including *hoopesi*), or *neglecta*.

The phylogenetic tree generated by SVDQuartets shows 2 distinct clades: the first included individuals of both *S. m. liliana* + *auropectoralis*, and the second included both *S. magna* and *S. neglecta* (Fig. 4). Beam et al. recovered full support for *S. magna* as sister to *S. neglecta* (Fig. 4). The subspecies *auropectoralis* was not monophyletic within *S. m. liliana*, nor were

hoopesi or *magna* within *S. magna* (Fig. 4). Notably, this is a different relationship than in Barker et al. (2008), who found that *S. magna* and *S. m. lillianae* were sister taxa with *S. neglecta* in a separate clade. This is not surprising, however, given that Barker et al. used 3 genetic markers whereas Beam et al. used a whole-genome approach and 484,816 variable SNP loci—higher resolution data that has only recently become feasible to generate.

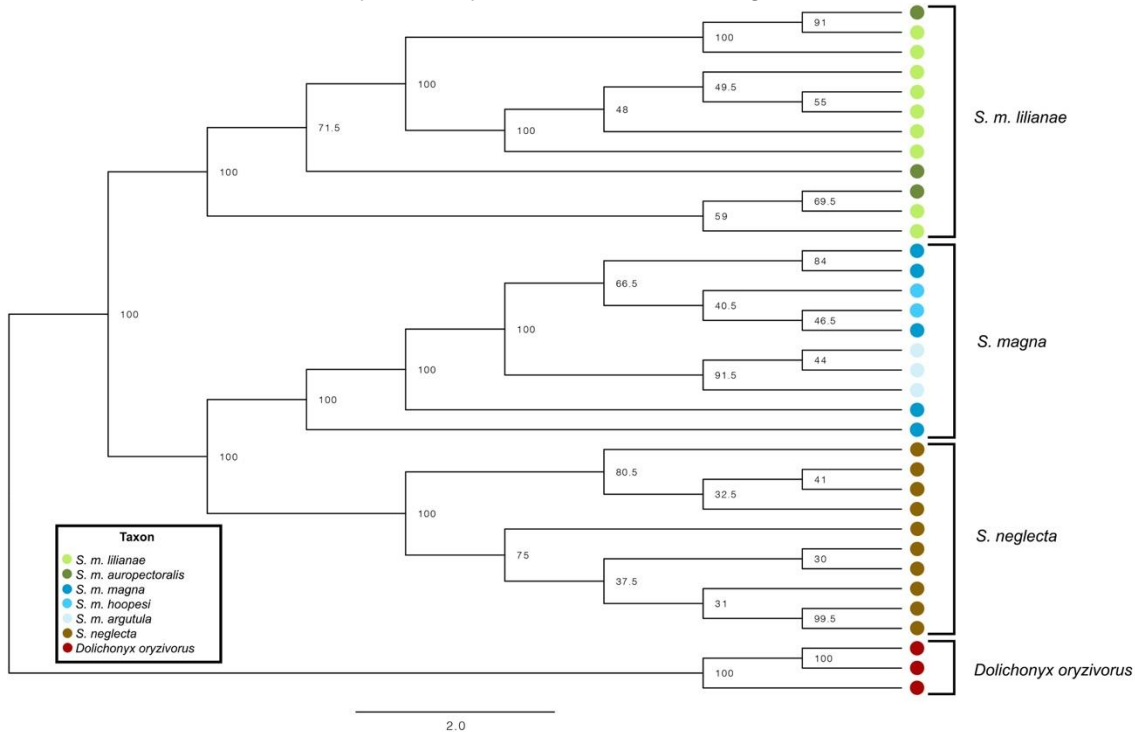


Figure 4. Phylogenetic tree created using PAUP* and SVDQuartets. Support values, from a bootstrap analysis, are labeled at each node. Bobolink was used as the outgroup (in red). *Sturnella magna lillianae* forms a separate clade from both *S. magna* and *S. neglecta*, which are sister taxa. There is full support for *S. m. lillianae* split off the *S. magna*/*S. neglecta* clade. Notably, the subspecies *S. m. auropectoralis* does not form a clade within *S. m. lillianae*, nor do the subspecies *S. m. magna* or *hoopesi* within Eastern. The subspecies *S. m. argutula* appears to be monophyletic within the *S. magna* clade but does not appear in the NGSAdmix plots (Figure 3C) at higher values of K. Figure and figure caption taken from Beam et al. 2021.

F_{ST} shows moderate and equal levels of divergence among *lillianae*, *magna*, and *neglecta*. *S. m. lillianae* shows just as much differentiation from *S. magna* as *S. magna* does from *S. neglecta*, which are two long established species (Fig. 3A). These F_{ST} (Fig. 3A) values are similar to many established species pairs, such as Black-capped and Carolina Chickadees ($F_{ST} = 0.1$, Taylor et al. 2014), Collared and Pied Flycatchers ($F_{ST} = 0.2$, Nadachowska-Brzyska et al. 2013), and Baltimore and Bullock's Orioles ($F_{ST} = 0.161$, Walsh et al. 2020). Sliding window F_{ST} plots (Fig. 5) show high background differentiation between all species groups. This suggests that *lillianae*, *magna*, and *neglecta* have been isolated for a long time and have accumulated many differences across their genomes.

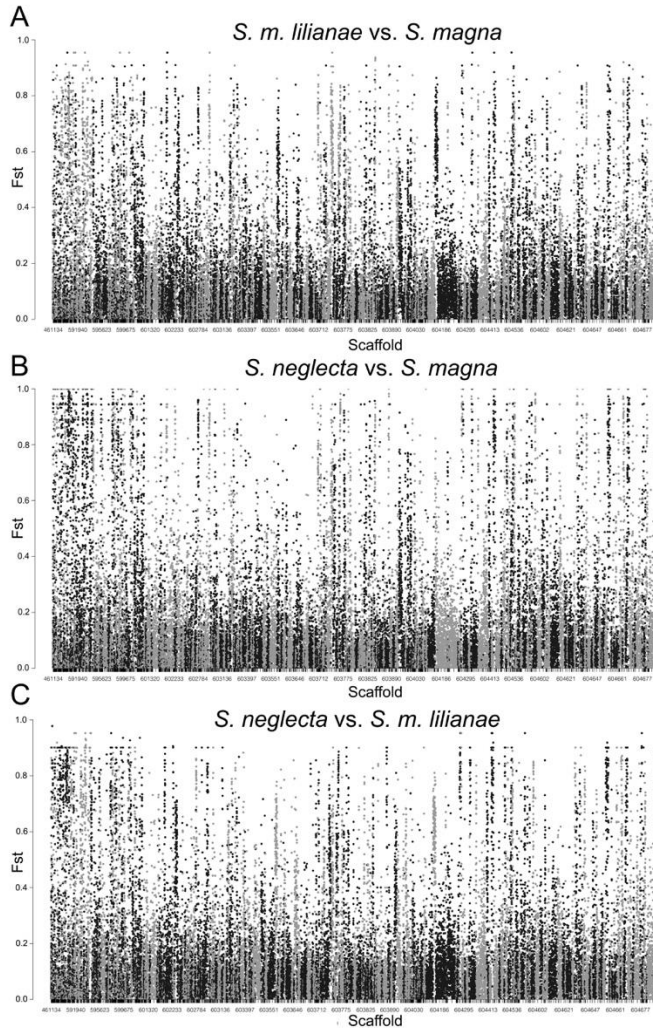


Figure 5. (A-C) A non-overlapping 25kb windowed scan of pairwise F_{ST} between (A) *S. m. liliana* and *S. magna*, (B) *S. neglecta* and *S. magna*, and (C) *S. m. liliana* and *S. neglecta*. Scaffolds have been arranged according to size. Figure and caption taken and adapted from Beam et al. 2021.

Lanyon's (1957, 1979) hybrid observations both in the wild and in captivity with *magna* and *neglecta* show that hybrid pairings are rare and that hybrids have low viability and fertility. No hybrids between *neglecta* and *liliana* have been found. *S. neglecta* and *magna* are more closely related to each other than they are to *liliana*, which suggests that if hybrids were to occur between either *liliana* and *neglecta* or *liliana* and *magna*, they would also be likely inviable or infertile. If hybrids were, or are, produced, they are not successfully reproducing with any parental species—Beam et al. (2021) found no contemporary introgression between any of *liliana*, *magna*, and *neglecta*.

It is likely that important geographic barriers are preventing gene flow across the ranges of meadowlarks. Rohwer (1972b) noted that the Llano Estacado in Texas acts as a barrier between *hoopesi* and *liliana* populations. eBird trends and abundance data (Fink et al. 2020) show gaps in the range of *S. magna* that correlate with the Llano Estacado, as well as gaps

between the ranges of *auropectoralis* and the purported subspecies *saundersi*, which correlate with the Sierra Madre Oriental.

Recommendation:

I recommend that the committee split *liliana* from *S. magna* and establish *Sturnella liliana* as species with two subspecies: *S. l. liliana* and *S. l. auropectoralis*. *Sturnella m. saundersi* would remain a subspecies under *S. magna* until further studies can establish its validity as a subspecies.

Options for the English name for *liliana* include:

- 1) Chihuahuan Meadowlark – Chihuahuan Meadowlark would follow taxonomy already in place on the Clements Checklist (Clements et al. 2021); however, the range of the Chihuahuan Desert fits with the subspecies *liliana*, but not with *auropectoralis*.
- 2) High Desert Meadowlark – Although there is no precedent for a name like High Desert, the range of *liliana* fits with the high elevation desert of southeast Arizona, New Mexico, west Texas, and northern Mexico.
- 3) Pallid Meadowlark – *Sturnella (m.) liliana* is noted as the palest of meadowlarks, with paler back, head, and tail than either *neglecta* or *magna*. A name such as Pallid Meadowlark would be fitting for such a pale bird.
- 4) White-tailed Meadowlark – *liliana* notably has the most white in its outer rectrices of all meadowlarks. Amount of white in the tail is also one of the key field marks when identifying meadowlarks (Lanyon 1962).

I recommend option 3) Pallid Meadowlark as the new English name for *Sturnella liliana*, and retaining Eastern Meadowlark for *S. magna* and Western Meadowlark for *S. neglecta*.

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Submitted by: Johanna K. Beam

Date of Proposal: 9 February 2022

Recognize *Riccordia elegans* as a species, subspecies, or doubtful taxon**Background:**

Riccordia elegans is known from a single specimen taken in 1860, but from an unknown locality somewhere in the Caribbean. Both *elegans* and *R. bracei* (also known from a single specimen) have a long history of taxonomic uncertainty, but the extinct *R. bracei* was recently recognized as a species by NACC based on Graves and Olson (1987). The sole specimen of *bracei* was taken on New Providence Island in the Bahamas in 1877.

Riccordia ricordii is common on Cuba and on islands in the northern and western Bahamas (Grand Bahama, Great Abaco, Andros, Green Cay), but is not known from New Providence (Bündgen and Kirwan 2021). The other three species of *Riccordia* are found elsewhere in the Caribbean on Hispaniola (*swainsonii*), Puerto Rico (*maugaeus*), and Dominica and Martinique (*bicolor*), and all are extant.

Both *Riccordia elegans* and *R. bracei* have been considered distinct species by some authors, but both have been controversial because the descriptions were based on unique holotypes that are poorly preserved (*bracei*), or for which the collecting locality remains a mystery (*elegans*). HBW-Birdlife considers *elegans* to be a valid species, with the following comment: “Described from a single specimen, dated 1860; recently shown to be a valid species (Weller 1999). Monotypic.” Clements also considers *elegans* to be a valid taxon, but treats it as a subspecies of *bracei*. *Riccordia elegans* was not included in previous editions of the AOU checklist (AOU 1983, 1998).

New information:

Weller (1999) examined the single specimen of *R. elegans* and determined, based on morphology, that it was unlikely to be a hybrid given that it was not intermediate between any known taxa, including Bahamas populations of *R. ricordii* (sometimes separated as the subspecies *aeneoviridis*). The specimen of *elegans* has a fairly distinctive (within the genus) copper-purple rump and upper side to the tail. That information, plus the fact that the other *Riccordia* are each found on different islands, led Weller (1999) to suggest that *R. elegans* was likely found on an island where there are (or were) no congeners, possibly Jamaica or elsewhere in the Bahamas. Although these hypotheses are certainly possible, the lack of a known distribution makes them difficult to assess. That paper, which included photos of the type specimen of *elegans*, is available here:

<https://www.biodiversitylibrary.org/page/40025454#page/215/mode/1up>

Additional photos of this specimen are inserted below, courtesy of Paul Donald.





Terry Chesser has also provided photos of the sole specimen of *R. bracei* (the specimen with the red tag) in comparison with a series of specimens of *R. ricordii* (specimens from Cuba on the left, Bahamas on the right). The type is a poor specimen, but you can see such features as the bronze dorsal coloration, the ventral green restricted to the gorget, the white spot behind the eye, and the bill shape and size:





The Birds of the World account (Greeney 2021) includes *elegans* as a subspecies of *R. bracei* with the following comments:

the subspecies *elegans* has been of questionable taxonomic status and generic affinity since its discovery. Gould (27) suggested that *elegans* was similar in many respects to *Chlorostilbon* species, and subsequent authors placed it in a variety of genera, most of which have now been merged with *Amazilia* (6, 16, 17, 28, 21). In general, however, during much of the past century *elegans* has either been ignored, overlooked, or viewed with reservations as to its validity (17, 21, 29, 30, 31). Although its precise status may never be fully elucidated, Weller's (4) careful examination of available evidence suggested that *elegans* is best placed in *Chlorostilbon* [= *Riccordia*], and is worthy of recognition, either as a full species (25) or as a subspecies of *bracei* (32).

Although the analysis of Weller (1999) does seem to indicate that the specimen is unlikely to be a hybrid, there is no strong evidence supporting its status as a species or subspecies. Without distributional information, considering it conspecific with another taxon (e.g., *bracei*, as the Clements list has done, or maybe *ricordi*) seems to be, at best, a guess. The fairly distinctive dorsal color is not shown by any other species in the genus, perhaps suggesting that if the taxon is valid, that it should be designated a separate species.

The IOU's Working Group on Avian Checklists (WGAC) recently considered this issue and voted to consider *elegans* as a "taxon of uncertain status". Comments on that proposal noted that the distinctive plumage (e.g., dorsal coloration) was very different from that of *R. bracei*, so a subspecific treatment was not indicated. Given that there are so many unknowns (e.g., no distributional or genetic information), treatment as a species was considered premature.

Recommendation:

We agree with the WGAC on this issue. Although Weller (1999) did a commendable job with the available data, there is considerable uncertainty about this specimen that precludes a taxonomic treatment with any certainty. Especially troublesome is the lack of a locality. Although Weller (1999) concluded, based on morphology, that the specimen was not likely the product of hybridization, this should be confirmed with genetic data. Stable isotope data could perhaps be used to determine the geographic source of the specimen.

We recommend treating *R. elegans* as a form of doubtful status (**YES on C** below), which would add the taxon to the checklist category of Appendix C. If voting for species status, a separate English name proposal would be necessary.

Please vote on the following:

- A) Treat *Riccordia elegans* as a species
- B) Treat *Riccordia elegans* as a subspecies of *R. bracei*
- C) Treat *Riccordia elegans* as a form of doubtful status

Literature Cited:

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Submitted by: Oscar Johnson, University of Texas, El Paso, and Blanca E. Hernández-Baños, Universidad Nacional Autónoma de México

Date of proposal: 24 February 2022

Treat *Anthracothorax aurulentus* as a separate species from *A. dominicus* (Antillean Mango)

Background:

Anthracothorax dominicus is a species with two fairly well-differentiated subspecies, *A. d. dominicus* of Hispaniola and *A. d. aurulentus* of Puerto Rico. These two subspecies have differences in color patterns in both sexes. In *A. d. dominicus*, the males have a metallic green throat and otherwise entirely velvet-black underparts, whereas males of *A. d. aurulentus* have green flanks and a dark brownish-gray belly, with the black restricted to a patch on the chest (Kirwan et al. 2020). In females, *dominicus* has a purplish base to the tail, while in *aurulentus* this area is largely brownish-gray (Kirwan et al. 2020). Unique amongst *Anthracothorax*, the females are pure white below, with only the young males having the black stripe down the venter typical of the mainland species of *Anthracothorax* (Kirwan et al. 2020).

The two taxa were considered separate species (e.g. Ridgway 1911, Wetmore 1916, Cory 1918) until lumped without comment by Peters (1945). Later authors have largely considered the two conspecific (AOU 1983, Raffaele 1989, Bond 1993, Raffaele et al. 1998, Dickinson 2003, Kirwan et al. 2020), until HBW-BirdLife split the two (see details below).

Under his account for *A. aurulentus*, Ridgway (1911) noted the following differences from *A. dominicus*: "Similar to *A. dominicus* but decidedly smaller; adult male with black of under parts confined to chest and breast, and middle rectrices usually much more coppery bronze; adult female with basal portion of lateral rectrices light grayish, or partly so, instead of more than basal half wholly chestnut-rufous, black of subterminal portion brightly glossed with bluish green, and under parts more extensively and uniformly grayish, the sides without green spotting or inter-mixture."

New evidence:

No recent publications.

HBW-Birdlife split *aurulentus* from *dominicus* based on the following rationale: "hitherto treated as conspecific with *A. dominicus*, but differs on account of (in male) blue-black not covering all of underparts below throat but just breast to mid-belly, with flanks green and lower central underparts to vent dark brownish-grey (3); (in male) central rectrices bronzy green vs glossy blackish-blue (2); (in female) outer tail dull brownish-grey, shading to darker subterminal tips and white tips vs violaceous-rufous, cutting sharply to blackish broad subterminal tips and white tips (3); markedly smaller size, although bill length virtually identical (effect size for wing -4.15, tail -5.63; score 3). Monotypic."

Terry Chesser and Paul Donald have graciously provided photos of the tails of the females, showing the differences between taxa. Note the more extensive purple coloration at the base of the tail in *dominicus* in the following photo taken by Paul:



Although the Birdlife account above indicates that lateral rectrices of female *aurulentus* are light grayish or grayish-brown basally, Terry noted that 50% of specimens of female *aurulentus* at the USNM (10/20) showed purple (or occasionally chestnut) at the base of the rectrices (although, as noted by Ridgway, not as extensively as in *dominicus*). A photo of three female *aurulentus* showing that purple coloration is below:



Photos on the Macaulay Library show the differences between the males quite well. Here are photos of male *dominicus*:

<https://macaulaylibrary.org/asset/176320171>
<https://macaulaylibrary.org/asset/176615901>
<https://macaulaylibrary.org/asset/241371311>
<https://macaulaylibrary.org/asset/397356871>

and male *aurulentus*:

<https://macaulaylibrary.org/asset/184585191>
<https://macaulaylibrary.org/asset/184585211>
<https://macaulaylibrary.org/asset/287874871>
<https://macaulaylibrary.org/asset/303680591>

Kirwan et al. (2020) listed the following morphometric differences between *aurulentus* and *dominicus*, with the data taken from Arendt et al. (2004). Based on these data, Kirwan et al. (2020) stated that “*aurulentus* has shorter wings and tail than nominate *dominicus*, but that bill length is comparable between the two taxa”. It appears, however, that there is some overlap in these measurements.

	Wing length	Tail length	Bill length	Tarsus length	Mass
<i>A. d. dominicus</i>					
Males	62–72 (64.8 ± 3.4, n = 3)				6.0–8.2 g
Females	59–67 (64.0 ± 2.7, n = 10)	35.3–36.4 (35.9 ± 0.7, n = 3)	18.0–25.3 (24.0 ± 2.1, n = 3)	5.1–7.3 (6.2 ± 1.6, n = 3)	4.0–7.0 g
<i>A. d. aurulentus</i>					
Males	57.3–69.0 (61.6 ± 2.0, n = 47)	22.7–36.4 (32.0 ± 3.7, n = 47)	21–27 (23.2 ± 1.4, n = 47)	2.3–7.3 (5.4 ± 1.0, n = 47)	4.8–7.2 g
Females	50.7–63.5 (57.9 ± 2.5, n = 60)	22.9–34.7 (32.0 ± 2.0, n = 60)	20.8–27.3 (24.5 ± 1.3, n = 60)	4.4–7.3 (5.6 ± 0.7, n = 60)	4.0–6.4 g

No genetic comparisons have been made between the two taxa, although given the plumage and morphometric differences, there are clearly some genetic differences. McGuire et al. (2014) did include a sample of *A. dominicus*, but unfortunately not of both subspecies. That study found *dominicus* sister to *A. viridis* of Puerto Rico, and in turn sister to the *Eulampis* Caribs of the eastern Caribbean (thus rendering *Anthracothorax* paraphyletic). This, unfortunately, provides no data on the species status of *dominicus* and *aurulentus*. However, the mainland *Anthracothorax* of Central and South America (sister to the aforementioned clade) provide an interesting comparison. The four species in that group are all differentiated (plumage-wise)

based on the relative extent of green and black coloration on the underparts, comparable to the differences in males of *dominicus* and *aurulentus*. However, the taxonomy of those *Anthracothorax* is not clear-cut, with some taxa having been considered conspecific in the recent past (e.g. *prevostii* and *veraguensis*).

It appears that no other studies on the taxonomy of this group have been conducted, such as research on song or genetics. The two taxa, like others in the genus, appear to vocalize infrequently, if at all (Kirwan et al. 2020). Thus, differences in plumage and morphometrics (described above) may be more relevant to species limits.

The IOU's Working Group on Avian Checklists (WGAC) recently considered this issue and voted to treat the two taxa as separate species. That decision was based on the differences in size and plumage, described above.

Recommendation:

We recommend a **YES**. Although more data would be desirable, the published plumage and morphometric data seem to indicate species status. Differences between the two taxa are consistent and diagnostic, and they are comparable to species-level differences in other taxa in the genus. However, although the differences in color pattern are clear, a study of genetics and quantification of plumage differences is desirable. Unfortunately, it does not appear that there is anyone working on this group at the moment. The two taxa are clearly closely related and are (together) distinctive within the genus.

If split, we recommend the following English names, used by HBW: Hispaniolan Mango for *dominicus* and Puerto Rican Mango for *aurulentus*. Ridgway (1911) and Cory (1918) used Haitian Mango and Porto Rican Mango, but the HBW names highlight the entire island on which *dominicus* is found, and the Ridgway/Cory name for *aurulentus* is an outdated spelling variant.

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Submitted by: Oscar Johnson, University of Texas, El Paso, and Blanca E. Hernández-Baños, Universidad Nacional Autónoma de México

Date of proposal: 24 February 2022

Transfer *Pitangus lictor* (Lesser Kiskadee) to the monotypic genus *Philohydor***Background:**

Lanyon (1984) described the genus *Philohydor* for Lesser Kiskadee (*Pitangus lictor*), which had typically been placed in the genus *Pitangus* together with Great Kiskadee (*Pitangus sulphuratus*), based on morphological and behavioral characters. In justifying his split of *Philohydor* from *Pitangus*, Lanyon (1984) noted differences in syringeal morphology that “far exceed intrageneric variation in syringeal morphology among tyrant flycatchers” – these included differences in the number of complete cartilage rings, as well as differences in the shapes of cartilage rings. In addition to syrinx morphology, *Philohydor* is described as having a very narrow skull and differing from *Pitangus* “to a degree greater than any other congeneric flycatchers examined” (Warter 1965 in Lanyon 1984). Lanyon (1984) also noted differences in nest shape between *Philohydor* and *Pitangus*: *Philohydor* constructs a shallow cup-nest, whereas *Pitangus* constructs a large and untidy domed structure. Despite these differences, many checklists have continued to recognize *lictor* as part of *Pitangus* (AOU 1998, Dickinson and Christidis 2014, Clements et al. 2021), although the IOC Checklist (Gill et al. 2022) and BirdLife International Checklist (del Hoyo and Collar 2016) now place *lictor* in *Philohydor*. Early genetic work did not provide much clarification of the issue; Tello et al. (2009) found that Great Kiskadee and Lesser Kiskadee were sister species, although with relatively weak support.

New Information:

In their UCE-based phylogeny of suboscine passerines, which included 1,287 of 1,306 suboscine species sequenced at 2,389 genomic regions, Harvey et al. (2020) found that Lesser Kiskadee and Great Kiskadee were not sister taxa; Lesser Kiskadee instead was sister to a large clade that included Great Kiskadee, *Myiozetetes*, *Tyrannus*, *Conopias*, and *Myiodynastes*, among others (see phylogenetic tree on next page). The node that unites *Pitangus sulphuratus* with these other genera to the exclusion of *lictor* (i.e., supports Lesser Kiskadee as sister to the rest of the clade) receives very strong support (98% RAxML bootstrap support; see Fig. 1 on the next page). Given that Lesser Kiskadee and Great Kiskadee are not sister species, and that neither species is particularly closely related to any other species, placing each in a monotypic genus seems to be the best solution. For Lesser Kiskadee, this involves resurrecting *Philohydor* Lanyon, 1984, and removing it from *Pitangus*, leaving Great Kiskadee as the sole member of *Pitangus*.

Recommendation:

I recommend that NACC transfer Lesser Kiskadee (*Pitangus lictor*) from the genus *Pitangus* to the monotypic genus *Philohydor*.

References:

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Figure 1. Portion of tree from Harvey et al. (2020) with tip names and support values. Lesser Kiskadee is indicated with a red arrow with the name “*Philohydor*” and Great Kiskadee is indicated with a light blue arrow and the name “*Pitangus*”

Submitted by: Shawn M. Billerman, Cornell Lab of Ornithology

Date of Proposal: 23 February 2022

Transfer *Grus monacha* (Hooded Crane) to the Main List

Background:

Hooded Crane (*Grus monacha*) is listed in the Appendix on the basis of well-documented records involving one or more birds over a 22-month period from April 2010 to February 2012, from Tennessee, Indiana, Nebraska, and Idaho. These records were accepted by at least three state committees (Nebraska, Indiana, and Tennessee), but on a split vote this species was not accepted by the ABA Checklist Committee (Pranty et al. 2014) on the grounds of origin, not identification. This led to some dissention from the chairs of the committees from Nebraska, Indiana, and Tennessee (Kendall et al. 2015), followed by a response from the ABA CLC Chair, Bill Pranty (Pranty 2015). The by-laws of the ABA CLC require substantive information before a non-accepted record is reconsidered. For some of us a new record was what was needed, preferably from Alaska.

New Information:

On 29 September 2020, Michael Lenze collected a Hooded Crane from a flock of 70+ Sandhill Cranes near Delta Junction, Alaska. The record is detailed by Withrow and Lenze (2021). The bird had been in the vicinity for several days, but its exact detected arrival date is unknown. The specimen (University of Alaska 45000) was a male weighing 3300 g, with light fat, and it appeared to be in good health. On the basis of plumage and molt it was in its second year, roughly 15 months old. This record was accepted unanimously by the Alaska Checklist Committee as a wild bird (decision not yet published) and by the ABA CLC (Pyle et al. 2022). Withrow and Lenze (2021) included color photos of the specimen, including dorsal and ventral sides of the severed right wing, showing the molt pattern.

Discussion:

There has never been controversy about the identification of any of the Hooded Cranes, a striking species. The debate has revolved around the origin of the records, particularly the ones from the “Lower 48.” Those who believed these birds were of wild origin postulated that the Hooded individuals got caught up with Sandhill Cranes (*A. c. canadensis*) breeding in Arctic Russia in Russian Far East (west to the mouth of the Yana River). However, Withrow and Lenze (2021) pointed out that this is 1000 km from the closest regularly occurring Hooded Cranes to the west and south. Most Hooded Cranes winter in Kyushu, southern Japan (Arasaki Crane Observation Centre, Kagoshima), with smaller numbers in South Korea and China. Withrow and Lenze (2021) noted that there are few known records of vagrancy, but that the two records they know of were both in 2020, from the Philippines in February (flock of 7) and one shot by a hunter in Pakistan in April. The species is also casual in Taiwan. Withrow and Lenze (2021) detailed that the Tanana River Valley is a major migratory corridor for Sandhill Cranes breeding in western Alaska and Siberia [Russian Far East; Yana River is in the Russian Far East, not Siberia]. They pointed out that these birds migrate somewhat later than those from the interior of Alaska and that the accompanying Hooded Crane was at the tail end of this movement. The authors stated that the area around Delta Junction is one of the few areas of Alaska that has

significant agriculture (primarily hay and barley, as well as pastures) and attracts large numbers of waterfowl and cranes. One of two Alaska records of Common Crane (*Grus grus*) was from this area, the other from Fairbanks. I agree with the opinion expressed by Withrow and Lenze (2021) that the Hooded Crane could well have joined Sandhill Cranes wintering in Japan, including Kagoshima Prefecture. They (*ibid*) cited a publication indicating that wintering Sandhill Cranes are increasing in Japan. The current world population of Hooded Crane is estimated to be about 15,000.

Recommendation:

I recommend that we transfer Hooded Crane from the Appendix to the Main List based on this well-documented record from Alaska. Since at least three other states have accepted their records of Hooded Cranes (not sure about the disposition of the Idaho records), I don't see a compelling reason not to accept those records also.

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Submitted by: J. L. Dunn

Date of Proposal: 4 March 2022

Add *Larosterna inca* (Inca Tern) to the U.S. List**Background:**

Inca Tern, a species found on the west coast of South America, is already on the Main List on the basis of records from Central America. There are multiple records from the Pacific coast of Panama and Costa Rica (detailed by Vallely and Dyer 2018). Pyle et al. (2021) cited records as far north as Guatemala.

New Information:

An individual of this species was discovered on South Point, Hawai'i Island, Hawaii, on 12 March 2021 and remained there through 3 June 2021. Details of this record are published in Pyle et al. (2021) and include color photos from 13 March and 29 April. During its stay this individual underwent its preformative or second prebasic molt, replacing its very worn juvenile flight feathers with fresher feathers. The record was accepted by the Hawaii Bird Records Committee in March 2021 and unanimously by the ABA CLC in June 2021. A second individual (based on detailed comparison of photographs) was first observed on Oahu on 24 June 2021 and was still present in November 2021.

Discussion:

Excellent published photos (2) of the bird on Hawai'i Island (Pyle et al. 2021) clearly document this striking species. There were some questions about origin and whether it could have been held captive on a ship from South America. Pyle et al. (2021) indicated that the bird was initially "somewhat tame" and took handouts from fishermen on a dock at South Point. They commented further that Chinese fishing fleets regularly transit between South American waters and those south of Hawaii. On the other hand, the bird flew strongly, and they noted that wild Inca Terns take handouts from fishermen in South America. (Long ago, I recall Guy McCaskie discussing sightings in the late 1960's of this species on or near Pt. Loma, San Diego, San Diego County, CA, but I have never seen them published in any substantive manner.)

Recommendation:

I **recommend** that Inca Tern be added to the U.S. list. Issues of origin are often difficult to resolve, but I see no compelling reason to reach a different decision from the Hawaii or ABA Checklist committees.

Literature cited:

Pyle, P., M. Gustafson, T. Johnson, A.W. Kratter, A. Lang, M.W. Lockwood, K. Nelson, and D. Sibley. 2021. 32nd Report of the ABA Checklist Committee. *Birding* 72 (2):10-17.
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Submitted by: J. L. Dunn

Date of Proposal: 5 March 2022

Remove the account for *Macronectes giganteus* (Southern Giant-Petrel) from the Appendix and replace it with an account for *Macronectes halli* (Northern Giant-Petrel) in the Main List

Background:

Accounts for the Giant Fulmar (*Macronectes giganteus*), the English name used through the 5th edition of the AOU (1957), can be found on the Main List through the first three editions of the AOU Check-list (1886, 1895 and 1910). This is based on a specimen record by Townsend off the coast of Oregon relayed by Audubon (Orn. Biog., V, 333). In the 4th edition of the AOU Check-list (1931), it had been moved to the Hypothetical List, likely based on Stone (1930), who stated that this and other specimen-supported claims from Townsend from the Oregon coast were likely from the South Pacific. Stone (1930) stated:

It will, I think, be evident that Townsend had no clear idea of the identity of the various species of Tubinares nor of where he secured the several specimens; that he sent Audubon no information about the four in question and probably did not label them at all; and that he had every opportunity to secure specimens of all four in the South Pacific, while his serious illness may have made it still more difficult for him to remember which specimens had been obtained at the mouth of the Columbia and which in the south Pacific. The fact that he sent Audubon a specimen of the Chilian Finch (*Brachyspiza*) as from Oregon (described as *Fringilla mortoni* by Audubon) further shows his carelessness or failure of memory. Audubon was in Edinburgh when Townsend arrived home, November 15, 1837, and his published letters show that he, or Edward Harris for him, purchased Townsend's second collection of birds and that they were sent over to Edinburgh. He had no personal intercourse with Townsend until after his great work was completed, if ever.

In view of all of these facts it seems far more likely that these four South Pacific birds actually came from the South Pacific and not from the coast of Oregon and that they should be dropped from our North American list or at least placed in the hypothetical section. (p. 415)

Other species claimed by Townsend off the Oregon coast (off mouth of Columbia River) and maintained on various North American lists included Yellow-nosed Albatross (*Thalassarche chlororhynchos*), Sooty Albatross (*Phoebastria fusca*), and Slender-billed Fulmar or Southern Fulmar (*Fulmarus glacialisoides*) (Stone (1930).

In addition to the Oregon record, an account of Giant Fulmar is found in Grinnell and Miller (1944) in their Supplementary List:

Known only from the statement by Cooper (Amer. Nat., 4, 1871:758; Baird, Brewer and Ridgway, Water Birds N. Amer., 2, 1884:365) that this "enormous Petrel "or 'Gong' (*Ossifraga gigantea*), could often be seen" in the summer of 1861 about the whale fishery in Monterey Bay, "swimming lazily near the try-works to pick up scraps of

blubber, sometimes accompanied by the dusky young of Short-tailed Albatross (*Diomedea brachyura*)." Cooper's identification has been discredited (Loomis, Proc. Calif. Acad. Sci., ser. 4, 2, 1918:87) because no specimen came actually to hand. Even so, considering the habits of the Giant Fulmar (see Murphy, Oceanic Birds S. Amer., 1936:584ff.) its occurrence in our latitudes would be but little more astonishing than that of several other birds of south-equatorial seas, of which specimens have been taken here. (p. 557)

The Monterey sightings published by Cooper got no mention in any of the editions of the AOU Checklist. Stone (1930) wrote that "A later alleged sight record of Giant Fulmar in Monterey Bay Calif., is hardly of serious consideration," advice the committee apparently followed.

By the 6th edition of the AOU Check-List (1983) the species was in Appendix A, but there was a section on *Sight records* in which records were listed from Midway Atoll, Hawaii, in December 1959 and again in December 1961, and records of what could have been the same bird from the northeastern beach of Eastern Island (Fisher 1965). Fisher (*ibid*) says that the first two sightings were thought to be this species, but that the latter was a "positive" identification. He then went on to complain about the treatment of the Oregon and California records saying that "despite the fact that these records have been discredited for one reason or another, the evidence against their acceptance seems to rest primarily on the fact that the occurrence was just too far away from the known range!" The species is not easily confused with any others of the North Pacific and its appearance there is no more surprising than is that of other "south-of-the-equator birds." AOU (1983) and again in the 7th edition of the Check-list (1998) dignified Fisher's rant regarding the 19th century records: "for a conflicting opinion, see also Fisher, 1965, Condor, 67, pp. 355-356). The only thing clear from Fisher was that either he didn't read Stone (1930) or Grinnell and Miller (1944), or chose to ignore what they said. It is interesting that Pyle et al. (2021) made no mention of the Midway records. I contacted Peter about this, and he said (in litt., 6 March 2022): "We do cover Fisher's reports at our monograph [on Hawaii]. As I recall either myself or my dad petitioned the AOU (probably Banks) to remove it from the main list, which he did for the AOU Checklist. You are right in that I should have mentioned these records in the ABA report, but, frankly, I had forgotten about them since I have so little faith in their validity."

New Information:

An individual of this species was photographed by a fisherman off Ocean Park, Washington, on 8 December 2019. The record (including photos) was reviewed and accepted by the Washington Bird Records Committee (WBRC) in November 2020 and unanimously accepted by the ABA CLC in February 2021 (Pyle et al. 2021).

Discussion:

For both the WBRC and the ABA CLC, there were concerns about the identification of the bird and whether it could be a Southern Giant-Petrel (*M. giganteus*), and the record was reviewed by seabird experts Steve N.G. Howell and Alvaro Jaramillo. They supported the initial identification based on the color of the bill tip (dark maroon rather than pale green) which is diagnostic at all ages. Pyle et al. (2021) indicated that the "rather fresh and dark plumage (as opposed to

grizzled white feathering on the face and chin) and dark eye indicate a younger individual, perhaps in juvenile or formative plumage.” Pyle et al. (2020, 2021) included different color photos that clearly show the size of the bird in comparison to a Black-footed Albatross (*Phoebastria nigripes*) and, in Pyle et al. (2021), part of a dark morph Northern Fulmar (*Fulmarus glacialis rodgersii*) in the background. The dark bill tip is clearly visible. Pyle et al. (2021) stated that this is the first confirmed record for the North Pacific Ocean, although they indicated that another (or the same) individual was photographed about 1000 nautical miles northeast of Honolulu, Hawaii, on 2 March 2021. The latter record is outside the AOS (and ABA) area.

Recently, a record of a Southern Giant/Northern Giant Petrel was recorded in County Durham, UK. It was sight record from shore of a passing bird, but sketches and details were provided (Newsome 2021) and, remarkably, the same bird was recorded that day farther north in the North Sea in Northumberland by two observers (Sexton 2021). The observers acknowledged that views were not sufficient to determine species. This record met the criteria for acceptance (detailed in Sexton 2021) by the British Birds Records Committee (BBRC), and is a first for the UK. This record was also discussed earlier with the sketches of the Northumberland sighting by French and Holt (2020). They indicated that the record had already been accepted by the BBRC, but at the time the article was written it was still being assessed by the British Ornithologists Union Records Committee (BOURC). Although an editorial comment is included by Paul French, BBRC Chair, in Sexton (2021), there is no mention of BOURC action there or in Newsome (2020). Newsome (2021) detailed five other sightings from the UK and indicated that there are two other published records from Europe (France and the Adriatic Sea between Italy and Albania), neither of which was attributed to species because they were before the species split. They also mentioned the Washington record detailed above and stated that it is the only accepted record north of the equator. Newsome (2021) also included excellent photos of both taxa. The bill tip of *M. giganteus* looks to be about the same color as the rest of the bill, perhaps with a tinge of green. The one color photo (full frame of swimming bird) provided of *M. halli* shows a bird with only a slightly darker bill tip, less so than the one photographed off Washington. For a bird seen at any significant distance, birds with a bill tip color like this one would not seem to be identifiable.

Recommendation:

I recommend that this species be added to the Main List. The bird is obviously a giant-petrel of some sort, and the dark bill tip indicates Northern Giant-Petrel (*M. giganteus*). This record has been accepted by both the Washington Bird Records Committee (decision not yet published) and the ABA CLC (Pyle et al. 2021). It is the only valid record for North America. The previous records are all doubtful either on provenance (Townsend’s Oregon record) or identification (California and Hawaii records). In any event none of the previous records, even if they were *Macronectes* (presumably the Townsend record is of this genus), are identifiable to species.

Placement on Checklist:

In Clements et al. (2021), Northern Giant-Petrel precedes Northern Fulmar (*Fulmarus glacialis*). The ABA CLC (Pyle et al. 2021) has tentatively placed it here. Dickinson et al. (2014) also place it here.

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Submitted by: J. L. Dunn

Date of Proposal: 5 March 2022

Add *Turdus naumanni* (Naumann's Thrush) to the Main List

Background:

In 2020, the NACC (Chesser et al. 2020), following most recent taxonomic treatments, split *Turdus naumanni* into two monotypic species: *Turdus eunomus*, retaining the English name of Dusky Thrush, and *Turdus naumanni*, with an established English name of Naumann's Thrush. All accepted records for North America of this group (mostly from Alaska but extending south to British Columbia and Washington) were of this species. In the 61st Supplement (Chesser et al. 2020) under **Notes**, stated that “a report of a vagrant individual of *T. naumanni sensu stricto* in Alaska (Gambell, St. Lawrence Island, 5 June 2015; photos, Lehman 2019) is under consideration by the Alaska Checklist Committee.” The rest of this proposal largely concerns this photo-documented (but with no specimen) record. For transparency, I have been actively and methodically involved with this record and was part of the sighting late on the night (it never gets dark on that date and latitude!) of 5 June 2015.

The Gambell record of 5 June 2015:

Rather late in the evening of 5 June 2015, a couple of participants of our *Wings* tour reported a dull individual of the genus *Phylloscopus* in the “Far Boneyard” at the base of the mountainous ridge to the east of the village of Gambell, St. Lawrence Island, Alaska. Although we did not re-find the bird that evening, it was found and identified the next morning as a Common Chiffchaff (*P. collybita*) that showed the characters of eastern form *tristis*, the “Siberian Chiffchaff.” While searching late on the night of the 5th, Rich Hoyer spotted a bright *Turdus* thrush which he tentatively identified as an American Robin (*Turdus migratorius*). This species is casual on Gambell in spring and very rare in fall (Lehman 2019). Both Gavin Bieber, my other co-leader, and I (also present) were skeptical. We soon obtained views of the bird, particularly when it perched for an extended period of time at one location on the side of the mountain. It was here that it was photographed. It was tentatively identified as a Dusky Thrush and showed the characters of *naumanni*, but I knew there were issues of intergradation between *T. n. eunomus* and *T. n. naumanni*, and I was not fully aware of the appearance of these intergrades.

Although others had split these two taxa as separate species, the NACC did not consider the issue until 2020. I eventually worked out a path forward with Daniel D. Gibson, first submitting a motion for the split to AOS, and agreeing that if it passed, the Alaska Checklist Committee would consider this record, the best substantiated of the three Alaska reports of *T. n. naumanni*. Prior to their consideration, I had sent the photos (all showing the front of the bird) to Per Alström on 7 March 2017. On 28 July 2017, Per responded saying in part: “Apologies for not replying to your original email. It had sedimented down below hundreds of other unread emails, and I had not even seen it (until now), when I searched for it. The Gambell thrush does indeed look like a pure Naumann's. Although it is little difficult to be absolutely certain based on [the] strongly cropped photos, I cannot see any indications of hybrid origin. In combination with your observations of the wings and tail, I would feel pretty happy to call this a Naumann's.”

Per's comments continue: "I do not have a firm opinion on the taxonomy of these birds. They are obviously very closely related and recently diverged, so any treatment is subjective. Birds with intermediate plumage between Naumann's and Dusky are VERY common around Beijing in winter, so based on that, interbreeding seems to be pretty common. I presume you got my Colston's and Lewington's European rare birds guide. If I remember correctly, we discuss the variation quite a bit." I have that guide, and although they treat them as subspecies, they give separate accounts. They don't illustrate or describe the intergrades but do comment under the notes of Naumann's: "Intermediates between Naumann's and Dusky Thrushes are frequently seen, showing the full range of intermediate characters" [Lewington, P. Alström and P. Colston. 1991. A Field Guide to the Rare Birds of Britain and Europe. HarperCollins Publishers].

The Problem of the photos and New Information:

Although a number of photos were taken with the bird facing us, showing the coloration and pattern of the underparts, and the upperparts were well seen (plain upperparts, including the wings), the upperparts did not show in the photos. Pure Naumann's are normally quite plain and non-contrasting above, whereas Dusky shows a prominent (duller on females) rufous panel on the wings (coverts and flight feathers) that contrasts with the back. Dunn and Bieber also noted the distinctly reddish outer tail feathers, visible in flight when the bird spread its tail prior to landing. This is another distinct feature that separate the two taxa. Because no photos were available that showed the dorsum, the Alaska Checklist Committee decided (two circulations) to put the species on the "Unsubstantiated List" in 2020.

After consultation with D.D. Gibson, Dunn wrote Pavel Tomkovich on 26 January 2021 to inquire about the extensive collection of both Dusky and Naumann's Thrushes, plus hybrids (27, or 15% of the total collection of these specimens) at the Zoological Museum of Moscow University (information from Clement 2000). I was curious if any of these hybrids had underparts that were essentially solid rufous red with no black scaling, which is characteristic of Dusky. Clement 's (2000) account of these two taxa is quite detailed and contains much information about hybrids, supplying information on intergrades at the Zoological Museum of Moscow University. He (*ibid*) described *naumanni*-like variations with the feathers of the breast usually having black centers with whitish fringes, becoming dark orange to chestnut on the lower breast, belly, and flanks. The color illustrations of hybrids (figures 121H and 121K on plate 41; illustrations by Ren Hathway) show two of the variations of hybrids, neither of which look like the Gambell bird, especially ventrally. Clement (2000) extensively discussed the appearance of hybrids; none were described as looking like the Gambell bird, particularly with regard to the appearance of the breast.

Some two weeks after I had sent the photos to Pavel, Dan Gibson sent me three additional photos of the Gambell thrush by James Levison, one of which showed the bird from the side, and although it is not razor sharp and not close, it does not show any rufous color on the wings. This photo, along with one of Rich Hoyer's photos, was published in Pyle et al. (2021). Hoyer's image was earlier published in Lehman (2019). I forwarded these new images by Levison to Pavel, who responded to me on 12 February and said in part: "It seems to me from this your e-mail that my previous message has not reached you. In brief, I forwarded your request to my museum colleague, Dr. Yaroslav Red'kin ... who studies passerines (my skills in shorebirds are

not very helpful in the case with thrushes). However Yaroslav was off for two weeks. I'll remind him soon about your interest in hybrids of thrushes; hopefully he will respond [to] you soon."

On 25 February 2021, Pavel sent another email to me. It says: "It took some time before Dr. Yaroslav Red'kin was able to check the collection in the Moscow Zoological Museum in search of thrushes similar with the bird seen at Gambell, St. Lawrence Island in June 2015. Being afraid of his poor English, Yaroslav asked me to express for you his opinion about his findings. It is rather simple. His conclusion is that the bird under question is a phenotypically pure Naumann's Thrush *Turdus naumanni*, but taking into account the lightly colored throat of the bird it is most likely in the age of one year. Yaroslav took photos (see attached) of similarly colored specimens of the same season in the museum; they originate mostly from the central and southern Yakutia (=Sakha) Republic in Siberia within the breeding range of the Naumann's Thrush. The photos also show a rather large variation of individual variation in the color of their plumage. Hopefully this information is helpful to you and the Alaska Checklist Committee for a decision."

Based on the new information, the Alaska Checklist Committee accepted (with one dissenting vote) the Gambell record in March 2021. This record will be published next year in *Western Birds* in a report that will cover multiple years. On 6 March Dan Gibson shared with me the draft account:

Turdus naumanni Temminck, 1820 {type locality: Silesia and Austria ... Hungary (Ripley 1964)}. Naumann's Thrush. Breeds in Siberia from mid-Yenisei valley to upper Lena basin, south to Baikal, n. Mongolia. Monotypic (Dickinson and Christidis 2014). **FIRST ALASKA RECORDS:** one bird observed 22 Oct 1982 at Adak Island, Aleutian Islands (C. F. and M. Zeillemaker, color sketch AKCLC); one bird observed 20-22 May 2000 at Attu Island, Aleutians (S. C. Heintz and others, digital photo by B. Carlson); and one bird observed, 5 Jun 2015 at Gambell, St. Lawrence Island (J. L. Dunn and others; five digital photos by R. C. Hoyer, one published—see Lehman 2019:268; and photos [AKCLC] by J. D. Levison). **NOTES:** Following elevation of *T. naumanni* to species from subspecies status by Chesser et al. (2020:18), the AKCLC—concerned that the possibility of hybrids with the closely related Dusky Thrush *T. eunomus* could not be eliminated by the available photos—added this species to the unsubstantiated list based on the three reports above. That decision was superseded after additional photos and a second 2021 vote, which added the species to the AKCL. No Alaska specimen.

The ABA CLC normally follows the decisions of state and provincial committees. One member of the ABA CLC, David Sibley, had asked to review the record, despite the AK CLC decision. This was pended when the Chair of ABA CLC was informed that the record, with the new photos, was being evaluated by Russian ornithologists familiar with this species. Once the AK CLC accepted the record, the ABA CLC followed suit and accepted the record unanimously in June of 2021 (Pyle et al. 2021).

Recommendation:

I recommend that the species be added to the Main List based on the Gambell record, but note that the AKCLC also now accepts two other records from the central (fall) and western Aleutians

(spring). These records are detailed by Gibson and Byrd (2007). I note from Pyle et al. (2021) that four reports are mentioned of Naumann's Thrush. The AKCLC totals three, so one additional sighting must be involved. It is perhaps from the Pribilof Islands in spring, and I remember G. Bieber mentioning a sighting to me from there. I suggest following the AKCLC.

Placement on checklist:

Pyle et al. (2021) noted that Clements et al. (2021) and the official list of British Birds place Naumann's Thrush after Dusky Thrush. On the other hand, Dickinson and Christidis (2014) and HBW (del Hoyo et al. 2010) placed Naumann's before Dusky Thrush.

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Submitted by: J. L. Dunn

Date of Proposal: 5 March 2022

Treat *Pharomachrus costaricensis* as separate species from *P. mocinno* (Resplendent Quetzal)

Background:

The Resplendent Quetzal (*Pharomachrus mocinno*) is a difficult species to study due to its restricted distribution in cloud forests of seven countries in Mesoamerica, and its conservation status. The two subspecies (*mocinno* and *costaricensis*) were described more than 150 years ago based on their plumage differences and allopatric distribution, and they were recognized as subspecies by Ridgway (1911), Cory (1919), Johnsgard (2000), Collar (2001), Forshaw & Gilbert (2009), and del Hoyo & Collar (2014). The NACC previously rejected a proposal to treat *mocinno* and *costaricensis* as separate species (2019-A-11), in part because of the lack of data on vocalizations, but a new study focusing on vocal data (Bolaños-Sittler et al. 2020) was recently published.

Using sequences of the control region of mitochondrial DNA, Solórzano et al (2004) recovered two reciprocally monophyletic clades corresponding to each subspecies and proposed that each subspecies be considered as an evolutionarily significant unit. Their data indicated a strong population subdivision ($F_{ST} = 0.37$) among subspecies. Although not mentioned in their Figure 2, a genetic distance of 2% or more was found. Their haplotype network also showed a difference of seven mutations between both clades in a fragment of 255 bp.

Solórzano & Oyama (2010) analyzed eight morphometric variables in museum specimens of 41 quetzals: body length, tarsus and wing chord, length, width, and depth of the bill, body weight, and in the case of the males, length of the long upper-tail covert feathers. Their multivariate analyses reported greater mass, longer wings, broader and deeper bill, and longer uppertail coverts in the northern subspecies. They also expanded their previous genetic work to four mitochondrial fragments (control region, subunit ND6, and tRNA^{Glu} and tRNA^{Phe}). Genetic differentiation showed two groups within *P. mocinno* that corresponded to the subspecies. According to their calculations, gene flow between subspecies was interrupted at least three million years ago. They proposed that *P. mocinno* should be divided in two species: *P. mocinno* (northern species, from Mexico to Nicaragua) and *P. costaricensis* (southern species, Costa Rica and Panama). The two taxa were diagnosable at 32 nucleotide positions (seven variable sites in ND6, one in tRNA^{Glu}, 23 in control region and one in tRNA^{Phe}). The estimated net distance of Nei was approximately 2%.

A study of width and length of the uppertail coverts of 73 adult male specimens in European ornithological collections by Schulz and Eisermann (2017) reaffirmed the sizeable difference in this character in these two populations, and suggested that they be considered species. Their paper prompted the 2019 NACC proposal, which did not pass.

New Information:

A reanalysis of the genetic data for these taxa in GenBank provided a 3.1% difference in the control region (Bolaños-Sittler et al. 2020). These authors also provided new evidence from vocalizations showing that *mocinno* and *costaricensis* have vocal differences indicative of species status.

A total of 36 individual territorial song recordings (*P. m. mocinno*, n = 21; *P. m. costaricensis*, n=15) was assembled for this species, and 21 recordings of four other species in the genus *Pharomachrus* were also included, for a total of 57.

Figure 1 shows the origin of the samples and taxa included in the study:



Figure 1. Map of Central America and north of South America showing the sites of recordings of *Pharomachrus* species and subspecies used for the comparative analysis (Google® background). Picture of *P. m. mocinno*, approximate body length 41 cm (picture reproduced with the authorization of Ricky Lopez).

Twenty two variables were obtained from the two successive notes of the syllable: note duration (s), inter-note separation (s), peak frequency (the frequency of highest energy, Hz), center frequency (Hz), highest and lowest frequencies (Hz), first and third frequency quartiles (the

frequencies that divide the selection into frequency intervals containing respectively 25% and 75% of the energy, Hz), frequency inter-quartile-range (difference between the first and third frequency quartiles), inter-syllable separation (s), and frequency modulation (FM). Acoustic differences among all taxa were examined with multivariate analyses and machine learning techniques.

Spectrograms of the typical territorial vocalizations of each *Pharomachrus* taxon were shown in Figure 3:

The differences found between the subspecies were mostly in frequency parameters.

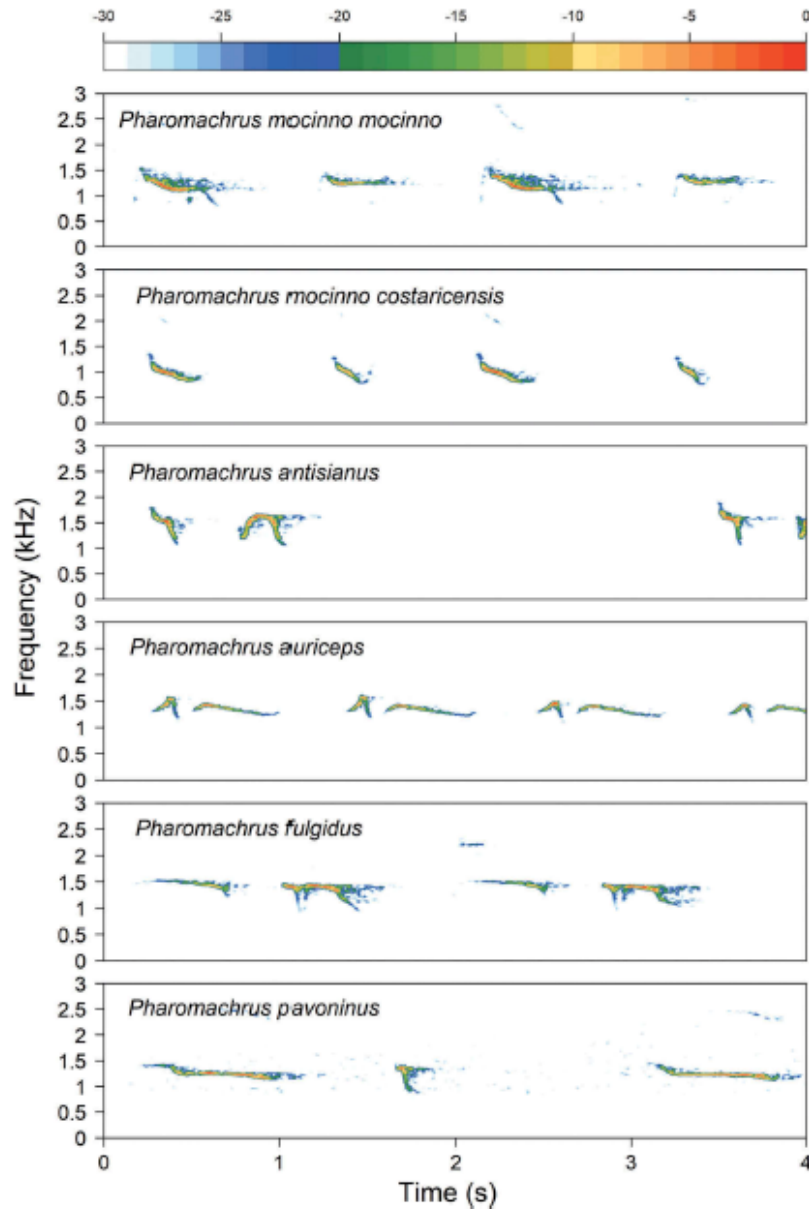


Figure 3. Spectrograms of the territorial vocalisation of *P. m. mocinno*, *P. m. costaricensis*, *P. antisianus*, *P. auriceps*, *P. fulgidus* and *P. pavoninus* (Sound recordists in the same order: P. Bolaños, L. Baptista, C. Marantz, V. Emanuel, M. Robbins, P. Boesman) (short-time Fourier transform parameters: Hanning window made of 2048 samples and 87.5% of overlap between successive windows). The vocalisation were aligned to fit into a 4 s window to allow temporal comparison.

The first two axes of the PCA, explaining 61.17% of the total variance are depicted in Figure 4, showing the difference between *P. m. mocinno* and *P. m. costaricensis*:

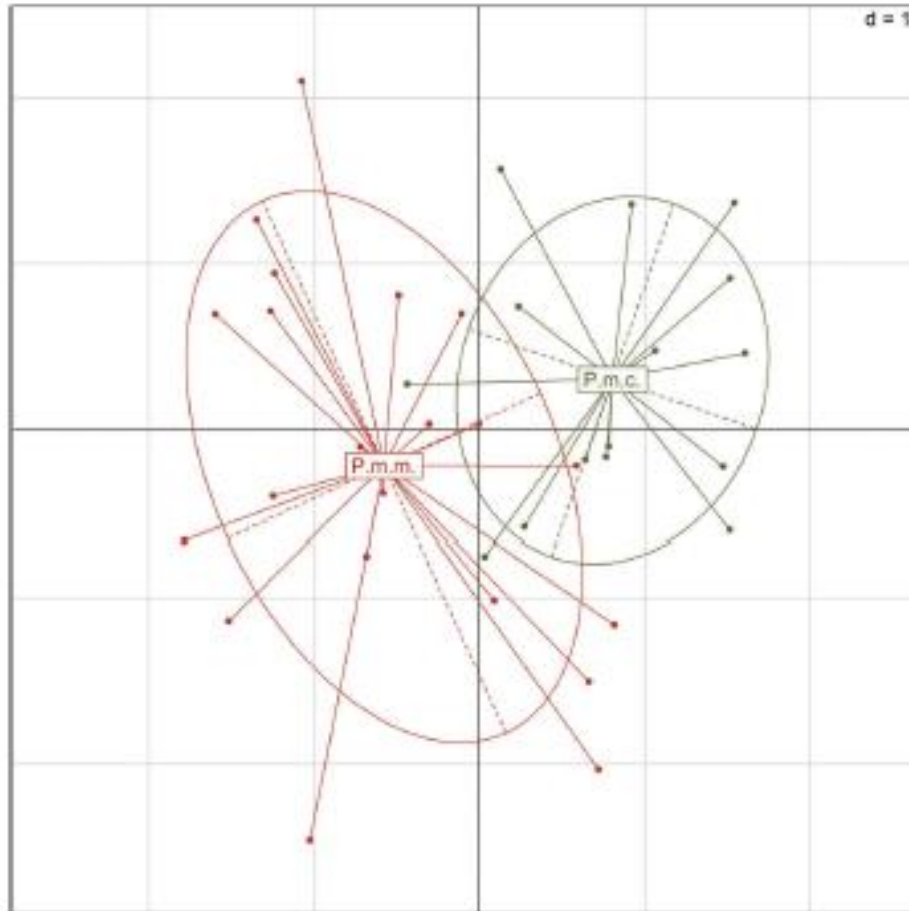


Figure 4. Principal Component Analysis (PCA) projection showing the space defined by the two first principal axes that explained 61.17% of the total variance. Each point corresponds to a single individual. *Pharomachus mocinno mocinno* (P.m.m.) individuals are indicated in red and *P. m. costaricensis* (P.m.c.) individuals in green. The ellipses surround the centroid of each taxa and delimit 67% of the vocalisation that are expected to be associated with each taxa.

Plotting the PCA scores with respect to latitude did not indicate that the territorial songs intergrade and did not show any trend according to latitude within each sub-species:

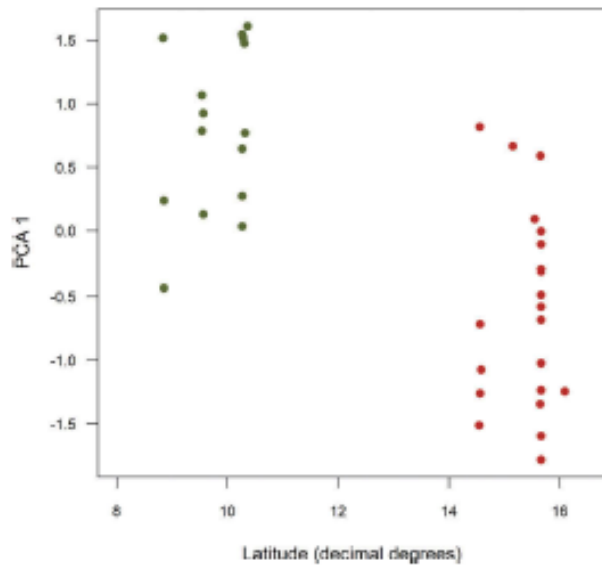


Figure 5. Scores obtained from principal component analysis (PCA) based on 22 acoustic measurements of the song of *P. m. mocinno* (red dots) and *P. m. costaricensis* (green dots), plotted as a function of latitude (total individuals is 21 *P. m. mocinno* and 15 *P. m. costaricensis*). The gap in latitude between 11° and 13° is a gap in the distribution of *P. m. mocinno* related to the lowlands of Nicaragua.

To test how well the 22 acoustic features could correctly classify *P. m. mocinno*, *P. m. costaricensis*, and the closely related species, two supervised classification methods were applied, a multiclass linear discriminant analysis (LDA) for the subspecies comparison (Fisher 1936 in Bolaños-Sittler et al. 2020), and a balanced random forest analysis (RF) (Breiman 2001 in Bolaños-Sittler et al. 2020) including the subspecies and the other *Pharomachus* species.

The LDA obtained from the PCA scores showed a clear differentiation between *P. m. mocinno* and *P. m. costaricensis*. The confusion matrix returned an 89.88% correct classification (*P. m. mocinno* 19 of 21 individuals assigned correctly, *P. m. costaricensis* 13 of 15 individuals assigned correctly), and exceeded the correct classification expected by chance (χ^2 test, d.f. = 1, $\chi^2 = 18.37$, $p < 0.001$) (Table 1):

Table 1. LDA confusion matrix used to classify the species belonging to *P. m. mocinno* or *P. m. costaricensis*, based on 22 acoustic measurements of the territorial vocalisation (21 individuals for *P. m. mocinno* and 15 individuals for *P. m. costaricensis*).

	<i>P. m. mocinno</i>	<i>P. m. costaricensis</i>
<i>P. m. mocinno</i>	92.86	0.07
<i>P. m. costaricensis</i>	13.1	86.9

The acoustic features of the two subspecies of *Pharomachrus mocinno* are given in Table 2:

Table 2. Characteristics of the territorial vocalisation of *P. m. mocinno* and *P. m. costaricensis* (21 individuals for *P. m. mocinno* and 15 individuals for *P. m. costaricensis*). Mean \pm SD (range).

Acoustic Feature	<i>P. m. mocinno</i>	<i>P. m. costaricensis</i>
Inter note separation (s)	0.53 \pm 0.12 (0.08–0.65)	0.63 \pm 0.12 (0.41–0.82)
Inter syllable separation (s)	0.68 \pm 0.16 (0.38–1.01)	0.6 \pm 0.09 (0.4–0.73)
Note 1		
Duration (s)	0.38 \pm 0.09 (0.27–0.59)	0.3 \pm 0.05 (0.23–0.39)
Centre frequency (Hz)	1094.8 \pm 99.4 (880.7–1205.9)	986.1 \pm 82.87 (865.9–1094.6)
Highest frequency (Hz)	1462 \pm 140.53 (1190–1728)	1409 \pm 182.28 (1147–1771)
Lowest frequency (Hz)	910.7 \pm 145.19 (678.8–1106)	723.6 \pm 65.75 (613–853.7)
First frequency quartile (Hz)	1051.5 \pm 102.98 (835.9–1169.1)	933.3 \pm 84.03 (816.5–1061.1)
Third frequency quartile (Hz)	1143.2 \pm 81.61 (954.3–1255.3)	1035.2 \pm 77.02 (905.6–1131.7)
Inter-quartile range (Hz)	91.76 \pm 55.9 (32.29–278.62)	101.88 \pm 40.22 (56.24–193.80)
Peak frequency (Hz)	1098 \pm 95.66 (889.3–1210.9)	991.4 \pm 84.23 (867–1109)
Negative FM (Hz)	1.65 \pm 0.43 (0.83–2.53)	1.5 \pm 0.33 (0.98–1.99)
Positive FM (Hz)	1.61 \pm 0.42 (0.95–2.49)	1.48 \pm 0.29 (1.03–1.99)
Note 2		
Duration (s)	0.34 \pm 0.09 (0.18–0.52)	0.31 \pm 0.06 (0.22–0.43)
Centre frequency (Hz)	1164 \pm 84.66 (1006–1343)	987.6 \pm 67.21 (893.6–1100.5)
Highest frequency (Hz)	1439 \pm 129.81 (1212–1643)	1324 \pm 131.78 (1154–1679)
Lowest frequency (Hz)	970.8 \pm 135.94 (731.2–1196.5)	774.9 \pm 68.65 (689.7–913.3)
First frequency quartile (Hz)	1115.5 \pm 100.73 (943.9–1319.7)	931.2 \pm 81.95 (802.1–1065.3)
Third frequency quartile (Hz)	1210 \pm 81.61 (1072–1366)	1046.2 \pm 77.02 (970.3–1134.1)
Inter-quartile range (Hz)	94.55 \pm 55.91 (30.88–343.56)	114.95 \pm 40.22 (37.49–199.95)
Peak frequency (Hz)	1168 \pm 81.47 (1036–1354)	992.8 \pm 68.29 (881.2–1108.4)
Negative FM (Hz)	1.64 \pm 0.49 (0.63–2.53)	1.54 \pm 0.32 (1.01–2.1)
Positive FM (Hz)	1.66 \pm 0.49 (0.66–2.6)	1.54 \pm 0.3 (1.13–2.1)

Results of the RF classification showed that the most important acoustic features to classify the *Pharomachrus* taxa were the peak and center frequency of the second note, followed by the center frequency of the second and first note (Figure 6):

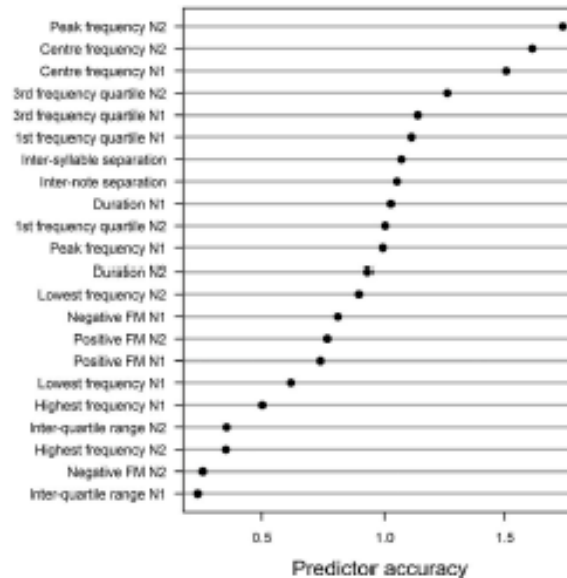


Figure 6. Random Forest analysis for *Pharomachrus* taxa. Relative importance of the explaining variables based on the mean decrease Gini impurity criteria. N1 and N2 refer to note 1 and note 2 respectively.

In Table 3, the confusion matrix built on the balanced RF classification revealed a high correct classification rate for all the species and subspecies with 81.9% for *P. m. mocinno* (17 of 21 individuals assigned correctly), 86.67% for *P. m. costaricensis* (13 of 15 individuals assigned correctly), 100% for *P. antisianus* (7 of 7 individuals assigned correctly), 100% for *P. auriceps* (6 of 6 individuals assigned correctly), 75% for *P. fulgidus* (3 of 4 individuals assigned correctly), and 100% for *P. pavoninus* (4 of 4 individuals assigned correctly) (Table 3). All rates exceeded classification expected by chance (χ^2 test, d.f. = 25, $\chi^2 = 221.1$, $p < 0.001$).

Table 3. RF confusion matrix used to classify the species belonging to *Pharomachrus* genus (total individuals is 21 for *P. m. mocinno*, 15 for *P. m. costaricensis*, 7 for *P. antisianus*, 6 for *P. auriceps*, 4 for *P. fulgidus*, 4 for *P. pavoninus*) on the basis of 22 acoustic features. Correct classifications are underlined.

	<i>P. m. mocinno</i>	<i>P. m. costaricensis</i>	<i>P. antisianus</i>	<i>P. auriceps</i>	<i>P. fulgidus</i>	<i>P. pavoninus</i>	Class error
<i>P. m. mocinno</i>	<u>80.95</u>	14.29	0.00	0.00	4.76	0.00	0.19
<i>P. m. costaricensis</i>	13.33	<u>86.67</u>	0.00	0.00	0.00	0.00	0.13
<i>P. antisianus</i>	0.00	0.00	<u>100.00</u>	0.00	0.00	0.00	0.00
<i>P. auriceps</i>	0.00	0.00	0.00	<u>100.00</u>	0.00	0.00	0.00
<i>P. fulgidus</i>	25.00	0.00	0.00	0.00	<u>75.00</u>	0.00	0.25
<i>P. pavoninus</i>	0.00	0.00	0.00	0.00	0.00	<u>100.00</u>	0.00

In particular, they

found a difference in the acoustic parameters of *P. m. mocinno* and *P. m. costaricensis*, similar as it has been reported for other learning and non-learning species where species status has been promoted (Cadena and Cuervo 2010; Millsap et al. 2011 [same geographic barrier]; Sandoval et al. 2014, 2017). The correct classification between the two taxa was high as revealed by the LDA classification and confirmed by the RF classification among all *Pharomachrus* taxa. In the particular case of the RF, the classification of the sub-species was slightly less successful than the classification of the other species except for *P. fulgidus* that included only four individuals. (p. 664)

They also noted, “Moreover, plotting the discriminant function scores with respect to latitude did not reveal trends that would suggest intergradation” or a cline.

The authors argued that these differences in acoustic parameters have been found in other species that have been elevated to species status, that the classification with the LDA was very high, and that results were similar for the RF analysis. In addition, the discriminant values did not show any latitudinal trend.

Recommendation:

Morphological differences between the two Resplendent Quetzal subspecies were recognized from the beginning, and recently were shown to be significant not only for male tail length but also for width of adult male uppertail-coverts (Schulz & Eisermann 2017), in addition to reports

of greater mass, longer wings, broader and deeper bill, and longer uppertail-coverts in the northern subspecies (Solórzano & Oyama 2010). For females, several genetic studies using mitochondrial DNA also showed clear separation of 3.1% (Bolaños-Sittler et al. 2020).

The acoustic differences between *P. mocinno* and *P. costaricensis* are in agreement with the morphological differentiation (LaBastille et al. 1972; Solórzano and Oyama 2010; Schulz and Eisermann 2017), and with the mitochondrial differentiation, in which a lack of a shared haplotypes implies no female mediated gene flow (Solórzano and Oyama 2009) and which establishes the absence of contact due to an important geographical and climatic barrier, of at least 3 My.

The comments of the NACC on the 2019 proposal recognized the contributions of the morphological and genetic studies, but the discussion dwelt mainly on whether the two allotaxa deserved species status under the BSC or whether they were phylogenetic but not biological species. Several committee members suggested that a vocal study comparing all quetzal species, which Bolaños-Sittler et al. (2020) have now provided, would be key to determining species status under the BSC.

I consider the data on phenotypic diagnosability, reciprocal monophyly, and mechanisms of reproductive isolation (vocalizations) to be sufficient to indicate species status for *P. m. mocinno* and *P. m. costaricensis*, in light of other examples in which this level of differentiation resulted in species status.

I recommend that the committee vote YES to treat *Pharomachrus mocinno* and *P. costaricensis* as separate species.

Suggested English names for the species are:

Pharomachrus mocinno de la LLave: Resplendent Quetzal or Northern Resplendent Quetzal
Pharomachrus costaricensis Cabanis: Costa Rican Quetzal or Southern Resplendent Quetzal

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Submitted by: Patricia Escalante, Instituto de Biología, Universidad Nacional Autónoma de México

Date of Proposal: 9 March 2022

Add *Pygochelidon cyanoleuca* (Blue-and-white Swallow) to the U.S. List**Background:**

The Blue-and-white Swallow is a Neotropical species with two groups (AOU 1998): the northern nominate group is found from in the foothills and highlands of Costa Rica (northwest to the Cordillera de Guanacaste) and western Panama (Chiriquí, Veraguas, and western Panamá province); and in South America from Colombia, Venezuela, Trinidad, and the Guianas south (except in central Amazonia) to northwestern Argentina, Paraguay, Uruguay, and southern Brazil. The migratory southern group (*patagonica*) breeds from central Chile and central (possibly north-central) Argentina south to Tierra del Fuego, with a disjunct resident population in coastal Peru. It winters from northern Chile and northern Argentina north regularly to northern South America and central Panama (west to the Canal area), casually to Nicaragua, Guatemala (sight report), and Chiapas, Mexico.

Record in the United States:

Blue-and-white Swallow

Date(s): 20-21 July 2020.

Location: south of Progreso, Hidalgo County, Texas.

Discovered by: Dan Jones.

Other Observers submitting documentation: Mary Beth Stowe (on 21 July 2020).

In December 2020 the Texas Ornithological Committee accepted this species to the state list based on a record of a first-cycle male present in Progreso Lakes, Hidalgo County, 20–21 July 2020 (Pyle et al. 2021). Its identification was supported by several expert opinions from those familiar with this South American species. The ABA-CLC accepted this record (#2020-09) in March 2021. Photographs of the bird accompanying the record (e.g., Fig. 5 in Pyle et al. 2021) were not ideal and caused one ABA-CLC member to prefer better documentation before accepting this species. However, the relative ease of identification (see Fig. 5), expert opinions, and the status of this species as a long-distance migrant that had been anticipated to occur in the ABA Area combined to be enough for seven members to vote for its addition, and the dissenting member did not wish to consider the record further.

Original posting on the internet generated lots of discussion, with near unanimous agreement with the identification of Blue-and-white Swallow. I have posted most of these discussions below, both in links to webpages and as files in our Google Drive.

Outside opinion for the TOC (especially Dan Lane):

<https://www.facebook.com/groups/357272384368972/permalink/3054889087940608> (or see file in Google Drive)

Kenn Kauffmann, Alvaro Jaramillo:

<https://www.facebook.com/kenn.kauffman/posts/10217605457145091> (or see file in Google Drive)

Add *Elaenia parvirostris* (Small-billed Elaenia) to the Main List**Background:**

The Small-billed Elaenia is a South American austral migrant, breeding in Bolivia, Argentina, Uruguay, Paraguay, and wintering in the breeding range but also ranging north in winter through northern South America east of the Andes. This proposal deals only with a 2012 record from Chicago, Illinois. In 2021, three new records were attributed to this species (17 May at Mustang Island Texas, 26 November – 7 December at Waukegan Beach, Illinois; and 26 October at Observatoire d'oiseaux de Tadoussac, Quebec (photos of these other birds are on eBird).

First record in the United States:

Small-billed Elaenia (*Elaenia parvirostris*)— 17-22 April 2012, Chicago, Illinois.

ABA-CLC Record #2020–04 (First Circulation: 6–2, Jun 2020; 5–3 Aug 2020; 5–3, Sep 2020; Second Circulation: 8–0, Sep 2021: Pyle et al. 2021). In 2020 the ABA-CLC did not add this migratory South American species to the *ABA Checklist*, despite its acceptance by the Illinois Ornithological Records Committee (IORC) in Mar 2020 (Pyle et al. 2020). The ABA-CLC was concerned that White-crested Elaenia (*Elaenia albiceps*), which can be difficult to distinguish from Small-billed, was not fully eliminated, although all members agreed that the identification of Small-billed was likely correct. Following publication of a paper clarifying the identification of these two species (Gorleri and Areta 2022), the ABA-CLC solicited the comments of Fabricio C. Gorleri, as well as Alvaro Jaramillo, each of whom provided lengthy commentary supporting the identification. The presence of white tipping to the lower row of lesser coverts (forming a “third wing bar”) is diagnostic to Small-billed Elaenia, especially on birds in worn formative plumage, as was the case with the Illinois bird (see Pyle et al. 2020 for further discussion and a photograph).

The body of work used by the IORC is included in the Google Drive (Proposal Sets > 2022 > 2022C > SBEL) and includes extensive comments from many experts on South American birds, including Terry Chesser and Doug Stotz. Pay particular attention to the comments of Bret Whitney, who stuck to his guns with his identification of the bird as *Elaenia albiceps*. Alvaro Jaramillo, among others, provides rebuttal. Note that these comments were made prior to the publication of Gorleri and Areta (2022). This paper is provided in the Google Drive, and Gorleri's comments are also included in the Google Drive.

I have put ten or so instructive images in the Google Drive folder. These were culled from over 150 photographs of the bird were included in the package assessed by the IORC. These can be seen at: http://geoffwilliamson.info/iorc/iorc2012_files/2012-007.html (username: abaclc; password: Elaenia).

Recommendation:

I recommend adding this species to the Main List; current sequence in the SACC has it placed after *Elaenia albiceps*.

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Submitted by: Andrew Kratter

Date of Proposal: 15 March 2022

Treat *Saxicola rubicola* and *S. maurus* as separate species from *S. torquatus* (Common Stonechat)

Note: This is a slightly revised version of Proposal 2021-A-11, which in turn was an updated version of Proposal 2014-B-11. The 2014 proposal was rejected 5-4 in favor of the status quo (no split) vs. a three-way split of *Saxicola torquatus* into *S. torquatus*, *S. rubicola*, and *S. maurus*. We reconsidered the case in 2021 because of new evidence indicating sympatry between the *rubicola* and *maurus* groups in the Western Palearctic (Shirihai and Svensson 2018, Loskot and Bakhtadze 2020) and new information on vocalizations in this complex (Opaev et al. 2018).

By the time of the 2021 proposal, the Howard & Moore, Clements, and IOC lists (Dickinson and Christidis 2014, Clements et al. 2019, and Gill et al. 2020) had adopted a three- (or four-) way split of this extralimital species complex. The NACC ultimately postponed our vote on this proposal, principally due to a lack of agreement on the taxonomy among global references (the IOC list split *stejnegeri* in addition to *maurus*, and the Clements list was considering but had not adopted this additional split, whereas Dickinson and Christidis had not split *stejnegeri* and the Birdlife-HBW list had not split *torquatus* at all), but also because of the lack of an established English name for *stejnegeri* and uncertainty about the placement of subspecies *przewalskii*. The IOU's Working Group on Avian Checklists (WGAC), which was established to consolidate the various global lists, recently voted to consider *maurus* a separate species from *torquatus*, but to treat *stejnegeri* as conspecific with *maurus*. This classification will now be followed by the Clements, IOC, and Birdlife-HBW lists, bringing all global lists into agreement on this issue.

Description of the problem:

The Common Stonechat *Saxicola torquatus* (*s.l.*) is highly polytypic over most of the Palearctic (except Australasia) from the British Isles and Africa through East Asia. Although treated as a single species for many years, this has been a contentious issue for decades, and much has been written on the subject of its taxonomy and identification, especially because of the frequent appearance of vagrant "Siberian" Stonechats of the *maurus* group in western Europe. Vaurie (1959) stated that two very different populations are in contact in the Caucasus without evidence of interbreeding, but he nevertheless treated all as a single species. Sibley and Monroe (1990) briefly split *maurus* from *torquatus* (including the western European taxa), but soon thereafter retracted this treatment (Sibley and Monroe 1993), and many authors have continued to treat all taxa as conspecific (e.g., Shirihai 1996, Clement and Rose 2016, del Hoyo and Collar 2016).

Although most taxa traditionally included in *torquatus* are allopatric or parapatric in breeding distribution as far as is known (see New Information 2020 for the exception), in South Asia the marsh specialist White-tailed Stonechat *S. leucurus* occurs sympatrically with the very similar *S. torquatus indicus* throughout its much narrower range in the Indus-Ganges-Brahmaputra-Irrawaddy valleys from Pakistan to Myanmar, segregated largely by habitat. Both occur in the same sites, where they choose different microhabitats, and they do not appear to hybridize (Rasmussen and Anderton 2012). The fact that *leucurus* (which looks very like *indicus* except

for its tail) is undeniably a valid biological species is one very good reason to doubt that all other stonechats (which show a lot of morphological variation; HBW illustrated 8 taxa) are best considered conspecific.

New information (as of 2014):

Several mtDNA analyses of the stonechat complex have been published in recent years (Illera et al. 2008, Woog et al. 2008, Zink et al. 2009, van Doren et al. 2017), to add to the less complete earlier ones (Wittmann et al. 1995, Wink et al. 2002a,b). Each of these focused on a particular section of the huge range of the species complex: for example, Illera et al. (2008) were especially concerned with the Iberian population, whereas Woog et al. (2008) focused on the Malagasy, Reunion (Indian Ocean), and African populations. Zink et al. (2009) had several samples from East Asian *stejnegeri* (Parrot, 1908) but none from the South Asian taxa *indicus* (Blyth, 1847) or Sino-Tibetan *przewalskii* (Pleske, 1889); the latter has not yet been included in any study [and a Nepal “*indicus*” specimen (see below for circumstances) in Illera et al. (2008) oddly enough clustered with some Iberian birds, which were distantly related to most other Iberian birds].

Illera et al. (2008) obtained 958 bp sequences of cytb from 11 of the 12 recognized species of *Saxicola* and 15 of the 45 described subspecies, of which “14 morphologically diverse and/or geographically disjunct populations (nine subspecies) were analysed” within *torquata*. Woog et al. (2008) obtained 915 and 1041 bp sequences of cytb and ND2 of 9 taxa of *Saxicola*, 5 of them normally treated within *S. torquata*. Both Illera et al. (2008) and Woog et al. (2008) evidently used mostly blood samples, although exactly how many seems unclear. Zink et al. (2009) sequenced ND2 from 171 specimens of the *S. torquata* complex, 27 from Eurasian and 3 from African sites. I did not find a statement of sequence length in Zink et al. (2009).

The only one of these studies to include the White-tailed Stonechat *S. leucurus* was Illera et al. (2008), and that was a blood sample of a single individual taken by “Bird Conservation Nepal”, according to the Acknowledgments. The same source is responsible for the only (blood) sample of putative *indicus* in any of the studies. Given that no indication is provided as to how they were identified, or what sex/age they were (relevant because female *leucurus* are not especially distinctive), and that the *leucurus* and *indicus* cluster close together on the tree in Illera et al. (2008), further corroboration using better documented samples is needed. However, what their tree putatively shows is that *leucurus* is very closely related to some taxa of *torquatus* (not surprisingly, given their morphological and vocal similarity).

All of the most recent studies included the insular Reunion Stonechat *S. tectes* and Fuerteventura Stonechat *S. dacotiae*, and it is clear that the former (not surprisingly based on geography) is sister to the African clade(s), whereas the latter is sister to the Western Palearctic clade (again, geographically not surprisingly). Although this could be taken to show that *tectes* and *dacotiae* should be lumped within an inclusive *torquatus*, the same cannot be said for the sympatric *leucurus*.

Table 1 (see below) from Zink et al. (2009) summarizes influential recent treatments of *Saxicola torquatus*. This table does not mention Woog et al. (2008), which focuses on Afro-Malagasy

taxa, although no explanation is given in Zink et al. (2009) as to why, and the paper is cited therein.

Taken together, these studies (see figs. below) show that *S. torquatus* (s.l.) is paraphyletic with respect to the distinctive-appearing taxa long considered to be separate species, the Canary Islands or Fuerteventura Stonechat *S. dacotiae*, the Reunion Stonechat *S. tectes*, and the sympatric White-tailed Stonechat *S. leucurus*. They also confirm the existence of the following distinct clades: the West European *rubicola* group, the mainly Central Asian *maurus* group, the African *torquatus* group, the Malagasy *sibilla* group, and the NE Asian *stejnegeri*, which is especially genetically distinct and sister to the others (according to Zink et al. 2009, the only study to sample *stejnegeri*). However, this latter finding is difficult to interpret without knowledge of where *przewalskii* fits in.

Author	Number of Spp. recognized	Suggested taxonomy and comments
Cramp (1988)	1	<i>S. torquata</i> (European stonechat; 9 subspecies)
Sibley and Monroe (1990)	2	<i>S. torquata</i> (western Palearctic) <i>S. maura</i> (eastern Palearctic)
Sibley and Monroe (1993)	1	<i>S. torquata</i> (including <i>maura</i>)
Wittmann et al. (1995)	3	<i>S. rubicola</i> (European stonechat) <i>S. maura</i> (Siberian stonechat) <i>S. axillaries</i> (African stonechat)
Wink et al. (2002)	5	<i>S. torquata</i> (European stonechat) <i>S. axillaris</i> (African stonechat) <i>S. tectes</i> (Reunion Is. Stonechat) <i>S. dacotiae</i> (Canary Is. Stonechat) <i>S. maura</i> (Siberian stonechat)
Urquhart (2002)	3	<i>S. maura</i> (Siberian stonechat) <i>S. torquata</i> (African stonechat) <i>S. rubicola</i> (European stonechat)
Illera et al. (2008)	3	<i>S. torquata</i> (European stonechat) <i>S. tectes</i> (Reunion Is. Stonechat) <i>S. dacotiae</i> (Canary Is. Stonechat) Recommended further molecular studies focusing on within- and between-subspecies relationships
This study	6	<i>S. rubicola</i> (European stonechat) <i>S. maura</i> (Western Siberian stonechat) <i>S. stejnegeri</i> (Eastern Siberian stonechat) <i>S. torquata</i> (African stonechat) <i>S. tectes</i> (Reunion Is. Stonechat) <i>S. dacotiae</i> (Canary Is. Stonechat)

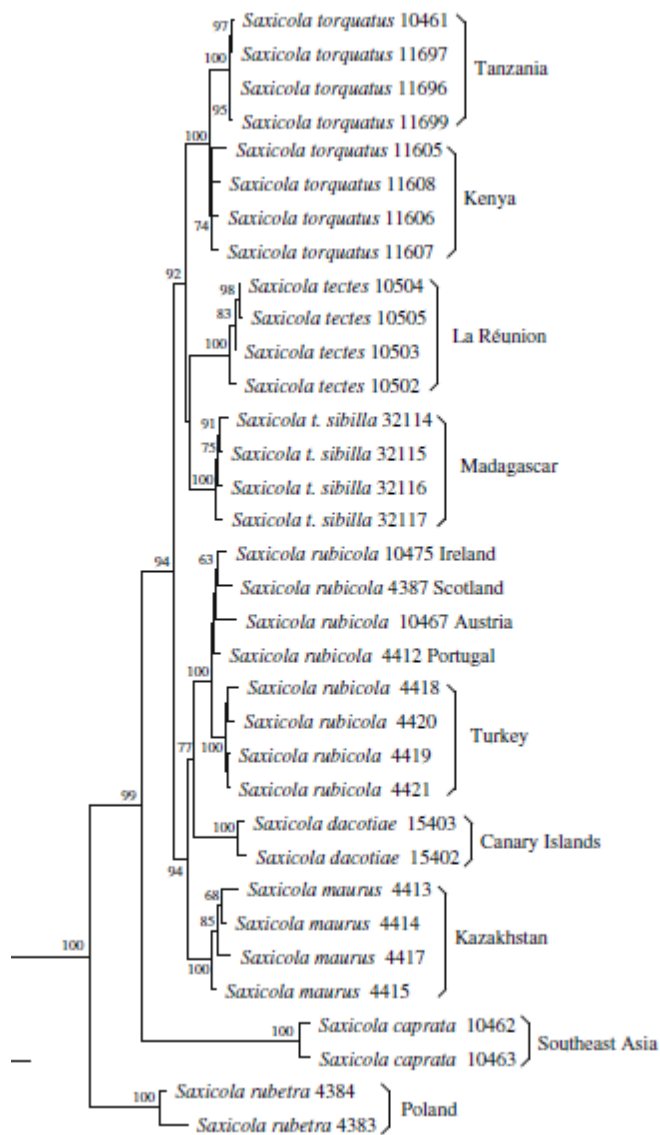


Fig. 2. Woog et al. (2008).

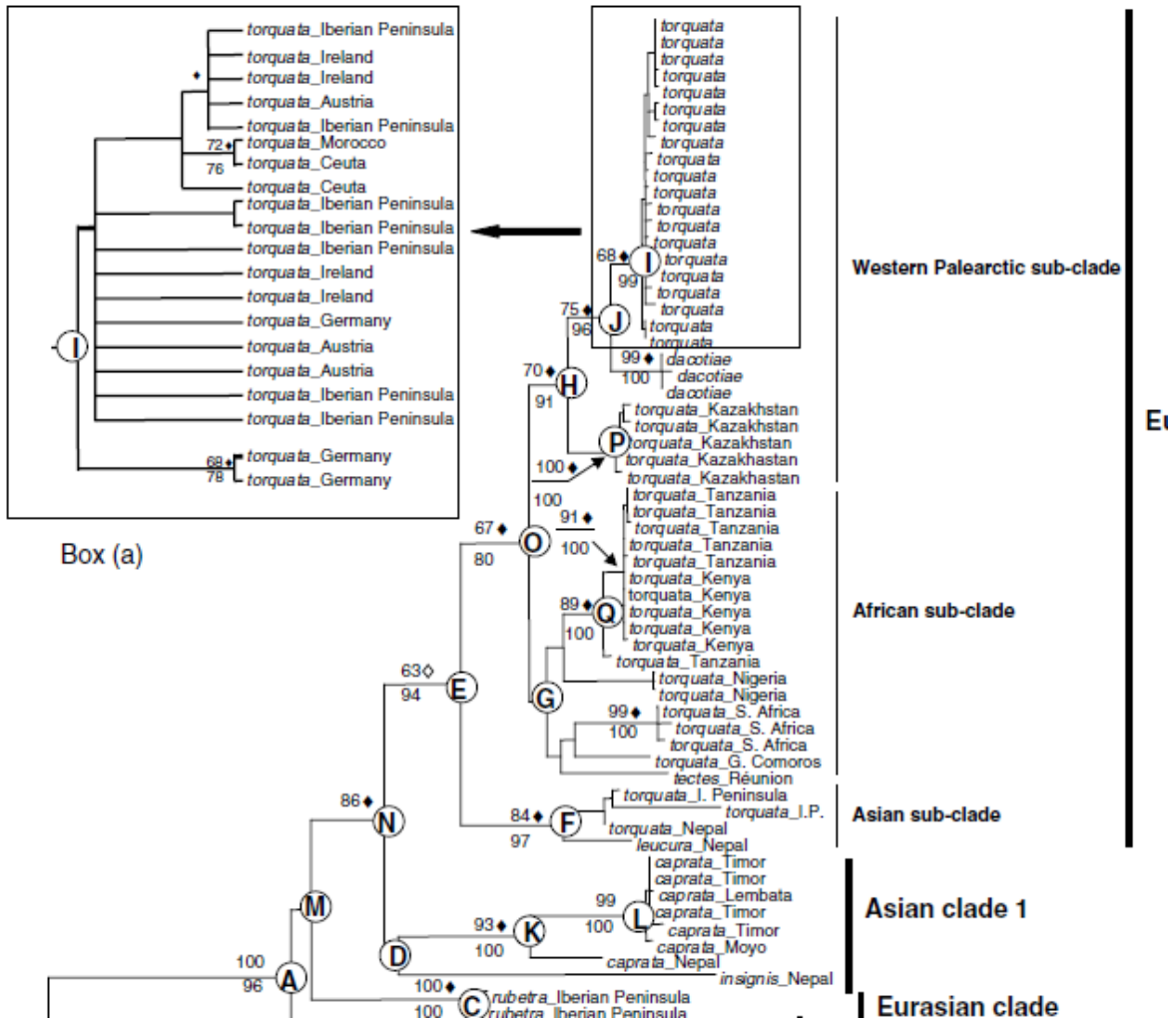


Fig. 1. Illera et al. (2008).

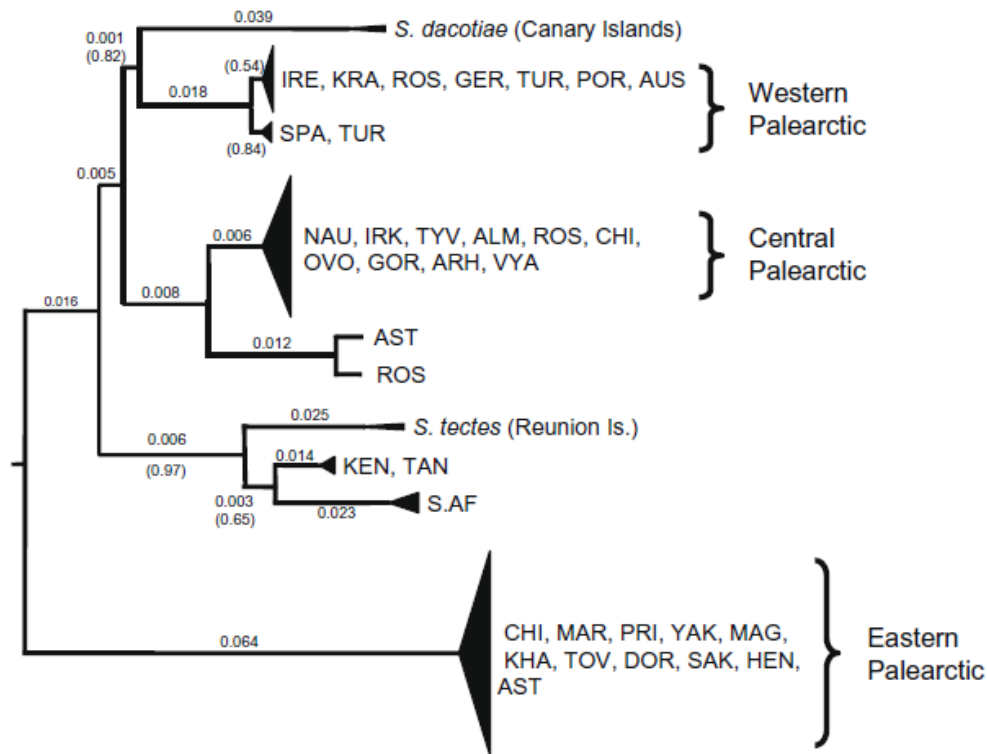


Fig. 2. Zink et al. (2009)

Subsequent treatments:

HBW (Collar 2005, and <http://www.hbw.com/species/common-stonechat-saxicola-torquatus>) and BirdLife International (<http://www.birdlife.org/datazone/speciesfactsheet.php?id=6682>; del Hoyo and Collar 2016) have refrained thus far from adopting any split of *torquatus* (*s.l.*).

In Sangster et al. (2011), *maurus* was split from the nominate and *rubicola*, but *stejnegeri* was maintained under *maurus* despite the deep divergence in Zink et al. (2009), because that paper did not include the key taxon *przewalskii*, which is morphologically quite distinct from both *indicus* and *stejnegeri* (which have a moderate level of morphological divergence between them; Rasmussen and Anderton 2012). Hence, splitting *stejnegeri* without knowing the placement of *przewalskii* is risky because *przewalskii* would have priority over *stejnegeri*, if they are united, and *indicus* over both. Rasmussen and Anderton (2012) followed the BOU on this matter.

IOC 4.1 (<http://www.worldbirdnames.org/chats-revised/>) basically followed Zink et al. (2009) by recognizing *rubicola*, *torquatus*, *maurus*, and *stejnegeri* as species, and in addition followed Woog et al. (2008) in treating Malagasy birds as a separate species. They also adopted the taxonomic recommendations of Svensson et al. (2012) concerning nomenclature of central Asian *maurus*, which was disputed by Opaev et al. (2018) and Loskot and Bakhtadze (2020).

New information (as of 2020):

Although no additional densely sampled phylogenies have been published in the years since we evaluated the 2014 proposal, major strides have been made in understanding the biology and phenotypes of the stonechat complex. Unfortunately, these studies did not include sub-Himalayan *indicus* or Tibetan *przewalskii*.

***rubicola/maurus* groups.**—Shirihai and Svensson (2018), on the basis of study of extensive museum series, over 3000 photographs, and field studies of almost all Western Palearctic taxa stated that “it eventually became clear that two morphologically diagnosable taxa coexist in NE Turkey, S Caucasus, and Transcaucasia (possibly also in extreme W Iran), *rubicola* and *variegatus*, with no intermediates evident, separated also by ecological preferences...”. Opaev et al. (2018; see map below) mentioned a zone of sympatry between *rubicola* and *variegatus* in Rostov Oblast, Russia, where “these two taxa bred in different although overlapping habitats without any signs of intergradations (Kazakov & Bakhtadze, 1999; Bakhtadze, 2002).” Loskot and Bakhtadze (2020) presented results of extensive morphological and field studies of stonechats in the Caucasus, and showed that where *rubicola* and *variegatus* occur in sympatry, *rubicola* is found mostly in drier habitats over a wide elevational range including in the mountains, whereas *variegatus* preferred more mesic and almost exclusively lowland habitats.

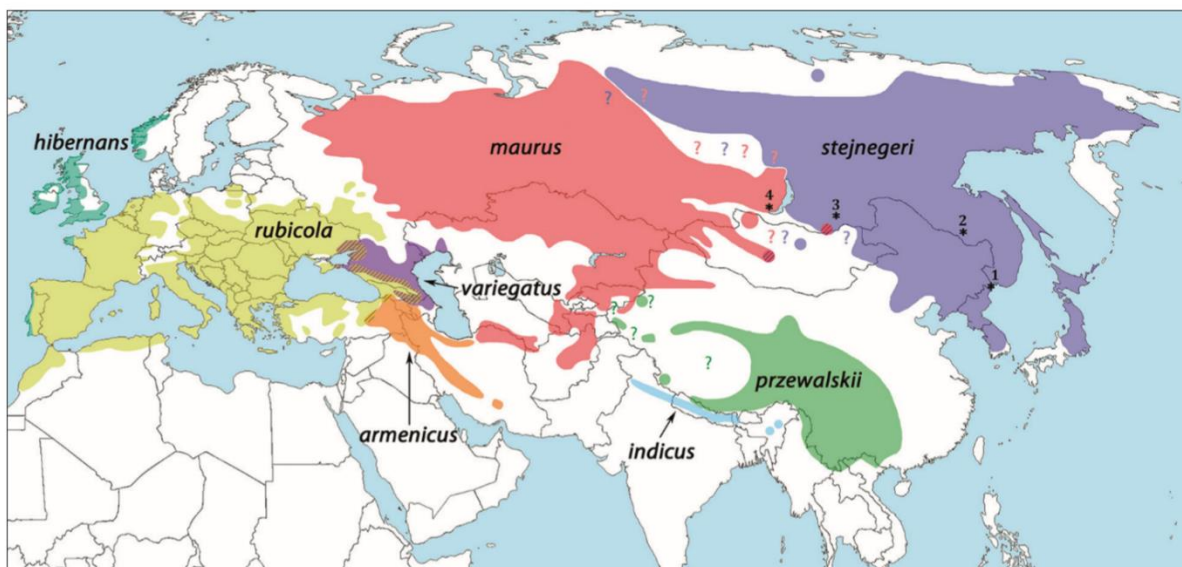


Fig. 1. Breeding ranges of the Eurasian taxa of the *Saxicola torquatus* complex. The hatched areas indicate zones of sympatry or possible sympatry. Numbers indicate the points of field work in Russian Federation: 1 – Khasan, Primorsky Krai, 2 – Khingan State Nature Reserve, Amur Oblast, 3 – Ivano-Arachleisk Nature Park, Chita Oblast, 4 – Irkutsk, Irkutsk Oblast.

From Opaev et al. (2018).

***maurus/stejnegeri* groups.**—Vaurie (1959) and Stepanyan (1990, not seen, as cited in Hellström and Norevik 2014) considered that there was a zone of intergradation between nominate *maurus* and *stejnegeri* from the lower Yenesei to the Irkutsk area, but neither author provided details. In fieldwork in parts of this area, Hellström did not find any apparent intermediate birds, and thus Hellström and Norevik (2014) suggested that the “transition from

maurus to *stejnegeri* in southern Siberia may perhaps be more abrupt (and with a lower frequency of hybridization) than implied in the literature.”

***rubicola/maurus/stejnegeri* groups.**—In a study comparing morphology and vocalizations of *rubicola*, *maurus*, and *stejnegeri*, Opaev et al. (2018) showed that both songs and calls were quite different between *stejnegeri* and the other two groups, and calls also differed between *rubicola* and *maurus*. They noted the strong congruence between the mtDNA phylogenetic results of previous authors and the results of their vocalization analyses and considered this supportive of specific status of *stejnegeri*, which they called a cryptic species.

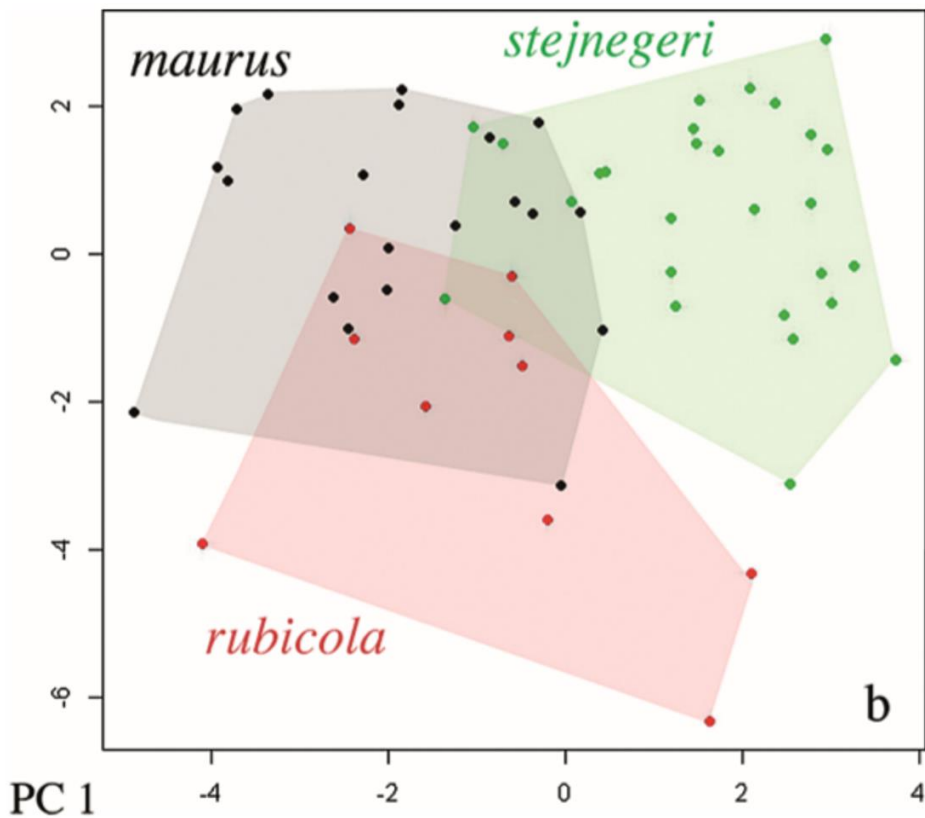


Fig. 2b of Opaev et al. (2018), a PCA of song characteristics.

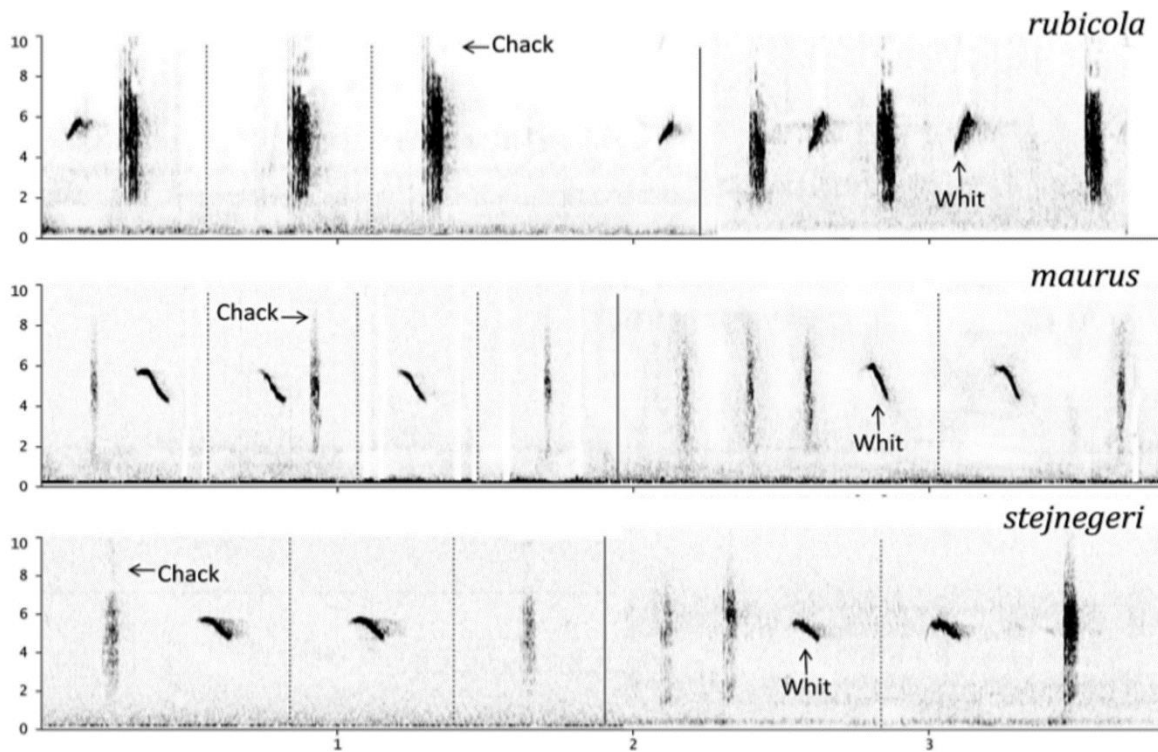


Fig. 5 of Opaev et al. (2018), showing alarm call types of the three Palearctic groups.

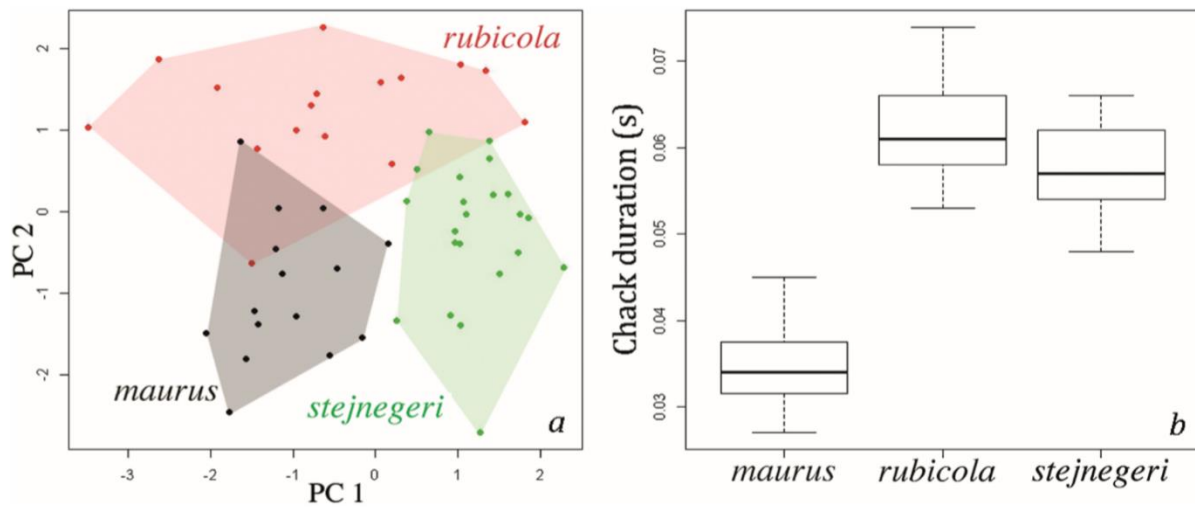


Fig. 6. PCA of four acoustic parameters of whit calls (a) and durations of chack calls (b) of three taxa of the *Saxicola torquatus* complex.

From Opaev et al. (2018).

New information (as of 2022):

The IOU's Working Group on Avian Checklists (WGAC) recently voted to treat *S. maurus*, *S. rubicola*, and *S. torquatus* as separate species, based in part on van Doren et al. (2017), who used genome-wide data to show conclusively that the distinctive *S. dacotiae* (Fuerteventura Stonechat) is embedded within the three continental forms. The WGAC, however, voted not to recognize *stejnegeri* as a separate species based on the lack of genomic and phenotypic data on other Asian forms, some of which have senior scientific names and may well be closely related to *stejnegeri*.

Effect on AOU-CLC area:

Stonechats of any taxon are very rare vagrants in the NACC area. The first North American record documented photographically was of a female in New Brunswick on 1 Oct 1983 (Wilson 1986). One slightly fuzzy photograph was published (<http://sora.unm.edu/sites/default/files/journals/nab/v040n01/p00016-p00017.pdf>) and, as noted in the original article, it fits the eastern taxon *stejnegeri*, although it could also be the Central Asian *maurus* s.s. (Wilson 1986). Because *maurus* is a frequent vagrant to western Europe (believed to be much more so than *stejnegeri*; Hellström and Norevik 2014), it seems perhaps more likely to be that rather than a Siberian *stejnegeri* having made its way all across Alaska and Canada, but it may never be possible to determine this. The Western European *rubicola* group is not highly migratory so is less likely to occur in North America.

The first North American specimen record of a stonechat (UAM 5301, a frozen bird found in spring in a Bank Swallow burrow in Galena, Alaska) was identified as *stejnegeri*, the taxon breeding in northeastern Asia (Osborne and Osborne 1987). As this form is highly migratory, it is not surprising that it turns up occasionally in Alaska, with several records from St. Lawrence I. and a few others in Alaska, and one from San Clemente I., California (http://www.wfopublications.org/Rare_Birds/Stonechat/Stonechat.html).

As far as I've been able to determine, all North American stonechat records have been identified as, or at least assumed to be, *stejnegeri* or *maurus*. Thus, splitting stonechats would lead to a name change in the Checklist and a revised account. If we were to split deeper, removing *stejnegeri* from *maurus*, at least the New Brunswick and perhaps other records would likely be indeterminable.

Recommendation:

It is recommended that the committee vote to adopt the three-way split between the *maurus* group (including all Central Asian races, *indicus*, *przewalskii*, and *stejnegeri*), the W European *rubicola* group, and the African *torquatus* group, the taxonomy accepted by WGAC and to be adopted by other global references. We also recommend adopting the English names European Stonechat for *S. rubicola*, African Stonechat for *S. torquatus*, and Asian Stonechat for *S. maurus*, which are the English names to be implemented by the IOC and Clements lists.

P.S.: There is a typo in the Check-list on p. 498: it should say "Winters: [*torquata*] group" rather than "*torquata*".

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Submitted by: Pamela C. Rasmussen, Michigan State University (with thanks to David Donsker and his library)

Date of proposal: 22 August 2020, modified by Terry Chesser on 17 March 2022

Recognize *Pseudocolaptes johnsoni* as a separate species from *P. lawrencii* (Buffy Tuftedcheek)

Note: This proposal is simultaneously under consideration by the SACC, as proposal 940 (<https://www.museum.lsu.edu/~Remsen/SACCprop940.htm>).

Background:

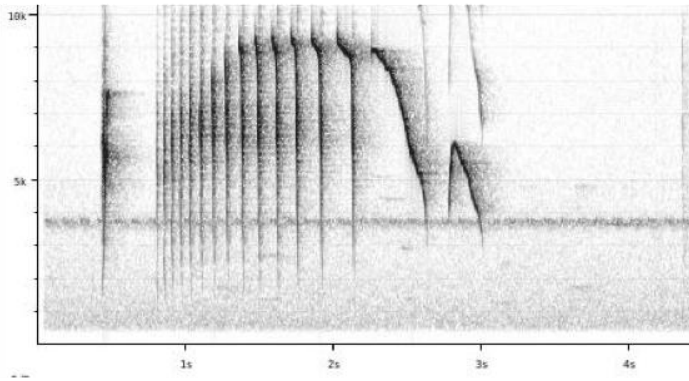
Pseudocolaptes johnsoni was described as a new species by Lönnberg and Rendahl in 1922 based on a specimen reportedly from Baeza, Ecuador (ca. 1800 m on the Eastern slopes of the Andes). Subsequently, Zimmer (1936) found four specimens that matched perfectly Lönnberg & Rendahl's description of *P. johnsoni* but collected on the western slopes of the Andes. The match was so striking that Zimmer (1936) not only concluded that *johnsoni* inhabits the western slopes but also cast doubts about the provenance of the type specimen, as all other specimens reported from that region are clearly *boissonneautii*. Zimmer (1936) also made clear that the distinctive plumage of *johnsoni* cannot be confused with the juvenal plumage of *boissonneautii*. Zimmer ended up considering *johnsoni* as a subspecies of *P. lawrencii* instead, but without providing any evidence other than presumed "closer affinities".

Based on plumage differences and elevational preferences Robbins & Ridgely (1990) suggested that *johnsoni* deserves species status, a treatment followed by few lists (Ridgely & Tudor 1994, Ridgely & Greenfield 2001, del Hoyo & Collar 2016). A previous SACC proposal based on this evidence was rejected because of lack of additional evidence such as vocalizations: <https://www.museum.lsu.edu/~Remsen/SACCprop28.htm>

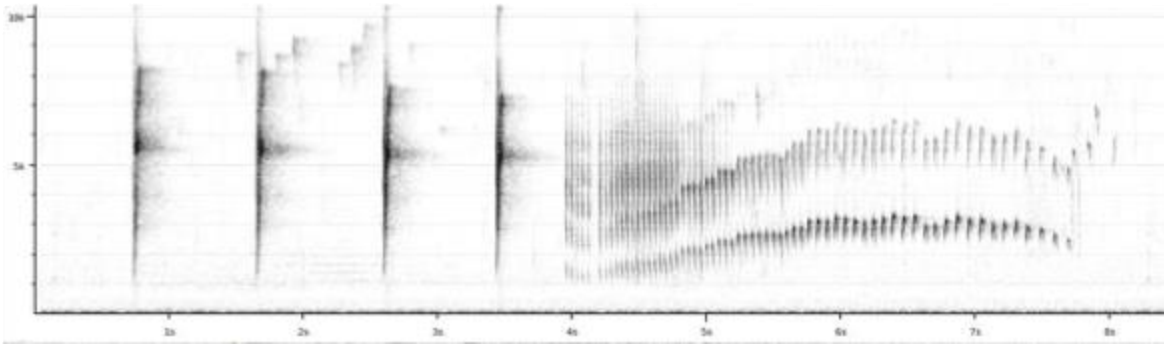
A more recent SACC proposal was based on results of playback experiments showing that the song of *johnsoni* does not elicit any response in *lawrencii* individuals, suggesting significant vocal differences potentially producing premating isolation (Freeman & Montgomery 2017): <https://www.museum.lsu.edu/~Remsen/SACCprop754.htm>

The analyses of Spencer (2011) and Boesman (2016) showed the differences in song characteristics between *johnsoni* and *lawrencii*. If the samples are representative of each taxon, they show well-marked differences:

johnsoni: Song is a high-pitched rattled series of notes slowing into stuttering and ending (always) with a characteristic high-pitched down-slurred note."



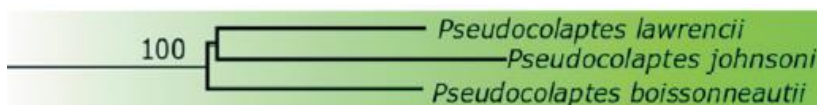
“*lawrencii*: Song is a number of well-spaced staccato notes (always present unlike *johnsoni*) followed by a trill, which usually first ascends in pitch and then slightly descends while slowing down in pace.” (Boesman 2016)



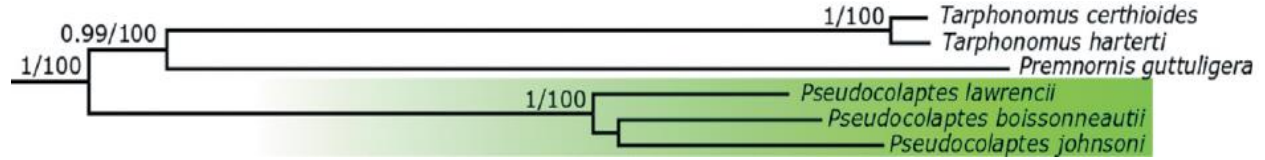
New Information:

Forcina et al. (2021) revisited the issue of the species status of *lawrencii* by reanalyzing DNA sequences from a previous study (Derryberry et al. 2011). They claimed that researchers so far have “neglected” the DNA evidence that indicates that *johnsoni* is a separate species. They found that the single sample of *johnsoni* showed levels of divergence comparable to those between *lawrencii* and *boissonneautii*. In other words, the three lineages diverged nearly simultaneously about 2 million years ago (using mitochondrial clocks; compare to ~ 4 Ma in Derryberry et al. 2011). The analysis could not resolve whether *johnsoni* is closer to *lawrencii* or to *boissonneautii*. They discussed all the evidence accumulated so far, including morphology, vocalizations, and habitat, and concluded that *johnsoni* should be elevated to species status.

Maximum likelihood analysis (Forcina et al. 2021, Fig. 1):



Bayesian analysis (Forcina et al. 2021, Fig. 1):



Discussion:

The data needed for evaluating the species status of *johnsoni* has accumulated slowly over decades, a little at a time, mostly due to the rarity of the species. But all pieces of evidence suggest that *johnsoni* is a distinctive species. It is clearly diagnosable by plumage; it is not a cryptic species by any means. I don't understand why Forcina et al. claim that this is a case of "cryptic diversity."

Photographs of the type specimen in the Stockholm museum are now publicly available here: <https://www.nrm.se/forskningochsamlingar/zoologi/samlingar/ryggradsdjur/typsamlingfaglar/tattningar/furnariidae/nrm569749.3562.html>

and these photographs confirm the original description and, in my opinion, the match between the type specimen and the AMNH series of 4 birds from western Ecuador.

Photographs available online of live birds may be a bit confusing because of the artificial variation in color produced by different light conditions and digital adjustments, and the presence of birds in juvenal plumage, but here are what I consider good representatives of adult *johnsoni* (very similar to the AMNH specimens):

https://macaulaylibrary.org/asset/178142751?_gl=1*1pz6d24*_ga*NjE4NTUxOTA5LjE2NDQ5NzU5MDk.*_ga_QR4NVXZ8BM*MTY0NzQwNzI3NC4yNS4xLjE2NDc0MDczMjkuNQ..#_ga=2.131747151.1345091137.1647401651-618551909.1644975909

https://macaulaylibrary.org/asset/41029281?_gl=1*30cct8*_ga*NjE4NTUxOTA5LjE2NDQ5NzU5MDk.*_ga_QR4NVXZ8BM*MTY0NzQ1Mjg5NS4yNi4xLjE2NDc0NTMwMTQuNDQ.#_ga=2.201353681.1345091137.1647401651-618551909.1644975909

In both the holotype and the photos, note the deep rufous tones on back and flanks (versus brown in the other two taxa), no light streaks on the mantle (vs. streaked in *boissonneautii*), whitish "cheeks" (vs. buffy in *lawrencii*), dark lower throat (not forming a gular band that is continuous with the light cheeks as in the other two taxa), inconspicuous superciliary stripe (versus thin but well-demarcated stripe in the other two taxa), blackish breast with white rhomboid spots and rest of the belly rufous (versus predominating buffy spots that coalesce to form a light-colored central belly in the other two taxa).

The song is clearly distinctive and not recognized by *lawrencii* in playback experiments (Freeman & Montgomery 2017). For both plumage and vocalizations, a more detailed analysis of geographic variation across the Colombian Andes would have been desirable but I think that the evidence is compelling.

Finally, the genetic evidence adds a bit of additional information. But contrary to what the title in Forcina et al. suggests, it doesn't "untangle" anything. Genetic data for just three individuals do not tell much about species limits. A random sample of three individuals from a single large and old population can produce a tree similar to the one found by Forcina et al. The species delimitation algorithm based on the Poisson Tree Processes (PTP) used by Forcina et al. is basically a mathematical formalization of a genetic divergence threshold/yardstick criterion, in itself a rather weak species delimitation criterion. The method classifies the nodes of the tree into speciation events and coalescent (intraspecific) events based on levels of divergence. It thus formalizes the observation that the three *Pseudocolaptes* are rather divergent.

The recovered topology doesn't help much either. A strongly supported sister relationship between *johnsoni* and *boissonneautii* would have clearly made the case for separating *johnsoni* from *lawrencii*, but there were conflicting topologies across methods, and clade support was nil. In sum, the genetic data are consistent with the species status of *johnsoni*, but the evidence is rather weak.

In any case, I think that plumage, songs, and genes together provide sufficient evidence suggesting that *johnsoni* deserves species-level status and there is not a hint of evidence that suggest that *johnsoni* is conspecific with *lawrencii* or with *boissonneautii*.

Recommendation:

I recommend the treatment of *johnsoni* as a separate species.

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Submitted by: Santiago Claramunt

Date of Proposal: 18 March 2022

SACC comments (only one so far):

Comments from Robbins: “YES for recognizing *Pseudocolaptes johnsoni* as a species. As we pointed out in our 1990 paper, we suspected that *johnsoni* deserved species status based on plumage and elevational differences. In the original SACC proposal, I voted against recognizing it as a species because of the lack of vocal data. However, given that Spencer (2011) and Boesman (2016) have established vocal differences, I now vote to elevate it to species status. As pointed out by Santiago, I consider the genetic data equivocal.”

Treat *Elaenia cherriei* as a separate species from *E. fallax* (Greater Antillean Elaenia)**Background:**

Elaenia fallax was described by Sclater in 1861 from Jamaica and *Elaenia cherriei* was described by Cory in 1895 from Hispaniolan material. Hellmayr (1927) lumped the two forms into a single species. They were treated as conspecific in all subsequent references until del Hoyo and Collar (2016) split them using the Tobias (2010) criteria.

New Information:

Rheindt et al (2008) did a broad molecular analysis of the genus *Elaenia* based on mitochondrial and nuclear DNA. In that study, *Elaenia fallax* and *E. cherriei* were sister, but joined by a relatively deep node. The estimated time of divergence was earlier than both the *E. chiriquensis/brachyptera* split and the *E. obscura/sordida* split, both recently treated as distinct species by SACC. However, in both of those cases, formal analysis of vocal differences had been done (Rheindt et al 2015 for *chiriquensis/brachyptera*, and Boesman 2016 and Minns 2017 for *obscura/sordida*), showing distinctly different songs and/or calls between the two taxa. This type of analysis has not been done in the case of *Elaenia fallax* and *E. cherriei*.

I am not going to do such a formal analysis, but I have reviewed available vocal material. The Birds of the World account for *Elaenia fallax* (Kirwan et al 2021; <https://birdsoftheworld.org/bow/species/graela1/cur/introduction>) has a good representative selection of calls and songs from both Jamaican *fallax* and Hispaniolan *cherriei*. The easiest to deal with is a common (at least often recorded) single call note. In *fallax*, this note is a descending clear whistle, sort of a “tseuu.” In *cherriei*, there is a short, abrupt, little bit buzzy “zwreep.” On the sonogram this note has an inverted V shape. In no recording to which I listened is there anything in any vocalization of *cherriei* that looks (in sonogram) or sounds like the *fallax* note. Similarly, the *cherriei* note does not appear to be found in the vocalizations of *fallax*. Songs are more complicated. *E. fallax* from Jamaica gives a fairly characteristic type of *Elaenia* song with distinct first note followed by something I would call a slow twitter. They also will take single elements of the twitter, or sometimes doubled, and give them by themselves. For *cherriei*, I did not hear anything that really seemed like a characteristic *Elaenia* song. A longer, simpler series on the same pitch or descending slightly has been called a song or even dawn song of *cherriei*. To me it doesn’t seem structured like songs in other *Elaenia*, so I am not sure it should be directly compared to the song of *fallax*. It may not be a homologous vocalization. Recordings of both taxa have a wide variety of calls/songs that don’t fit cleanly into categories.

Kirwan et al (2021) stated that “there is no evidence to date that the songs of nominate *fallax* in Jamaica and subspecies *cherriei* on Hispaniola differ, but they have not been studied in detail.” This appears to be quoting Kirwan et al (2019), but I have not seen that book. del Hoyo and Collar (2016) also stated that there exists “evidence of [*cherriei*] not responding to *fallax* playback.” However, I do not know the basis for this statement.

Morphologically the two taxa are quite similar, not a surprise in *Elaenia*. However, del Hoyo and Collar indicated the following: (1) *fallax* has a mandible that is half or more pink, whereas it is entirely black (or very nearly so) in *cherriei*; (2) gray breast in *cherriei* versus yellowish gray in *fallax*; and (3) white abdomen in *cherriei* versus pale yellowish-white in *fallax*. I looked at a fair number of photos from e-bird/Birds of the World (so from Cornell). To be honest, I do not really see the plumage differences as being very clearly defined. I also looked at Field Museum specimens. Unfortunately, we only have old material of *cherriei*, which look discolored. The recent material of *fallax* from Jamaica that we have does show the yellowish tones described by del Hoyo and Collar (2016), but I just can't confirm that they are different from *cherriei*. Based on photos, I'd say the difference in bill color is real, not dramatic but real. I would also note that SACC had no morphological data to support the split of *brachyptera* from *chiriquensis*, which was entirely based on voice and genetics. In general, the great similarity of the various species of *Elaenia* means that I think the very subtle plumage differences between *fallax* and *cherriei* effectively tell us nothing about their specific status.

Recommendation:

The vocal data and the genetic data look similar to those that supported the split of *E. brachyptera* from *E. chiriquensis* adopted by SACC in 2016. However, Rheindt et al (2015) specifically analyzed vocal differences between *brachyptera* and *chiriquensis*. Such a detailed analysis has not been done for *fallax* and *cherriei*. It appears to me that the genetic divergence is consistent with those of other taxa we have separated as species in *Elaenia* and much greater than in any populations that are considered conspecific. Vocally, they are distinct with very different calls, but we lack a formal analysis of these vocal differences. Despite the less than ideal vocal evidence, I recommend treating *E. fallax* and *E. cherriei* as distinct species based on genetic and vocal differences.

English name:

The obvious English names if the two species are split would be Hispaniolan *Elaenia* for *E. cherriei* and Jamaican *Elaenia* for *E. fallax*. Unfortunately, the name Jamaican *Elaenia* is already in use for *Myiopagis cotta*, also endemic to Jamaica. The names Large Jamaican *Elaenia* for *E. fallax* and Small Jamaican *Elaenia* for *M. cotta* were suggested by del Hoyo and Collar (2016). However, I think those names are very misleading regarding taxonomy, suggesting a much closer relationship between *cotta* and *fallax* than exists. Retaining the current Greater Antillean *Elaenia* for *fallax* doesn't follow our guidelines regarding names for daughter species in splits. Also, although Greater Antillean *Elaenia* is perhaps not the ideal name for the broader *fallax*, found on only two of the main Greater Antillean islands, I can't see maintaining it for a single island endemic. What we need is a name characteristic of Jamaica but not Jamaican. Locally in Jamaica the name Sarah Bird is used for this species. I do not know the basis of this name. However, the French name used for *E. fallax* in the AOU Checklist is "Elenie sara," so that name appears to have some currency. Unfortunately, Raffaele et al (1998) listed Sarah Bird as an alternate English name for both *E. fallax* on Jamaica and *M. cotta*, so it doesn't seem that Sarah *Elaenia* would be a good choice, because it is apparently not specific to *Elaenia fallax*. Boyd (<http://john-boyd.com/Taxo/changes.html>) suggested the name Sclater's *Elaenia* for *fallax*. We have done similar things in the past when making species level changes, but I don't think a new patronym is a good idea at this point.

In sum, I don't think that I currently have an acceptable name for *fallax* if this split is approved. I am not enthusiastic about Large Jamaican *Elaenia* because of the misleading sense of the taxonomy it creates, plus the fact that we'd also need to change the name of *M. cotta*. Sarah *Elaenia* is based on a vernacular name in the literature, but has no clear meaning associated with it that I can find, and it may not be specific to *Elaenia fallax*. If anybody has thoughts on a good English name for *fallax*, please speak up.

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Submitted by: Douglas F. Stotz

Date of proposal: 25 March 2022

Treat *Mionectes galbinus* as a separate species from *M. olivaceus* (Olive-striped Flycatcher)

Background:

Mionectes olivaceus is a small fruit-eating flycatcher with a range from Costa Rica to eastern Venezuela and Bolivia along lower montane slopes and nearby lowlands. The species was described in 1868 by Lawrence from Costa Rica. There are 5 recognized subspecies, all of which were originally described as subspecies of *olivaceus*.

New Information:

Boesman (2016) examined the voices of the various subspecies of *olivaceus* and concluded that there were 4 vocal groups. One was the nominate subspecies, *olivaceus*, found in eastern Costa Rica and western Panama. A second consisted of the taxa *hederaceus* and *galbinus*. The subspecies *hederaceus* occurs from Veraguas, Panama, south largely on the western side of the Andes to southern Ecuador, whereas *galbinus* is known from the Santa Marta Mountains of Colombia. The third vocal group consists of *venezuelensis* from northern Colombia and northern Venezuela and *fasciaticollis* on east slope of Andes from southern Colombia to Bolivia. The fourth group is from Santander, Colombia and is not clearly associated with any of the recognized taxa. Boesman evaluated the groups using the Tobias (2010) criteria and scored *olivaceus* versus the other taxa as 8. He scored *hederaceus/galbinus* versus *venezuelensis/fasciaticollis* as 6.

The sonograms on the next page are from the Birds of the World account (Fitzpatrick et al 2020). A is nominate *olivaceus*, B is *hederaceus* (presumably *galbinus* is similar, but voice apparently unrecorded), C is *fasciaticollis/venezuelensis*, D is the Santander population of uncertain subspecies, and E is a single recording from the far eastern end of the northern Venezuela mountains, which currently would be assigned to *venezuelensis*. Recordings of songs from populations in the Perija Mountains and Trinidad do not seem to be available.

These songs are squeaky and extremely high pitched, basically between 8 and 10 thousand MHz. I personally cannot hear the sounds on recordings of nominate *olivaceus* (at least through my computer) at all, and I am not hearing the other populations' vocalizations well. The literature describes these songs as insect or hummingbird-like.

Morphological variation among the five subspecies is minor. The main variation is in the brightness of the green upperparts, the brightness and tone of yellow on abdomen, the extent of streaking, and paleness of streaking. None of this variation would be apparent in the field. In del Hoyo and Collar (2016), they assign some points toward the Tobias criteria score based on plumage. However, I would say, from examining specimens and the discussion in Fitzpatrick et al (2020), that *olivaceus* is not at the extreme in any of the characters varying across the 5 subspecies. It is generally pale and bright, but to my eye, *galbinus* is the palest and brightest of these taxa, while *hederaceus* is overall the dullest.

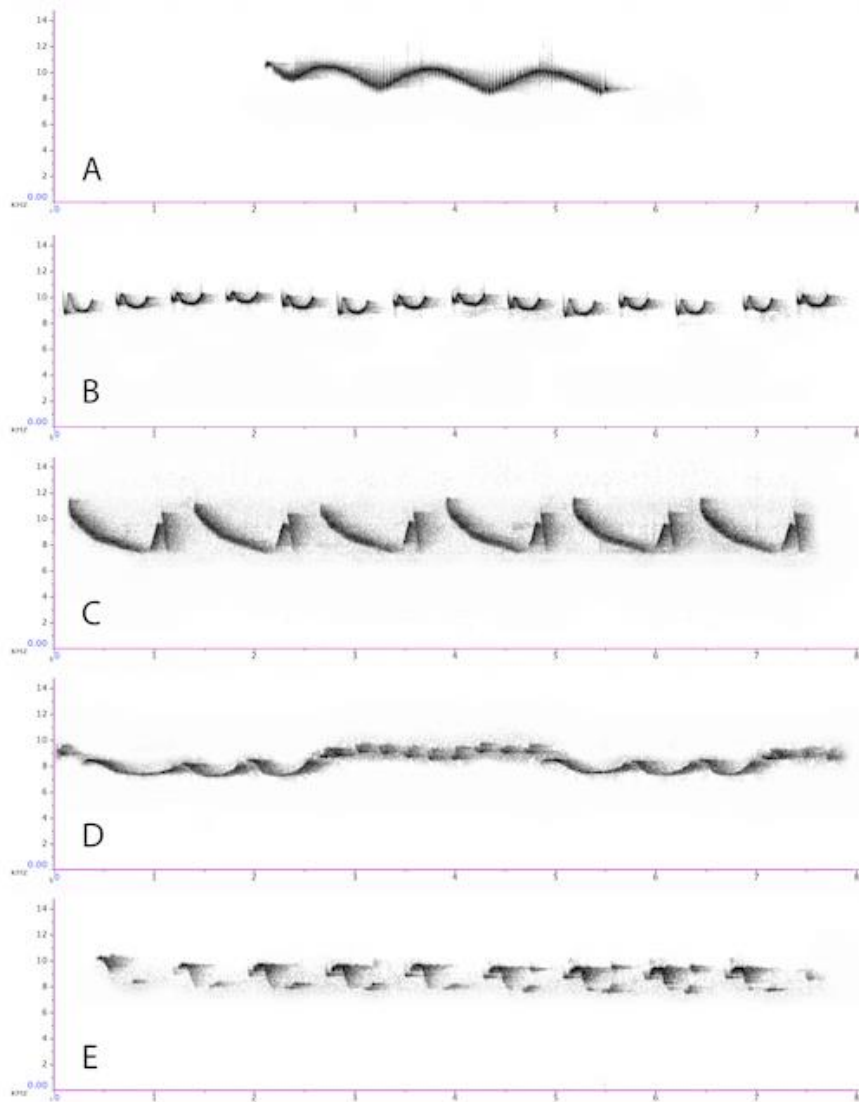


Figure 1. Sonograms from the Birds of the World account (Fitzpatrick et al. 2020). A is nominate *olivaceus*, B is *hederaceus*, C is *fasciaticollis/venezuelensis*, D is the Santander population of uncertain subspecies, and E is from a population currently assigned to *venezuelensis*. See text for more details.

At the time of del Hoyo and Collar (2016) there was no genetic evidence available for this complex. However, Harvey et al (2020) examined multiple samples of *olivaceus* as well as the other species of *Mionectes*. In their analysis, *Mionectes olivaceus* was paraphyletic, with nominate *olivaceus* sister to a clade with *Mionectes striaticollis* and samples corresponding to *galbinus* and *venezuelensis*. *Mionectes striaticollis* is a similar species broadly sympatric with *olivaceus* in South America, overlapping with the subspecies *hederaceus*, *fasciaticollis*, and *venezuelensis*.

Recommendation:

This is a complicated issue. I think it is very likely that there are multiple species within the current species *Mionectes olivaceus*. Splitting nominate *olivaceus* is supported by a distinctive voice and the genetic evidence that it is not sister to the rest of the species. If NACC did this, we would add a species to the checklist, because *olivaceus* occurs in Costa Rica and western Panama, and *hederaceus*, representing *Mionectes galbinus*, occurs in central and eastern Panama. However, it seems likely that there are multiple species to be recognized in *galbinus*. Unfortunately, I think we currently lack sufficient information to define the various species that would be left in *galbinus*. There are no genetic analysis at a relevant scale for that question, and many populations (including *galbinus*) do not have recordings in the Xeno-canto or Macaulay collections. One vocal group (D from Santander above) has not been clearly assigned to a named taxon. For NACC, the issue is that the name *galbinus* may not be applicable in the end to the populations in Panama. This case reminds me of *Schiffornis turdinus* for SACC. A proposal to split in 2007 failed to pass, but with additional data, a new proposal to split *Schiffornis turdinus* into 5 species did pass in 2011.

My weak recommendation is a NO vote, awaiting further evidence that will allow us to define more clearly the multiple species that likely make up *Mionectes olivaceus*.

English names:

Del Hoyo and Collar (2016) used Olive-streaked Flycatcher for *M. olivaceus* and retained Olive-striped Flycatcher for *M. galbinus*. Because the ranges are very uneven in size, with *M. galbinus* much more widespread than *M. olivaceus*, I think the use of Olive-striped Flycatcher for *M. galbinus* is justified under our English name criteria. Further, given that the splitting of *galbinus* into two or more species seems likely eventually, we (or SACC) would have to coin new names for the daughter species at a later time. I recommend using Olive-streaked Flycatcher for *Mionectes olivaceus* and Olive-striped Flycatcher for *Mionectes galbinus* if we decide to split these two groups. These are the names used by del Hoyo and Collar 2016 and also used for the groups corresponding to the species recognized by del Hoyo and Collar in the Birds of the World account (Fitzpatrick et al. 2020).

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Submitted by: Douglas F. Stotz

Date of Proposal: 25 March 2022

Treat *Canachites franklinii* as a separate species from *Canachites canadensis* (Spruce Grouse)

Description of the problem:

Until 1955, *Canachites canadensis* and *C. franklinii* were considered separate species on the basis of plumage and structural differences, e.g., the obvious large white spots on uppertail coverts and usual lack of a chestnut terminal tail band in the *franklinii* group, coupled with its nearly truncate-tipped and broader rectrices than in the *canadensis* group, which lacks the white uppertail covert spots, usually has a distinct chestnut terminal tail band, and has narrower, rounder-tipped rectrices (Ridgway and Friedmann 1941). Rand (1948) stated that the zone in which intermediates occur is very narrow and that intergradation seemed not to be common even there. Brooks and Swarth (1925) stated “Franklin and Spruce grouse are reported as occurring together at the headwaters of the Parsnip and the Big Salmon rivers [the former at least in eastern British Columbia] (F. K. Vreeland, MS)”, which could be taken to suggest sympatry. However, since the 30th Supplement of the Check-list in 1955, the Spruce Grouse has been considered to comprise a single polytypic species (AOU 1955), based on the rationale that intergradation occurs between the *canadensis* and *franklinii* groups (Jewett et al. 1953). A Note in Jewett et al. (1953:203) states “There is now abundant evidence that the Franklin grouse is a race of the spruce grouse rather than a distinct species as has always been maintained in the literature. Intergradation between these supposedly distinct species takes place chiefly in north-central British Columbia and western Alberta, but tendencies toward chestnut tail tips seem to appear occasionally almost anywhere within the range of *franklinii*. A large series of specimens in the U. S. National Museum shows complete intergradation in all characters between *franklinii* and *canadensis*.”

There does not seem to be mention of this variation in Ridgway and Friedmann (1946), which would have been based on much the same USNM material, and these authors (presumably Friedmann, Ridgway being by then deceased) did not indicate uncertainty as to species status of *franklinii*, but Terry Chesser noted that the identifications of several birds as hybrids were made in the early 1950s. Furthermore, Short (1967) stated that in many respects the differences between *canadensis sensu lato* and *Falcipectnis falcipectnis* (now known not to form a monophyletic group with *Canachites*; Persons et al. 2016) are no greater than those between *canadensis* and *franklinii*, and Short even suggested that *falcipectnis* might prove to be conspecific with these.

For comparison, it should be noted that Jewett et al. (1953) give a similar though less detailed Note regarding Dusky and Sooty grouse *Dendragapus obscurus* and *D. fuliginosus*: “We have found that the characteristics of the blue grouse of the Pacific Coastal region intergrade completely with those of the Rocky Mountain region and so can see no reason for maintaining them as distinct species. The area of intergradation is in the mountains of northern Okanogan County.” The AOU had previously (AOU 1944) lumped the *fuliginosus* group within the *D. obscurus* group in the 19th Supplement, following Peters (1936:28) without other comment, but at that time continued to maintain *Canachites franklinii* as a full species, as did Peters (1936). The split between *Dendragapus obscurus* and *D. fuliginosus* enacted in Banks et al. (2006)

followed a detailed analysis of the phylogeography of the genus (Barrowclough et al. 2004), but no such comprehensive analysis has yet been produced for *Canachites*.

New information:

Gutierrez et al. (2000) found 1% sequence divergence in mtDNA between *franklinii* and *canadensis*, and, noting that this is greater divergence than between any species of prairie grouse *Tympanuchus*, they considered that both *Canachites* and *Dendragapus* constitute two species each. Drovetskii (2001) considered his genetic analyses to support the specific status of *franklinii* as much as for several other taxa of grouse that have been variously treated as species or subspecies, but almost all of which are now treated as species (except *Tympanuchus [cupido] attwateri*). Barry and Tallmon (2010) found what they considered to be significant genetic variation in mtDNA and nuclear microsatellites between the insular south-east Alaska population *C. c. isleibi* of Prince of Wales Island in the Alexander Archipelago (on

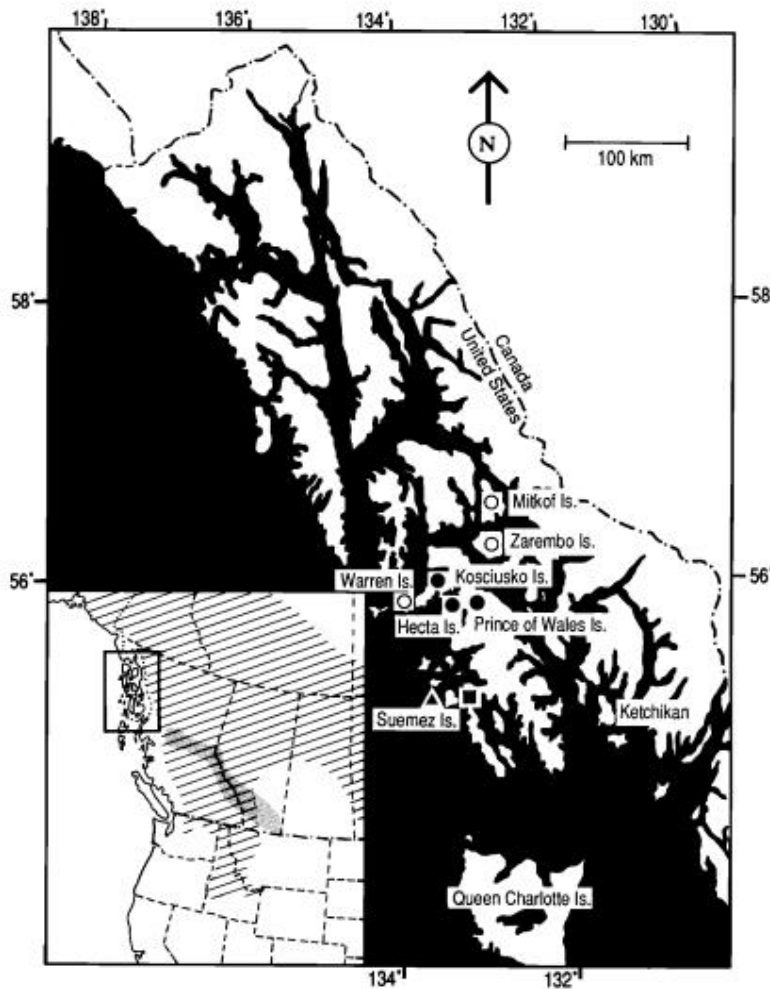


Figure 1. Range of the Spruce Grouse in western Canada and Alaska, showing range of *Falcipennis canadensis isleibi* and zone of intergradation between the *canadensis* and *franklinii* subspecies groups (inset). Solid dot, specimen record; open dot, sight record; triangle, bones; square, nest.

Figure 1 from Dickerman and Gustafson (1996), showing the range of *isleibi* (small boxed area) and the continental hybrid zone (shaded area).

morphology considered to be a member of the *franklinii* group) and both *franklinii* and *canadensis*. Barry and Tallmon (2010) found *franklinii* and *canadensis* to be more closely related to each other than either is to *isleibi*, but this may have been because their *franklinii* samples originated from the hybrid zone in British Columbia. However, the apparently intermediate phenotype of *isleibi* also suggests introgression and not necessarily valid subspecific status, and this would be consistent with its geographic position.



Figure 2. Upperparts of males of the Spruce Grouse. Left, *F. c. canadensis*. Based on two adults, MSB 880, from Thomas Lake, 30 mi. NE of Ely, St. Louis Co., Minnesota, 19 December 1924, and MSB 679, from mile 50 along Richardson Highway, 150 mi. NE of Anchorage, Alaska, 3 September 1961. Middle, *F. c. isleibi*. Based on AMNH 830554, an adult, and 830555, an immature, both from Kosciusko Island, about 50 mi. SE of Ketchikan, Alaska, in fall 1991. Right, *Falcipennis canadensis franklinii*. Based on two adults, UWBM 36214, from Skull and Crossbones Ridge, Okanogan Co., Washington, November 1981, and UWBM 50206, from Freezeout Ridge, 9 mi. W and 7.5 mi. N of Conconully, Okanogan Co., Washington, 27 August 1987.

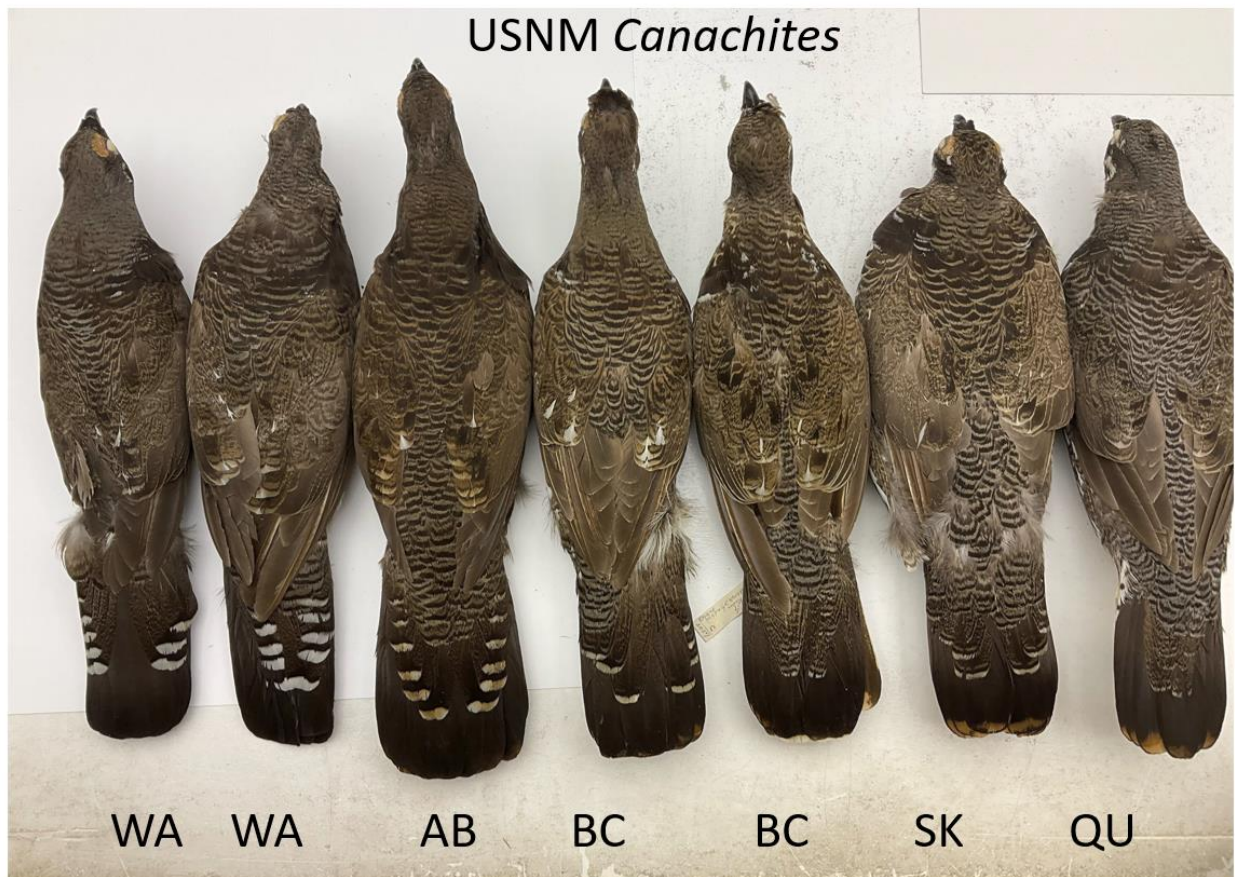
Figure 2 from Dickerman and Gustafson (1996); *F. c. canadensis* is pictured on the left, *isleibi* in the center, and *franklinii* on the right..

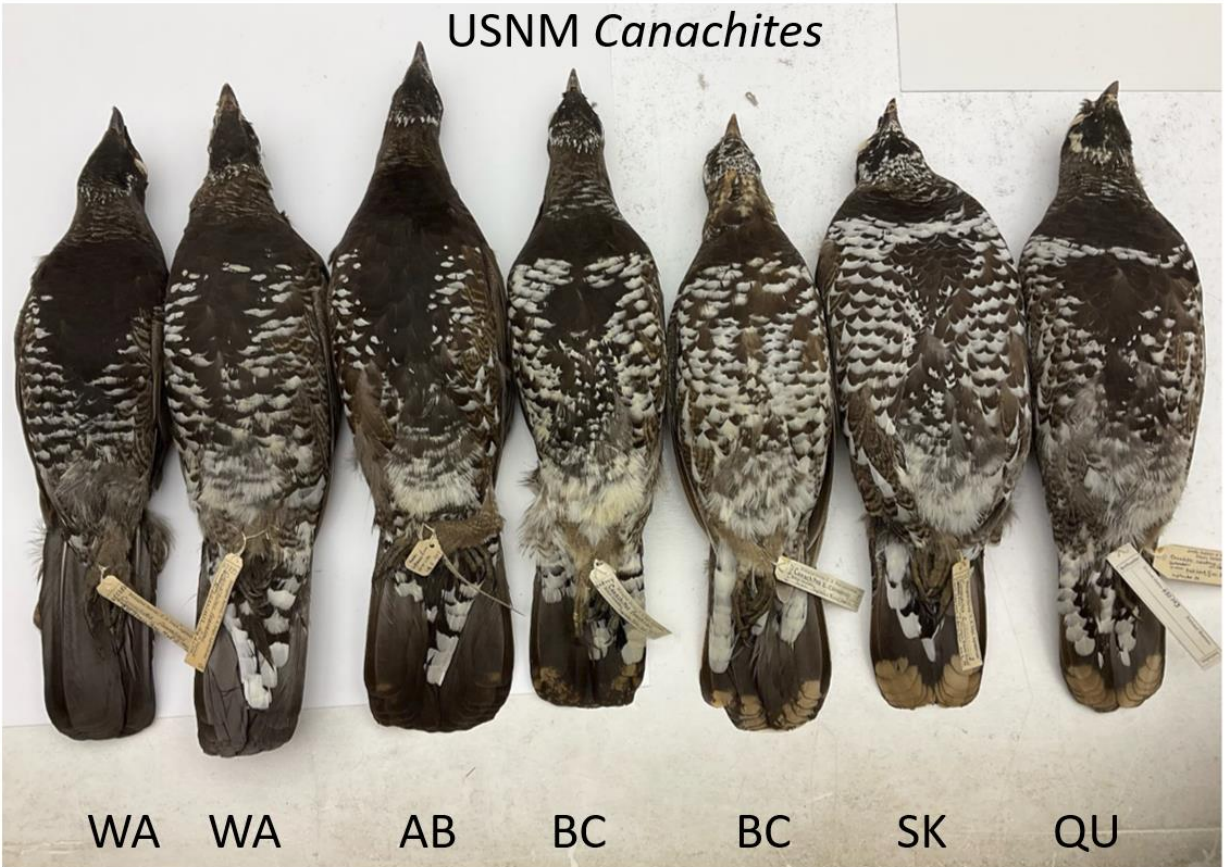
The Spruce Grouse was split by del Hoyo and Collar (2014) into *Falcipennis canadensis* and *F. franklinii*, citing: “all-dark vs broad orange-buff tips of rectrices (3); bold white (vs all-dark) tips of elongate uppertail-coverts (3); thin broken vs strong continuous white line across breast (1); broader rectrices (effect size based on published data¹⁶³ 1.67; score 1); possession of wing-clap territorial display vs none¹⁶³ (3); moreover, long zone of hybridization occurs at boundary, where two taxa inhabit different habitat (*franklinii* in montane conifers, *canadensis* in taiga¹⁶³) (2).” Reference 163 is the BNA account (Boag and Schroeder 1992). The noticeably darker, blacker central underparts of male *franklinii*, apparent from some photographs (e.g. <https://macaulaylibrary.org/asset/263068381>; <https://macaulaylibrary.org/asset/184617751>) was illustrated in the plate in del Hoyo and Collar (2014) and seems obliquely indicated in these authors’ character list by the “thin broken vs strong continuous white line across breast”.

Note also that males of the *canadensis* group even from the far east of their range often nearly lack chestnut tail tips; this can readily be seen in eBird photos. Here's one (<https://macaulaylibrary.org/asset/102027511>) with different amounts of chestnut on the two sides of the tail (presumably from different feather generations). Feather wear might account for some of the variation in amount of chestnut on tail tips (see, e.g., <https://macaulaylibrary.org/asset/159178181>).

And here's a male from Michigan with small but obvious whitish spots on uppertail coverts: <https://macaulaylibrary.org/asset/383073331>, but this could represent natural variation within *canadensis* rather than intergradation with *franklinii*.

Terry Chesser examined and photographed some of the extensive USNM series (photos of a selected few below) and considered that, at first glance anyway, Jewett et al.'s interpretation seems justified. It does not seem to uphold Rand's (1948) statement of a very narrow hybrid zone in which hybridization is uncommon.





It is well-established that southern *franklinii* populations give a (usually) double wing-clap as part of the flight display when descending to the perch, and this initially would appear to support species status for this taxon, but according to unpublished data (of M. A. Schroeder; Schroeder et al. 2021), northern *franklinii* do not wing-clap. This difference, however, is not mentioned in the original BNA account (Boag and Schroeder 1992) that was cited by del Hoyo and Collar (2014), and it appears to remain unpublished except as included in BOW (Schroeder et al. 2021). Birds from the zone of intergradation have been noted to give either single wing claps or to wing-clap in flights between trees (Schroeder et al. 2021).

There does not appear to be any true song in the Spruce Grouse, although the cackle of females can be considered a song (Schroeder et al. 2021), and other vocalizations mainly consist of clucks, chick calls, incidental wing noise, male wing-whirrs, stomps, short bouts of drumming, and the double wing-clap of southern *franklinii*. Reports of a very low-pitched hooting song appear to be mistaken (Schroeder et al. 2021).

Subsequent treatments:

The WGAC has voted to split Franklin’s Grouse, and hence the issue needs to be addressed by AOS-NACC. The NACC has recognized *Dendragapus obscurus* and *D. fuliginosus* as separate species since 2006 (Banks et al. 2006); this treatment, in addition to the recognition of three

species of *Tympanuchus*, with their very low genetic divergences, could be used to argue that *Canachites* should be treated as two species. However, a comprehensive phylogeographic analysis (Barrowclough et al. 2004) was available for the Blue Grouse complex, whereas no such analysis yet exists for the Spruce Grouse complex.

Effect on AOU-CLC area:

If the split is accepted, the result would be the addition of a species to the AOS area. Neither of the daughter species occur outside of the AOS area.

Recommendation:

Given the seemingly extensive introgression over a large area suggested by plumage (including the putative subspecies *isleibi*) and by the observed variation in the wing-clapping display of *franklinii*, at this time there is not a convincing case to be made that *Canachites* should be accorded the same type of two-species treatment as *Dendragapus*. I am thus recommending a NO vote, but I hope that a comprehensive analysis will soon clarify the picture.

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Modify the linear sequence of genera in the tribe Mergini, adjusting the placements of (a) *Camptorhynchus labradorius* (Labrador Duck), (b) *Clangula hyemalis* (Long-tailed Duck), and (c) *Histrionicus histrionicus* (Harlequin Duck)

Background:

The current linear sequence of the Anatidae, and in particular the extinct Labrador Duck (*Camptorhynchus labradorius*), is largely based on morphological data together with limited genetic data from mitochondrial DNA sequences. Broadly, Anatidae has been divided into various subfamilies and tribes, with most “ducks” falling into the subfamily Anatinae; within Anatinae, there are several tribes recognized among many authorities, including the Mergini (broadly the sea ducks: *Mergus*, *Bucephalus*, *Melanitta*, *Somateria*, *Clangula*, etc.), Aythyini (broadly the pochards: *Aythya*, *Netta*, etc.), and Anatini (broadly the dabbling ducks: *Anas*, *Mareca*, *Spatula*, etc.) (Eo et al. 2009, Gonzalez et al. 2009, Dickinson and Remsen 2013, del Hoyo and Collar 2014, Mitchell et al. 2014, Buckner et al. 2018). Within this broad framework, the extinct Labrador Duck (*Camptorhynchus labradorius*) has long been placed within the Mergini, and morphological studies suggested that it was closely related to the scoters (*Melanitta*) (Livezey 1996). In the linear sequence of the AOS Check-list, Labrador Duck comes after Harlequin Duck (*Histrionicus histrionicus*) and before the scoters (*Melanitta*) (AOU 1998).

Our current linear sequence of genera within the tribe Mergini is as follows:

- *Polysticta*
- *Somateria*
- *Histrionicus*
- *Camptorhynchus*
- *Melanitta*
- *Clangula*
- *Bucephala*
- *Mergellus*
- *Lophodytes*
- *Mergus*

New Information: Using whole mitogenome sequences of target species, together with sequences of select mitochondrial loci from a wider sampling of species, Buckner et al. (2018) studied the phylogenetic relationships among the Anatidae, focusing mostly on the subfamily Anatinae and resolving the relationships of two extinct taxa, Labrador Duck (*Camptorhynchus labradorius*) and *Chendytes lawi* (a taxon known only from fossil remains from California). In their phylogeny, they found that Labrador Duck was strongly supported as sister to Steller’s Eider (*Polysticta stelleri*), with these two species together sister to the *Somateria* eiders (Fig. 1). These results require a change in the linear sequence for Labrador Duck. Based on the phylogeny of Buckner et al. (2018), with additional support from Gonzalez et al. (2009), Mitchell et al. (2014), and Eo et al. (2009), I propose the following linear sequence for genera within Mergini, requiring moving *Clangula hyemalis* (Long-tailed Duck), *Histrionicus*, and *Camptorhynchus*:

- **Mergini** (well-supported group; note in particular the new positions of *Clangula* and *Camptorhynchus*)

- *Clangula*
- *Histrionicus*
- *Polysticta*
- *Camptorhynchus*
- *Somateria*
- *Melanitta*
- *Bucephala*
- *Mergellus*
- *Lophodytes*
- *Mergus*

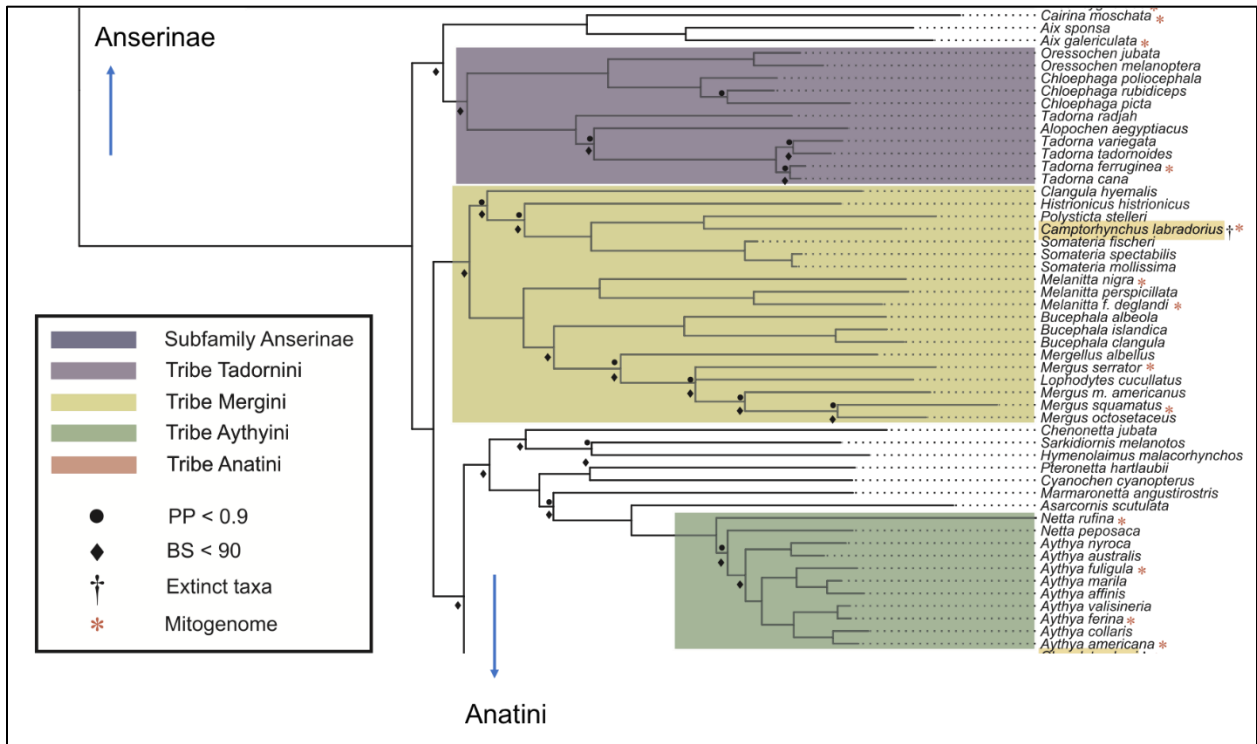


Figure 1. Part of Figure 2 from Buckner et al. (2018) showing Bayesian inference tree. Note position of Labrador Duck (highlighted in yellow) as sister to Steller’s Eider (*Polysticta stelleri*).

Recommendation: I recommend that NACC votes to adopt the new linear sequence for the Mergini, including the new placement for Labrador Duck as well as *Clangula* and *Histrionicus*. However, understanding that this sequence is based entirely on mitochondrial DNA (mitogenomes in some cases), I understand if the committee decides to wait on the larger-scale sequence changes. Therefore, I am splitting the vote up into three, one for Labrador Duck only, one for *Clangula*, and one for *Histrionicus*.

- A) Vote yes to move *Camptorhynchus labradorius* in the linear sequence so that it follows *Polysticta stelleri*.
- B) Vote yes to change the placement of *Clangula* so that all other genera in this group follow it.
- C) Vote yes to change the placement of *Histrionicus* so that all genera except *Clangula* follow it.

These studies also hint at broader changes in the arrangement of subfamilies and the genera within subfamilies in the Anatidae, but because these results are based entirely on mtDNA and some are not well supported at deeper levels, I will wait to propose these changes.

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