

AOS Classification Committee – North and Middle America

Proposal Set 2021-A

10 November 2020; final revision 15 April 2021

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Revise the classification of the Euphoniinae (Fringillidae): transfer *Euphonia musica* and *E. elegantissima* to resurrected genus *Cyanophonia* or to *Chlorophonia*, and revise the linear sequence of the subfamily

Note: These issues, in slightly different form, are being considered by SACC in Proposal 856. See SACC votes and comments at <https://www.museum.lsu.edu/~Remsen/SACCprop856.htm>

Effect on NACC:

YES votes on part a and Option b-1 would resurrect *Cyanophonia* and transfer *Euphonia musica* and *E. elegantissima* to this genus, whereas YES votes on part a and Option b-2 would transfer these species to *Chlorophonia*. A YES vote on part c would revise the linear sequence of species within the subfamily Euphoniinae to reflect new phylogenetic information.

Background and New Information:

Prior to the recent publication of a phylogenomic study of the true-finch subfamily Euphoniinae, the most comprehensive molecular phylogeny of the group (Zuccon et al. 2012) had found that *Euphonia* was paraphyletic with respect to *Chlorophonia*, the other genus in the subfamily. Specifically, *E. musica* was found to be sister to *C. cyanea*. The authors noted this taxonomic conflict but suggested that further sampling of species would be necessary to adequately resolve this issue. More recently, Imfeld et al. (2020) used target-capture and enrichment to

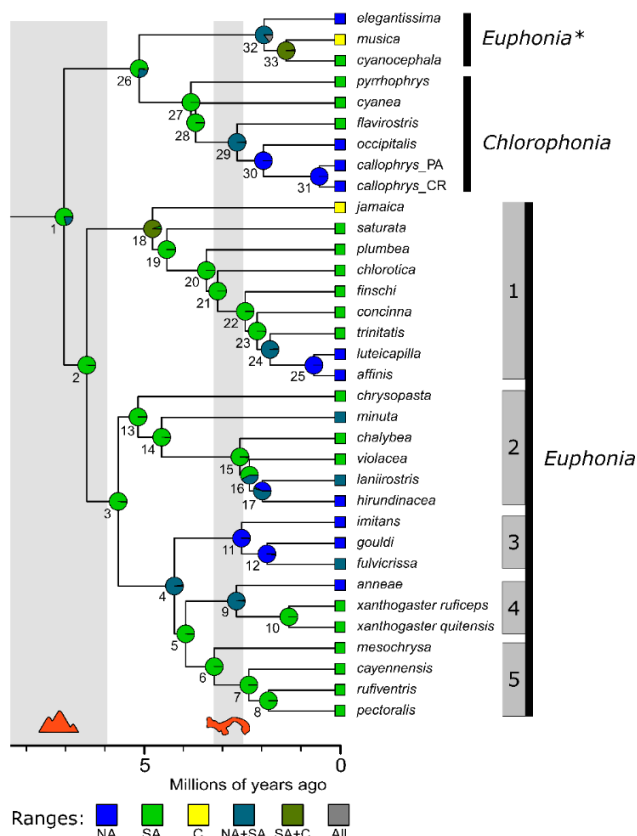


Figure 1. Time-scaled phylogeny of Euphoniinae. This tree is from Imfeld et al.'s Figure 4. The topology of this phylogeny was inferred by maximum likelihood estimation of a species tree from 4,944 UCE loci, and its branch lengths were optimized and time-scaled by a fossil-calibrated Bayesian analysis of 150 completely sampled UCE loci and cytochrome-b sequences. The blue-hooded euphonia species, noted by an asterisk, form a monophyletic clade sister to the genus *Chlorophonia* to the exclusion of the remaining *Euphonia* species. All nodes in this tree received localized posterior probability of 1 and bootstrap support of 100% except for nodes 19 (0.76, 87%) and 21 (0.98, 90%).

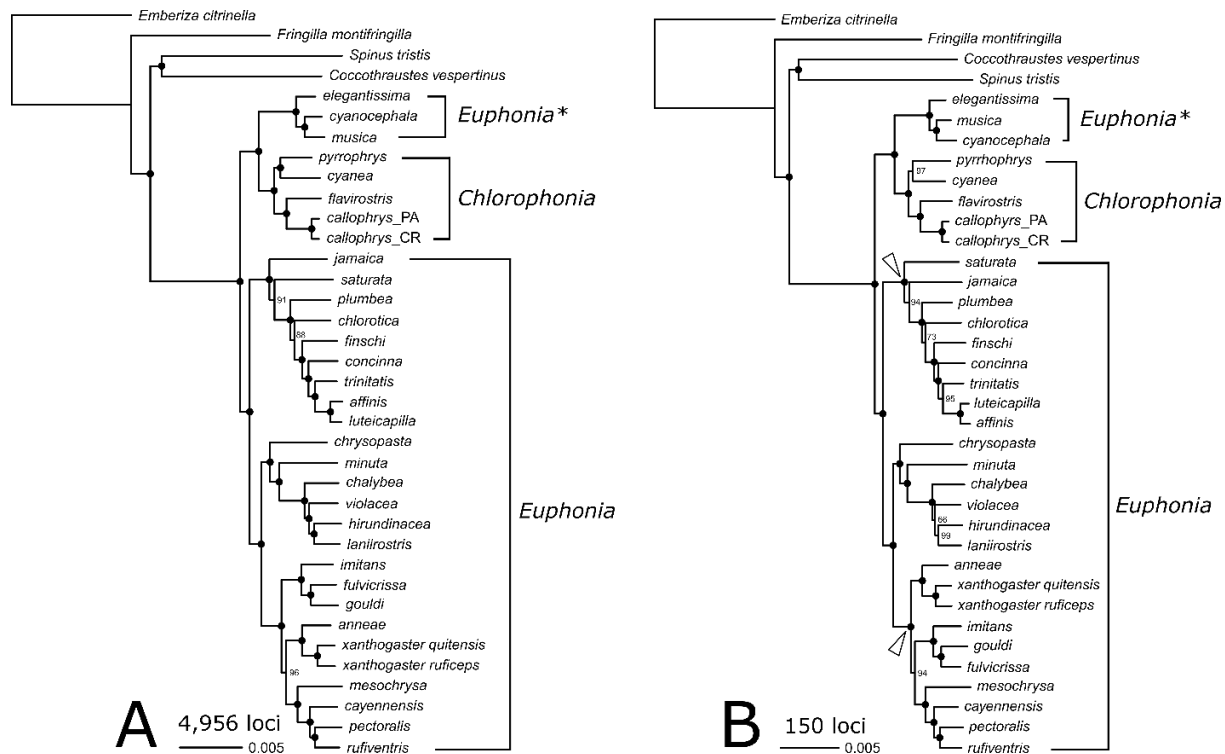


Figure 2. Maximum-likelihood phylogenies of the Euphoniinae generated from concatenated UCE loci. These trees are from Imfeld et al.'s Figure 1. Black nodes indicate bootstrap support of 100%, and any node receiving <100% support has its value reported. The topologies of these trees, especially the one inferred from all UCE loci, are largely similar to the species tree topology presented above. Triangles adjacent to the right tree indicate conflicting nodes between the concatenated phylogenies.

sequence thousands of ultraconserved elements and mitogenomes for every species of *Euphonia* and *Chlorophonia* presently recognized by the checklist committees of the American Ornithological Society. Every phylogenetic analysis performed in this study, whether with concatenation or species-tree methods, maximum likelihood or Bayesian approaches, or using nuclear or mitochondrial sequence data, found the three species of blue-hooded euphonias (*E. cyanocephala*, *E. elegantissima*, and *E. musica*) to form a monophyletic clade sister to the five *Chlorophonia* species to the exclusion of all other euphonias (see Figs. 1, 2). Thus, generic placement of this blue-hooded euphonia clade requires revision.

Two blue-hooded species, *E. elegantissima* and *E. musica*, occur in the NACC area and would be affected by this revision. Imfeld et al. (2020) discussed three possible scenarios to resolve the paraphyly of *Euphonia*: lumping all species in Euphoniinae into the genus *Euphonia*, placing the blue-hooded euphonias in the genus *Chlorophonia*, or resurrecting the genus *Cyanophonia* for the blue-hooded euphonias. *Euphonia* has priority over *Chlorophonia*, being established in 1806 versus 1851, respectively; however, the first option would remove a long-standing genus for chlorophonias and was not recommended. This option also would change the names of five species, three of which occur in the NACC area. The second option would require a revision of the blue-hooded species only, but the authors argued that the name *Chlorophonia* would not describe the phenotypes of these species particularly well. Adult males, except for the Lesser

Antillean subspecies of *E. musica*, lack any green plumage. Imfeld *et al.*'s third option, and the recommendation of this proposal, is to resurrect the genus *Cyanophonia* and place the 3 blue-hooded species in it. *Cyanophonia* was established by Bonaparte (1851) for the blue-hooded euphonias in the same volume as *Chlorophonia* and, thus, has equal priority to *Chlorophonia*. Additionally, given that all plumages of these three species possess blue hoods, even juveniles, the name is a better descriptor than *Chlorophonia*.

Recommendation:

Based on the new phylogenetic information presented in Imfeld *et al.* (2020), we recommend:

- (1) that *E. elegantissima* and *E. musica* be transferred to the genus *Cyanophonia*, and
- (2) that a new linear sequence be adopted for the subfamily Euphoniinae:

Cyanophonia (or *Chlorophonia*) *elegantissima*
Cyanophonia (or *Chlorophonia*) *musica*

Chlorophonia flavirostris
Chlorophonia occipitalis
Chlorophonia callophrys

Euphonia jamaica
Euphonia affinis
Euphonia luteicapilla
Euphonia minuta
Euphonia hirundinacea
Euphonia laniirostris
Euphonia imitans
Euphonia gouldi
Euphonia fulvicrissa
Euphonia anneae
Euphonia xanthogaster

Please vote on the following:

- (a) YES/NO: transfer *Euphonia musica* and *E. elegantissima* to a new genus;
- (b) Option 1/Option 2: transfer these species (1) to resurrected genus *Cyanophonia* or (2) to *Chlorophonia*; and
- (c) YES/No: revise the linear sequence of the subfamily.

Literature Cited:

Bonaparte, C.L. 1851. Note sur les Tangaras, leurs affinités, et descriptions d'espèces nouvelles. *Revue et Magasin de Zoologie Pure et Appliquée* 2(3): 129-138.
Clements, J. F., T. S. Schulenberg, M. J. Iliff, S. M. Billerman, T. A. Fredericks, B. L. Sullivan, and C. L. Wood. 2019. The eBird/Clements Checklist of Birds of the World: v2019.
<https://www.birds.cornell.edu/clementschecklist/download/>

Zucon D., Prÿs-Jones R., Rasmussen P.C., and Ericson P.G.P. 2012. The phylogenetic relationships and generic limits of finches (Fringillidae). *Molecular Phylogenetics and Evolution* 62(2): 581-596.

Submitted by: Tyler S. Imfeld and Nicholas A. Mason

Date of Proposal: 5 May 2020, revised October 2020

Split Band-rumped Storm-Petrel *Hydrobates castro***Background:**

The Band-rumped Storm-Petrel complex (*Hydrobates castro sensu lato*) contains seven named taxa distributed across the Atlantic and Pacific Ocean basins. The complex has long been thought to contain multiple cryptic species due to vocal differences between populations and the presence of both hot-season and cool-season breeding populations present on single islands or archipelagos. However, plumage patterns and morphometrics in the group are highly conserved, making it extremely difficult to assign individuals to taxa under field conditions, especially away from breeding colonies.

The named taxa in the group, in order of date of description, are:

castro (Harcourt, 1851) – widespread North Atlantic breeder

jabejabe (Bocage, 1875) – Cape Verde Islands

cryptoleucura (Ridgway, 1882) – Hawaii

bangsi (Nichols, 1914) – Galapagos Islands

helenae (Mathews, 1934) – southern Atlantic islands

kumagai (Mathews, 1938) – Japan

monteiroi (Bolton et al., 2008) – Azores hot season breeders

Additionally, at least two breeding populations lack formal taxonomic descriptions. The first consists of North Atlantic cool-season breeders (Howell 2012, Taylor et al. 2019) sometimes called “Grant’s” Storm-Petrel (hot-season North Atlantic breeders are nominate *H. castro*). The second is a population breeding on islands in the Gulf of Guinea (Flood et al. 2012).

The NACC tackled this problem as recently as 2019 in proposal 2019-C-10, which resulted in the unanimous acceptance by the committee of the split of Monteiro’s Storm-Petrel, *H. monteiroi*, from all other taxa in the group. This split was based on the findings of Bolton et al. (2008), who showed convincingly that populations of *monteiroi* and *castro* breeding on the Azores segregated temporally, did not recognize one another vocally, and exhibited very low levels of gene flow, thus qualifying as distinct species under the Biological Species Concept. *Hydrobates monteiroi* has also been recognized by global lists (Clements et al. 2019, HBW and BirdLife International 2019, Gill et al. 2020). Additionally, the population breeding on the Cape Verde Islands has been recognized as a species by several authorities (Clements et al. 2019, HBW and BirdLife International 2019, Gill et al. 2020) under the name Cape Verde Storm-Petrel, *H. jabejabe*, but this split has not yet been considered by the NACC.

A series of publications has tackled the phylogeography of the complex using mitochondrial DNA, microsatellite markers, and small numbers of nuclear loci (Friesen et al. 2007, Sangster et al. 2012, Silva et al. 2016, Smith et al. 2007, Smith and Friesen 2007, Wallace et al. 2017), but each has had either a narrow geographic focus or has lacked genetic samples from some populations or named taxa. Additionally, the complex has been the focus of vocal playback studies (Bolton 2007), which are described in detail below.

As an aside, another recent proposal accepted by the committee (2019-B-7) transferred all species in the genus *Oceanodroma* to *Hydrobates*, due to paraphyly in the former genus (Wallace et al. 2017; *Hydrobates* has priority and is embedded within *Oceanodroma*). The

decision to lump the genera in place of splitting *Oceanodroma* was made in part due to the fact that no name was thought to be available for one of the clades in *Oceanodroma*. That clade contained samples of *monteiroi* and *jabejabe* (= the old *castro*), for which a name is in fact available: *Thalobates* (Mathews 1943), which has *castro* as the type species (Mathews and Hallstrom 1943). Although the current proposal contains insufficient information with which to revisit the generic-level classification of the Hydrobatidae, this is simply to note that should *Hydrobates* be split in the future, the *H. castro* complex could be transferred to *Thalobates*.

New Information:

Taylor et al. (2019) provided, for the first time, a phylogenetic study of Band-rumped Storm-Petrels that included all named populations, both hot- and cool-season breeders, and many thousands of nuclear loci, all of which allows for a more complete revision of the taxonomy of the group. The only unsampled population consists of the as-yet unnamed breeders on islands of the Gulf of Guinea. Taylor et al. (2019) sequenced 3,707 nuclear loci using ddRAD-Seq and two mitochondrial loci (cytochrome *b* and the control region). They estimated phylogenies from the nuclear SNPs using RAxML and SNAPP, and from the mitochondrial data in BEAST.

In both the nuclear and mitochondrial phylogenies, they recovered *monteiroi* as embedded within the currently defined *H. castro* (Figs. 5-7). These phylogenies found with high support that *jabejabe* was sister to the remainder of the group. The topology of the rest of the tree was rather less resolved, with different analyses placing *monteiroi* either as sister to the remaining five taxa (nuclear RAxML tree) or as sister to *castro sensu stricto* (nuclear SNAPP tree, mitochondrial tree).

Two methodological shortfalls are worth mentioning, both of which may affect the taxonomic conclusions. The first is the selection of an outgroup taxon and the second is the model used for the estimation of the RAxML phylogeny. None of the phylogenies estimated by Taylor et al. (2019) used a sample outside of the Band-rumped Storm-Petrel complex as an outgroup. Instead, they opted to root all of the trees with their samples of *jabejabe*, a decision that was based on the mitochondrial cytochrome *b* phylogeny in Wallace et al. (2017), who found *jabejabe* to be sister to the rest of *castro (sensu lato)* and also did use an outgroup. Although rooting the mitochondrial phylogeny with *jabejabe* in Taylor et al. (2019) is likely a safe assumption given the similar locus-sampling of the two studies, it is certainly not the case for the tree based on the nuclear SNPs, given the many documented cases of topological discordance between mitochondrial and nuclear phylogenies across the tree of life. Different analyses of the nuclear data in Taylor et al. (2019) show conflicting results with regard to the genetic distinctiveness of each taxon, which would have been clarified by the use of an outgroup. Both the STRUCTURE and PCA results of nuclear SNPs in Taylor et al. (2019) show that *castro (sensu stricto)* is the most genetically distinct taxon analyzed (Figure S3, Figure 3), and *jabejabe* doesn't show up as genetically distinct from the rest of the group in the STRUCTURE results until K=4 (Figure S3A). While PCA and STRUCTURE analyses do not implicitly test phylogenetic relationships, this does suggest that the nuclear and mitochondrial genetic patterns differ, and that rooting the nuclear phylogeny with *jabejabe* is not a safe assumption. However, the SNAPP phylogeny of nuclear data (which does not require the setting of an outgroup) did recover *jabejabe* as sister to the rest of complex. The second factor is the model used to infer the RAxML phylogeny. RAxML provides a SNP-specific model that corrects for the ascertainment bias of using DNA datasets that contain variable sites only, but this appears to have not been used. This, plus the amount of missing data in SNP datasets, has been shown to affect both topology and branch lengths of SNP-based phylogenies (Leaché et al. 2015) and

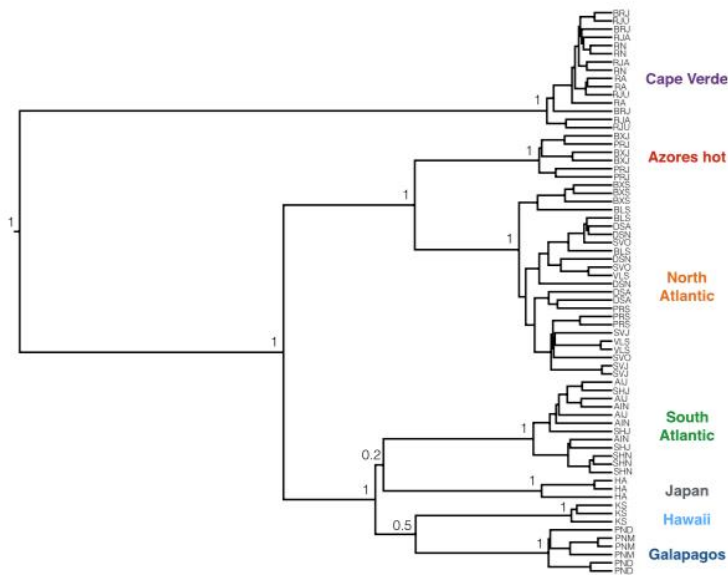


Fig. 5. Bayesian phylogenetic reconstruction of concatenated cytochrome *b* and control region mitochondrial DNA sequences of the band-rumped storm-petrel species complex, generated in BEAST. Posterior probability values are given above nodes to show support for the seven groups uncovered in our analyses.

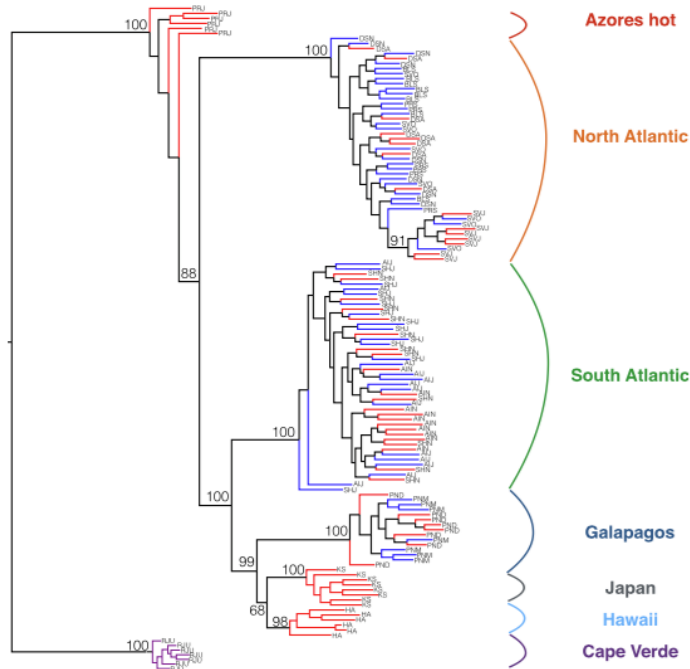


Fig. 6. Maximum likelihood phylogenetic reconstruction of relationships among the band-rumped storm-petrels generated in RAxML. Bootstrap support is given for all nodes with a value above 50. Branches are coloured by the breeding time of the individual bird: red for a bird sampled during the hot season, blue for a bird sampled during the cool season, and purple for a bird sampled from a colony with year-round breeding. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

Figures 5, 6 (both above), and 7 (on next page) from Taylor et al., presenting phylogenetic results from Bayesian, maximum likelihood, and SNAPP analyses. For ease of interpretation, I provide here the taxonomic names that correspond to their sampling populations: “North Atlantic” = *castro*, “Azores hot” = *monteiroi*, “South Atlantic” = *helena*, “Cape Verde” = *jabejabe*, “Galapagos” = *bangsi*, “Hawaii” = *cryptoleucura*, “Japan” = *kumagai*.

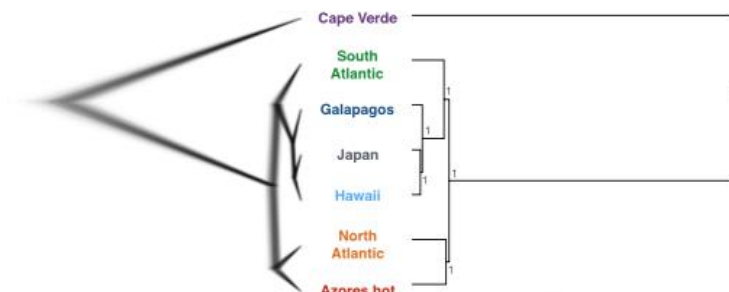
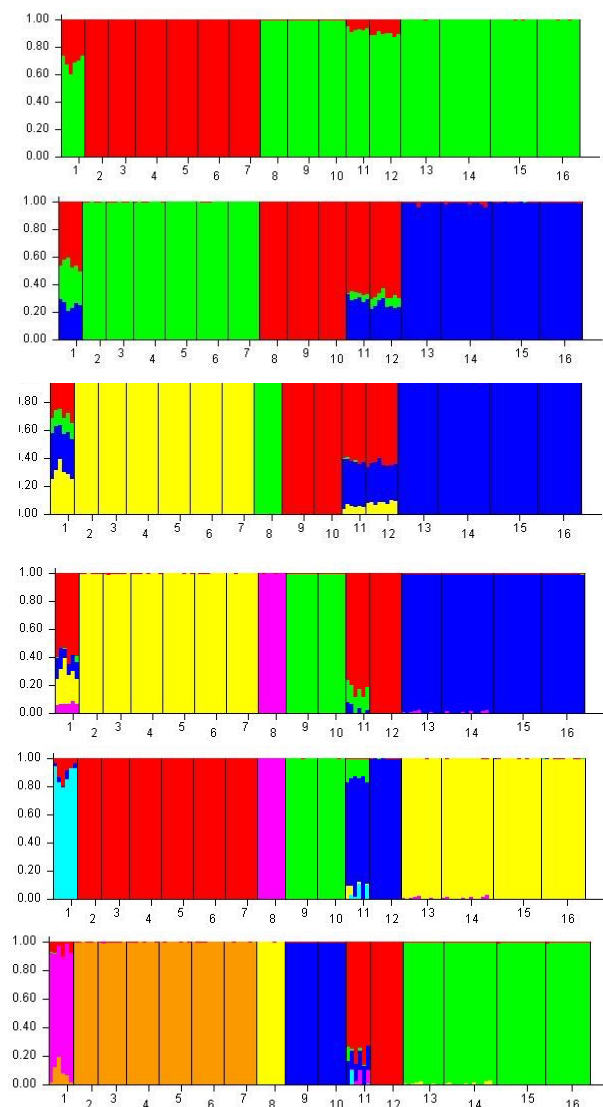


Fig. 7. Phylogenomic reconstruction of the seven genetic groups of band-rumped storm-petrels generated in the SNAPP package in BEAST. The left-hand side shows the densitree and the right-hand side shows the consensus tree with posterior probabilities labelled on the nodes.



Figures S3A and S3B from Taylor et al. (2019). The STRUSTRUCTURE results presented in the main paper show all populations for only $K=2$ (the K value with the lowest log likelihood), while $K = 2$ through $K = 7$ are presented only in the supplemental material pasted here. Population assignments: 1 = *monteiroi*, 2-7 = *castro*, 8 = *jabejabe*, 9-10 = *bangsi*, 11 = *cryptoleucura*, 12 = *kumagai*, 13-16 = *helena*.

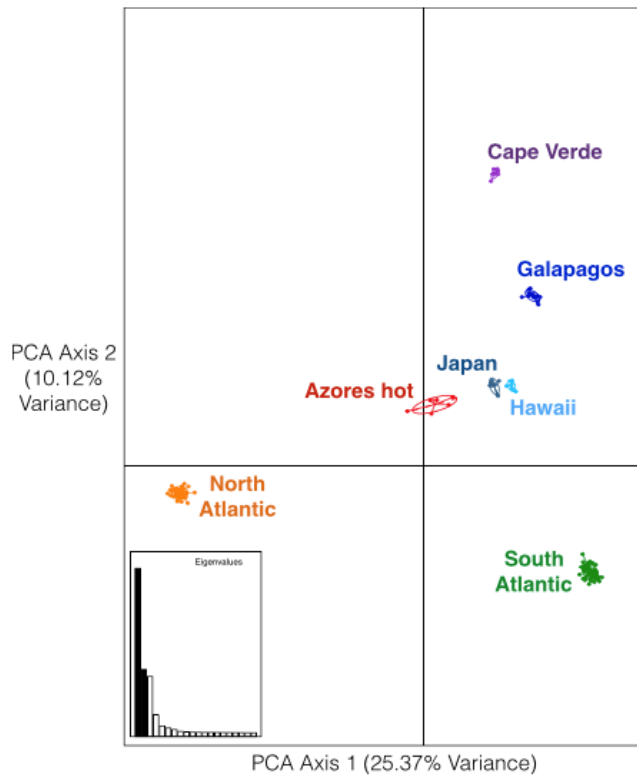


Fig. 3. Results of a principal component analysis of the band-rumped storm-petrel species complex seven genetic groups. Ellipses and colours have been chosen to label the six resultant non-overlapping clusters.

R.S. Taylor, et al.

Molecular Phylogenetics and Evolution 139 (2019) 106552

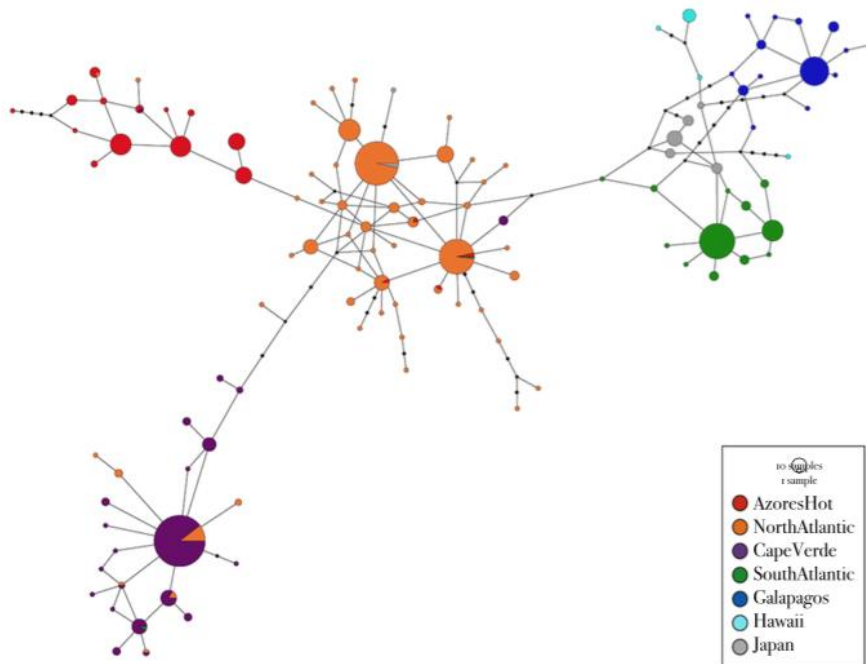


Fig. 4. Statistical parsimony network of 333 bp of the mitochondrial control region of 754 band-rumped storm-petrels. Circle size relates to the number of samples with each haplotype. Black circles represent unsampled or now-extinct haplotypes.

may account for the non-monophyly of *monteiroi* in Figure 6. In fact, using different locus filtering strategies, Taylor et al. (2019) recovered an identical topology to Figure 6, but with all samples of *monteiroi* as monophyletic and in the same position in the tree (Figure S7A, S7B). It is unclear why these phylogenies were presented as supplementary material and not in the main paper. For these reasons, the SNAPP phylogeny should, I think, be given greater weight than the RAxML phylogeny.

The STRUCTURE results produced some interesting patterns, with some taxa showing assignments from multiple populations. In particular, all individuals of *monteiroi* showed a proportion of genetic assignments from all other populations, perhaps due to incomplete lineage sorting after a recent divergence or to introgression. Even at K=7 the Japanese and Hawaiian populations do not fully segregate, a finding corroborated by the variable phylogenetic position of *kumagai*. No explicit tests of gene flow were performed, however.

Based on the results of Taylor et al. (2019), the current treatment by the NACC results in a paraphyletic *Hydrobates castro*, although this may be expected given the recent divergence times between taxa in this group (see below), perhaps due to peripatric speciation and rapid evolution of reproductive isolation, at least between some taxa (e.g. *monteiroi*). The three phylogenies in Taylor et al. (2019) contain discordant topologies that differ with regard to the position of *monteiroi* and the three Pacific taxa, but a three-way split of *H. castro* would result in monophyletic species according to each phylogenetic hypothesis. Given the strong evidence of reproductive isolation between *monteiroi* and *castro* presented in Bolton et al. (2008) and the unanimous acceptance of *monteiroi* as a species by this committee, the merging of *monteiroi* back into *castro* is not a valid option. A three-way split of *castro* would result in the elevation of *H. jabejabe* (which has been accepted by other global bird checklists) and *H. cryptoleucura* (including *kumagai*, *bangsi*, and *helena*) to species, leaving a monophyletic *H. castro*. Both hot-season and cool-season North Atlantic breeders clustered together in the mitochondrial and RAxML SNP phylogenies, indicating that “Grant’s” Storm-Petrel is not genetically distinct from *castro* and should probably not be treated as a distinct taxon. Clustering the Pacific and South Atlantic taxa under one species makes little biogeographic sense, so an argument could be made to also elevate the South Atlantic taxon *helena* to species level. However, the mitochondrial phylogeny did not recover monophyletic Pacific and South Atlantic groups, but instead recovered *kumagai* as sister to *helena* (to the exclusion of *cryptoleucura* and *bangsi*), albeit with low support. Although the two phylogenetic analyses of nuclear data did recover monophyletic Pacific basin or South Atlantic groups, the discordant mitochondrial phylogeny suggests incomplete lineage sorting or introgression between Pacific and South Atlantic populations. The Pacific and South Atlantic populations also cluster together quite closely in the mitochondrial haplotype network (Figure 4).

Based on the reciprocal monophyly of each taxon in all three phylogenies, Taylor et al. (2019) suggested a six-species solution, elevating all taxa to species level with the exception of maintaining *kumagai* as a subspecies of *cryptoleucura* based on the low levels of genetic differentiation between the two taxa in their STRUCTURE analyses. Taylor et al. (2019) did not provide an estimate for the divergence times in the group, but a date is available from Silva et al. (2016) who estimated the divergence of *castro*, *monteiroi*, *kumagai*, and *bangsi* at ~200,000 years using a strict mitochondrial molecular clock. Given how recent the entire radiation is, as well as the lack of explicit tests of introgression between taxa, I think it best to proceed more conservatively for the time being.

Vocal analyses have not been conducted for all taxa, but Bolton (2007) did conduct playback experiments on Azores (*monteiroi*), Galapagos (*bangsi*), and Cape Verde (*jabejabe*) populations

by presenting each of these populations to playback of other taxa (including recordings of *castro*) and control sounds. Some of this evidence was used to support the splitting of *monteiroi* from *castro*. Bolton's results indicated that *monteiroi* and *bangsi* both did not respond to playback of other populations any more than they responded to a control. Cape Verde *jabejabe* did respond more to their own calls than to those of other populations, but showed slightly elevated response to *castro*. Although these data are incomplete for our purposes, they do suggest a pre-zygotic isolation for Pacific Ocean taxa and for *monteiroi*, but are equivocal for *jabejabe*. This is interesting because some of the phylogenies suggest that *jabejabe* is the most genetically differentiated taxon of the group. It does provide support for species status for *cryptoleucura* (which would include *bangsi*), but additional playback experiments that include *helenae*, *cryptoleucura*, and *kumagai* are desirable. In the Figure 2 from Bolton (2007) shown below, GD=*bangsi*, AH=*monteiroi*, AC=*castro*, CV=*jabejabe*, and CS, SL, and LS are calls from control taxa.

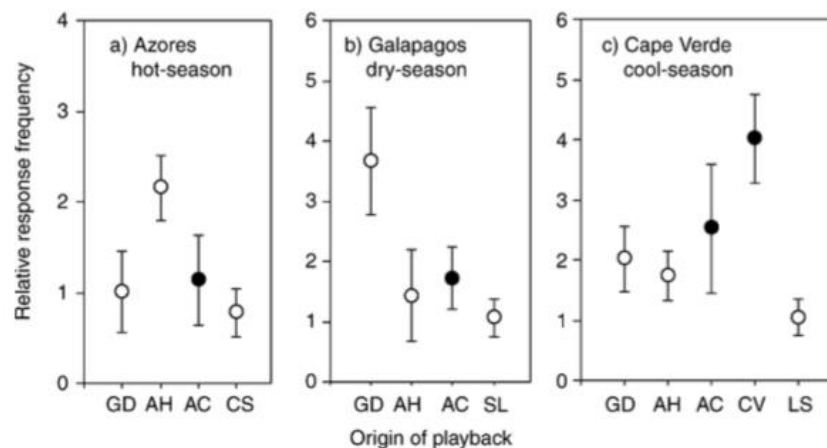


Figure 2. Relative response rate (mean \pm 95% CL) of Madeiran Storm-petrels to playback of Burrow Calls from different populations. (a) Experiment conducted on the Azores hot-season population in June, presenting playback from the Galapagos dry-season (GD), Azores hot-season (AH), Azores cool-season (AC) and Cory's Shearwater (CS) as a control. (b) Experiment conducted on the Galapagos dry-season population in May, presenting playback from the Galapagos dry-season (GD), Azores hot-season (AH), Azores cool-season (AC) and Galapagos Sealions (SL) as a control. (c) Experiment conducted on the Cape Verde cool-season population in December, presenting playback from the Galapagos dry-season (GD), Azores hot-season (AH), Azores cool-season (AC), Cape Verde cool-season (CV) and Little Shearwater (LS) as a control. The relative response rate is the ratio of number of calls during the 5-min playback period to the average number of calls before and after the playback trial (see text for more details). Open symbols = populations nesting May–September, closed symbols = populations nesting October–February. As response rates are calculated relative to background rates, a value of 1 represents the background rate (i.e. in the absence of any playback). Where the confidence limits overlap 1.0, there was no significant increase in Flight Call rate above the background level.

In summary, mitochondrial DNA data supported four clusters corresponding to *castro*, *cryptoleucura*, *monteiroi*, and *jabejabe*, but with some shared haplotypes between *castro* and *jabejabe*. The nuclear phylogenies supported these same four groups, but may also support *helenae* and *bangsi* as distinct. The SNAPP phylogeny of nuclear data, in particular, supported *jabejabe* as quite distinct from all other taxa. Branch lengths for all of these groups (except for *jabejabe*) were very short, indicating very recent divergence times for most taxa. The STRUCTURE analysis of nuclear data, however, showed extensive shared population assignments (i.e., indicative of introgression or incomplete lineage sorting) in some cases. In particular, *monteiroi* showed shared population assignments with most other taxa (which is of note, considering its documented reproductive isolation from *castro*), and *cryptoleucura/kumagai* show shared population assignments with *bangsi*, *helenae*, and perhaps

to a lesser degree with *castro*. The taxa *castro*, *jabejabe*, *bangsi*, and *helen*a showed no (or minimal) shared population assignments with any other taxa at any value of K. Vocal playback experiments suggested that *monteiroi* and *bangsi* are each distinct (no vocal recognition) from *castro* and *jabejabe*, but were equivocal with regards to *jabejabe* being distinct from *castro*. Vocal playback data are lacking from the other taxa.

This is an extremely complex system, and evidence from the mitochondrial DNA, nuclear DNA, and vocal recognition data do not present a clear taxonomic solution. Despite the many studies published on the group, much work remains to be done. Particularly relevant to taxonomic decisions would be studies that include estimates of rates of gene flow between taxa, detailed analyses of song structure, and vocal recognition experiments including all taxa.

Recommendation:

At least four taxonomic treatments are available given the results from Taylor et al. (2019) and Bolton (2007), and the relative importance given to each line of evidence. These are discussed below as options A-D:

- A (the recommended option) – 3 species (*castro*, *jabejabe*, *cryptoleucura*)
- B – 2 species (*castro*, *jabejabe*)
- C – 4 species (*castro*, *jabejabe*, *cryptoleucura*, *helen*a)
- D – 5 species (*castro*, *jabejabe*, *cryptoleucura*, *helen*a, *bangsi*).

Given the arguments outlined above, in particular the nuclear DNA evidence supporting the distinctiveness of *jabejabe* and the vocal data indicating the lack of vocal recognition between *bangsi* and the North Atlantic taxa, **I recommend a four-species treatment for the complex**, which would divide the current *Hydrobates castro* into three species, *H. monteiroi* having already been elevated to species status. This is **option A**, which would result in recognition of the following species:

Hydrobates castro: Widely distributed in the North Atlantic. Contains both hot-season and cool-season breeding populations. The English name Madeiran Storm-Petrel is widely used, although the name is not ideal as the species occurs on other North Atlantic islands.

Hydrobates jabejabe: year-round breeder on the Cape Verde Islands. Known at sea only from the vicinity of the breeding islands. The English name Cape Verde Storm-Petrel is widely used.

Hydrobates cryptoleucura: widely distributed in the Pacific and South Atlantic Oceans, including both hot-season and cool-season breeding populations. Includes the subspecies *bangsi*, *kumagai*, and *helen*a. No common name is in wide use for this group. Given that the distribution does not conform to any one biogeographic region and that there are few morphological differences to separate it from other taxa, no obvious name is available. If the committee votes to split *cryptoleucura*, I suggest a separate proposal be submitted to address the name for this species.

Alternatively, given that vocal playback data are not available for some taxa (*helen*a in particular), a more conservative treatment would be to hold off on splitting *cryptoleucura* until more vocal data are available. This **three-species treatment** would split *H. jabejabe* from the current *H. castro*. This is **option B**:

Hydrobates castro: Widely distributed in the Atlantic and Pacific basins. Contains both hot-season and cool-season breeding populations of *castro*, and the subspecies *cryptoleucura*, *bangsi*, *kumagai*, and *helenae*. The English name Madeiran Storm-Petrel is widely used, although the name is not ideal as the species occurs on many other Atlantic and Pacific islands. In keeping with NACC policy and previous decisions, I recommend that the name Band-rumped Storm-Petrel be retained for this widespread species, as the splitting of *jabejabe* would elevate a range-restricted taxon from a much more widespread form.

Hydrobates jabejabe: same as in option A.

Two alternative species treatments are available, but I believe that both would need additional evidence from playback experiments, morphological studies, or estimates of gene flow before the splits be considered. I have included them here for the sake of completeness. These treatments are **not recommended**, given the current data available.

C) A five-species treatment, which would be the same as the four-species treatment above, with the additional split of the southern Atlantic *helenae* from the three Pacific taxa. Possible English name for *helenae*: Saint Helena Storm-Petrel.

D) A six-species treatment, following the recommendation of Taylor et al. (2019), which is the same as C with the additional split of the Galapagos taxon *bangsi* from the other two Pacific taxa. Possible English name for *bangsi*: Darwin's Storm-Petrel.

Committee members should vote on the following:

- (a) maintain *castro* as currently constituted; if voting NO on (a), continue to (b)
- (b) split *castro* into three species (*castro*, *jabejabe*, *cryptoleucura*), as recommended in the proposal; if voting NO on (b), continue to (c)
- (c) split *castro* into 2, 4, or 5 species; if voting YES, specify how many (and which) species to be recognized.

Status in the AOU region

Hydrobates jabejabe is known at sea only from the vicinity of the breeding islands, so is best considered extralimital. Both *H. jabejabe* and *H. monteiroi* could occur in the AOU region, but given the difficulty in field identification, either species would likely require DNA sequence data or a band recovery to confirm their occurrence.

Hydrobates castro is thought to be the taxon that occurs regularly as a non-breeding visitor off the east coast of North America and in the Gulf of Mexico. This is supported by a specimen recovered in Alabama that had been banded as a breeding adult in the Azores in September, so is referable to *castro* (Woollfenden et al. 2001).

Hydrobates cryptoleucura breeds in Hawaii. A single record from California (Singer et al. 2020) certainly pertains to one of the Pacific breeding taxa and is thus referable to *H. cryptoleucura* but remains unidentified to subspecies. The South Atlantic taxon *helenae* is widespread at sea in the South Atlantic but lacks documented records for our area and is unlikely to occur.

Effect on the AOS Checklist:

Option A would add one species to the AOS Checklist; *H. cryptoleucura*. Option B would add no species to the AOS Checklist.

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Submitted by: Oscar Johnson, Louisiana State University Museum of Natural Science

Date of proposal: 13 May 2020

Split Mew Gull *Larus canus brachyrhynchus* and rename as Short-billed Gull**Description of the problem:**

The western North American form now considered a subspecies of the Mew/Common Gull, *Larus canus brachyrhynchus*, was treated as a species through the third edition of the AOU checklist, but was lumped with the widespread Palearctic *L. canus* in the fourth edition (AOU 1931; <https://avibase.bsc-eoc.org/species.jsp?lang=EN&avibaseid=342F6965&sec=summary&ssver=1>; Peters 1934). The finding of a 2% mtDNA divergence between *brachyrhynchus* and the east Siberian *kamtschatschensis* (Zink et al. 1995) has encouraged the treatment of *brachyrhynchus* as a separate species by some (Olsen and Larsson 2004) or treatment as three separate field-identifiable groups at least (Carey and Kennerley 1996, Howell and Dunn 2007). The lack of inclusion of the nominate in the Zink et al. (1995) study (which only included one individual of *brachyrhynchus* and three *kamtschatschensis*), the lack of a more recent and densely sampled published phylogeny including these taxa, the poor state of knowledge of the characters of the eastern Palearctic forms *heinei* and *kamtschatschensis*, and the suggestion that the American and W Palearctic forms might form a single species-group to the exclusion of E Palearctic *kamtschatschensis* (AOU 1983, Sibley and Monroe 1993) has contributed to stasis in their treatment as a single species (Dickinson and Remsen 2013, del Hoyo and Collar 2014, Clements et al. 2019, Gill et al. 2020).

New information:

By far the most comprehensive molecular phylogenetic analysis of gulls of which I am aware is in a dissertation (Sternkopf 2011) as yet unpublished in a peer-reviewed journal but available in full online (https://epub.uni-greifswald.de/frontdoor/deliver/index/docId/770/file/Dissertation_Viviane_Sternkopf_Uni_Bib.pdf). This dissertation includes an entire section on the *Larus canus* clade, which also includes Ring-billed Gull *Larus delawarensis*. Samples included 36 *canus*, 12 *heinei*, five *kamtschatschensis*, and four *brachyrhynchus*. Although *brachyrhynchus* is not included in the several phylogenetic trees of the whole subfamily, the haplotype networks (e.g., Fig. 3.33, below) support the genetic similarity of all three Palearctic forms to the exclusion of *brachyrhynchus*. An AMOVA of genetic variances showed that the best model was that in which *L. delawarensis* and *brachyrhynchus* were treated as separate species, and the three Palearctic taxa *canus*, *heinei*, and *kamtschatschensis* united (Sternkopf 2011). Based on these results and previously available data, Sternkopf recommended the treatment of *brachyrhynchus* as a distinct species, while keeping all Palearctic taxa in *L. canus*.

A recent paper on the *Larus canus* complex (Adriaens and Gibbins 2016), published as a special issue of *Dutch Birding*, provided an extremely comprehensive 63-page study focusing on morphology and identification, but incorporating review of vocalizations as well, and it involved field study of all taxa. A repeatable plumage scoring system with published reference photos was used for numerous characters of large museum specimen series of all taxa (e.g., figs. 9-12 below from Adriaens and Gibbins 2016). Several characters (e.g., diagrams 9 and 12) showed clear but not quite diagnostic differences between *brachyrhynchus* and the other taxa, whereas other characters (e.g. diagrams 10 and 11) did not. Non-metric multi-dimensional scaling analyses (NMDS) of wing-tip pattern showed near-complete separation between *brachyrhynchus* and the Western Palearctic taxa, but a little overlap with *kamtschatschensis*

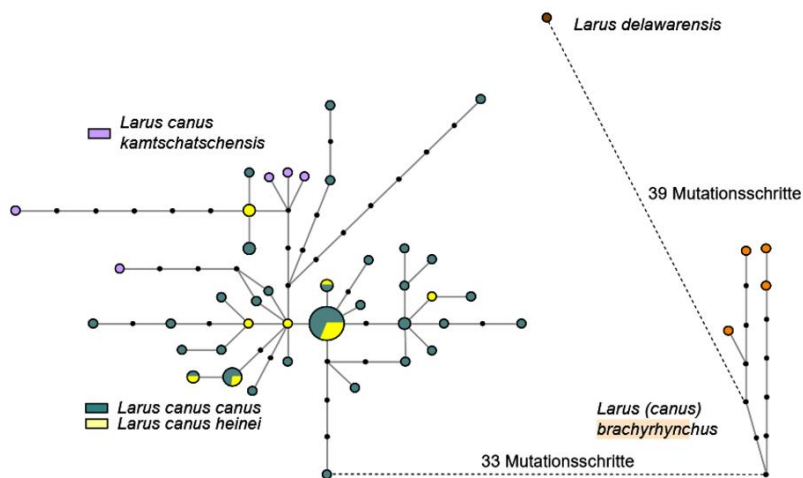
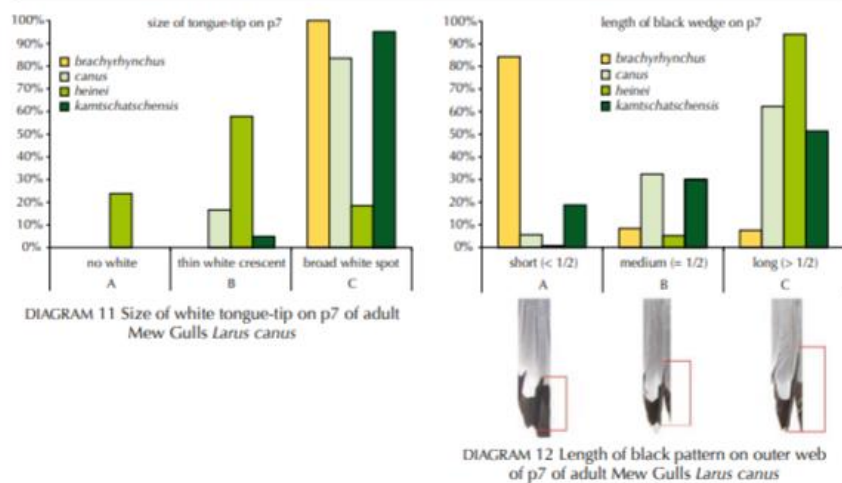
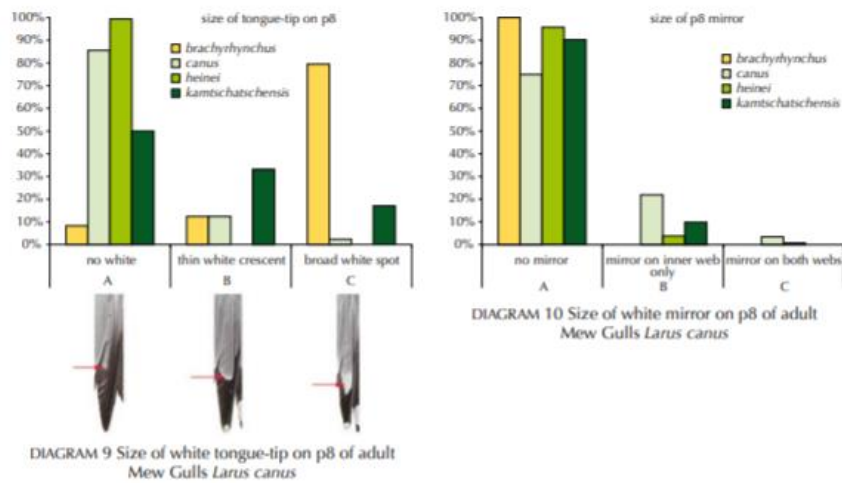


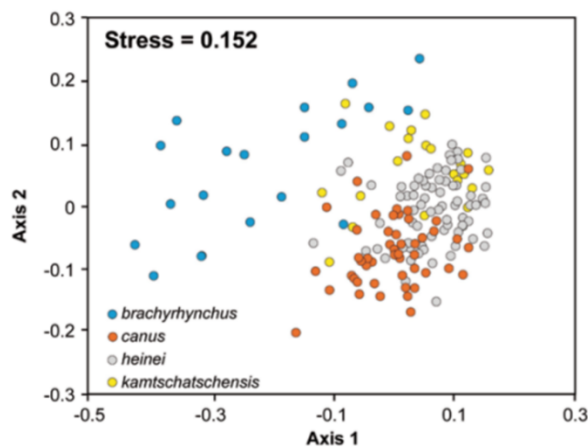
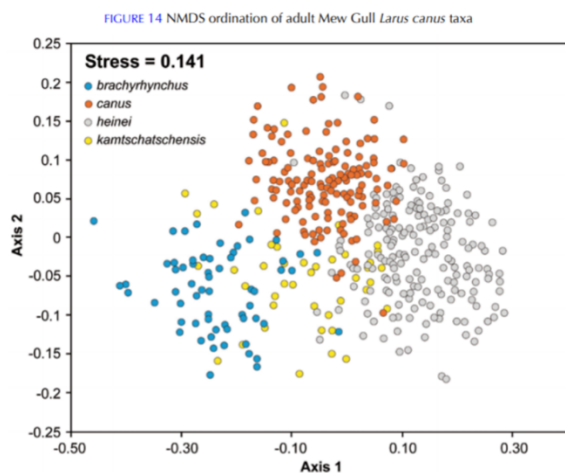
Fig. 3.33 in Sternkopf (2011): Median-joining tree for cytb, ND2 and HVR-1.

Identification of the Larus canus complex



Diagrams 9-12 from Adriaens and Gibbins (2016).

(figs. 14 and 15 of Adriaens and Gibbins 2016), which it should be made clear is the most distinct from *brachyrhynchus* in proportions (Adriaens and Gibbins 2016: p. 7).



Figures 14-15 from Adriaens and Gibbins (2016).

Further, display vocalizations were shown to differ between the Palearctic group (with *kamtschatschensis* being the most different) and *brachyrhynchus* (as in figs. 10 and 12 from Adriaens and Gibbins 2016, below). Qualitative vocal differences were previously noted by Sibley (2000) and Constantine & The Sound Approach (2006).

Identification of the *Larus canus* complex

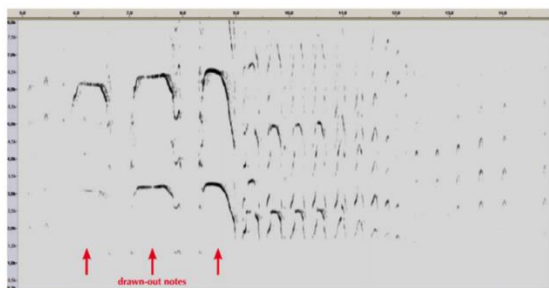


FIGURE 10 Long call of Russian Common Gull / Russische Stormmeeuw *Larus canus heinei*, adult, Medvedevskiy rayon, Mari El Republic, Russia, 22 June 2014 (Albert Lastukhin/www.xeno-canto.org/187416). Drawn-out notes extremely similar in structure, length and pitch to those of nominate *canus*.

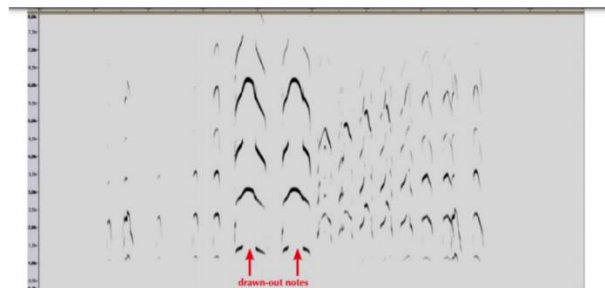


FIGURE 12 Long call of Short-billed Gull / Amerikaanse Stormmeeuw *Larus (canus) brachyrhynchus*, adult, Watson lake, Yukon, Canada, 2 June 2014 (Andrew Spencer/www.xeno-canto.org/189385). Drawn-out notes of long call have symmetrical, conical shape.

Adriaens and Gibbins (2016) considered that the morphological diagnosability, geographic isolation, distinctive vocalizations, and genetic divergence of *brachyrhynchus* is consistent with its treatment as a separate species. They did not rule out the possibility that *kamtschatschensis* may also be specifically distinct, as it has some vocal differences and is generally readily distinguishable morphologically, but it does appear to intergrade with the central Palearctic form *heinei* and groups genetically with the *canus* group.

Effect on AOS-CLC area:

The American form *brachyrhynchus* occurs along the west coast of North America, with widely reported vagrancy, including to the Azores (Alfrey and Ahmad 2007). Acceptance of this proposal would require providing a separate species account for *brachyrhynchus*. In addition, the European nominate has been widely reported in eastern North America at least, and there are numerous North American records of the east Siberian *kamtschatschensis*, mainly from Alaska, but also, e.g., from Hawaii and northeastern North America.

Nomenclatural issues:

Mlíkovský (2012) considered the name *kamtschatschensis* Bonaparte, 1857, to be both a junior synonym to *Gavina kamtschatchensis* Bruch, 1855, and a *nomen nudum*, and Bruch's name was adopted by del Hoyo and Collar (2014), but was neither adopted nor commented upon by Dickinson and Remsen (2013), nor by Gill et al. (2020). Dick Schodde kindly reviewed this case (in litt. 25 Jun 2020) and opined that, while Bonaparte's earlier usages of *kamtschatschensis* all remain *nomina nuda*, his 1857 usage is potentially available because it was taken up by Peters (1934) before 1961. However, because *kamtschatchensis* Bruch, 1855, is the first available name, Bruch is the author, but the incorrect subsequent spelling *kamtschatschensis* is in prevailing usage and thus protected by ICZN Article 33.3.1. Thus, on Schodde's advice the name should be *Larus canus kamtschatschensis* (Bruch, 1855).

English names:

Common Gull has long been used for Palearctic birds, and Mew Gull was earlier used for North American *brachyrhynchus*. However, recent extensive usage of Mew Gull for all these taxa (e.g., Gill et al. 2020, Moskoff and Bevier 2020) and for *Larus c. canus* (not including *brachyrhynchus*) by AOU (1886) has made its use exclusively for *brachyrhynchus* as a daughter species problematic and not in keeping with our stated policy. Short-billed Gull, however, has been used extensively in recent literature and is the name used in the first edition of the Check-list (AOU 1886) to refer to *brachyrhynchus* alone, and is apt given that its small bill is one of its most apparent identification features. The English name Common Gull has been used for the entire complex as well, but has never become entrenched for *brachyrhynchus*, while being extremely entrenched for the Palearctic taxa.

Recommendation:

In my opinion the integrative evidence favors treating *brachyrhynchus* as a separate species that is best known as Short-billed Gull. The evidence for a split of *kamtschatschensis* is notably weaker and would require further analyses.

Please vote separately on each of the following recommendations:

- a) Split *Larus brachyrhynchus* as a monotypic species from the *Larus canus* group.
- b) Retain *kamtschatschensis* within the *Larus canus* group.
- c) Change the authorship of the east Siberian form to *kamtschatschensis* (Bruch, 1855).
- d) Adopt the now widely familiar English name Short-billed Gull for *Larus brachyrhynchus*.
- e) Maintain Common Gull as the English name for *Larus canus* s.s.

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Submitted by: Pamela C. Rasmussen, Michigan State University

Date of proposal: 25 June 2020

Revise generic limits in the Phalacrocoracidae (cormorants)

Description of the problem:

For many years, all cormorants were placed in a single genus (e.g., AOU 1886, Mayr and Cottrell 1979), a treatment that presumably seemed warranted due to their relative homogeneity of form and plumage. Siegel-Causey (1988), on the basis of an osteological analysis, divided the family into two subfamilies: the Phalacrocoracinae, with four genera; and the Leucocarboninae, with five genera, but this treatment was not widely adopted. Kennedy et al.'s (2000) early DNA phylogeny did not recover most of Siegel-Causey's (1988) clades, including at the subfamily level. This led Worthy (2011), who sought to determine the relationships of certain Late Oligocene-Early Miocene (26–24 mya) Australian fossil cormorants (*Nectornis* and *Nambashag*, the latter a new genus), to base his osteological analysis of modern taxa on a different set of newly scored characters. Worthy's (2011) osteologically based phylogenetic tree recovered many but by no means all of the clades in Kennedy et al. (2000, 2009). Because many taxa were still missing from their phylogenies, Kennedy et al. (2009) recommended continuing to retain all species in the genus *Phalacrocorax*, although they suggested that ultimately two or more genera might be justified. Most world lists, however, now recognize at least two genera, *Microcarbo* and *Phalacrocorax* (Dickinson and Remsen 2013, del Hoyo and Collar 2014, Clements et al. 2019, Gill et al. 2020); *Microcarbo* does not occur in the NACC area.

More recently, Kennedy and Spencer (2014) produced a nearly complete phylogeny of Phalacrocoracidae, which formed the basis for Remsen's (2014) proposal #648 to SACC to recognize 7 genera in the Phalacrocoracidae (which nearly passed, failing at 6-4 to attain a 2/3 vote; see votes and comments at <https://www.museum.lsu.edu/~Remsen/SACCprop648.htm>), as well as to Remsen's recent proposal (2020-A-12) to NACC that led us to resequence the NACC-area cormorants (Chesser et al. 2020). The latter proposal did not address generic limits in the Phalacrocoracidae but did mention the need for such a proposal.

New information:

As NACC has not yet formally considered the issue of generic limits raised by the phylogenies (see screenshots below) of Kennedy et al. (2009, 2019), Kennedy and Spencer (2014), and Worthy (2011), the new NACC-relevant issues involved include the findings, concordant among these studies, that:

- 1) *Phalacrocorax carbo*, the type species, forms a well-supported clade with many Old World taxa that remain in *Phalacrocorax sensu stricto*;
- 2) *Phalacrocorax auritus*, *P. brasilianus*, and *P. harrisi* form a well-supported clade, with *P. harrisi* (not included in Worthy 2011) sister to the other two, and with the generic name *Nannopterum* taking priority; and
- 3) The Pacific taxa *P. penicillatus*, *P. pelagicus*, and *P. urile* form a well-supported and highly divergent clade, with *P. penicillatus* sister to the other two; the name *Urile* takes priority for this clade.

The morphological phylogeny of Worthy (2011) and the molecular phylogenies of Kennedy and Spencer (2014) and Kennedy et al. (2019), despite all recovering these clades, differ in other respects, such as the relationships of *Nannopterum* (sister to *Phalacrocorax* s.s. in the

osteological phylogeny, but sister to Southern Hemisphere *Leucocarbo* in the molecular phylogenies) and of *Urile* (sister to *Leucocarbo* in the osteological phylogeny but sister to *Phalacrocorax* s.s. in the molecular phylogenies). Nevertheless, these clades are well-supported and strongly divergent, and are Miocene in age (see NACC proposal 2020-A-12).

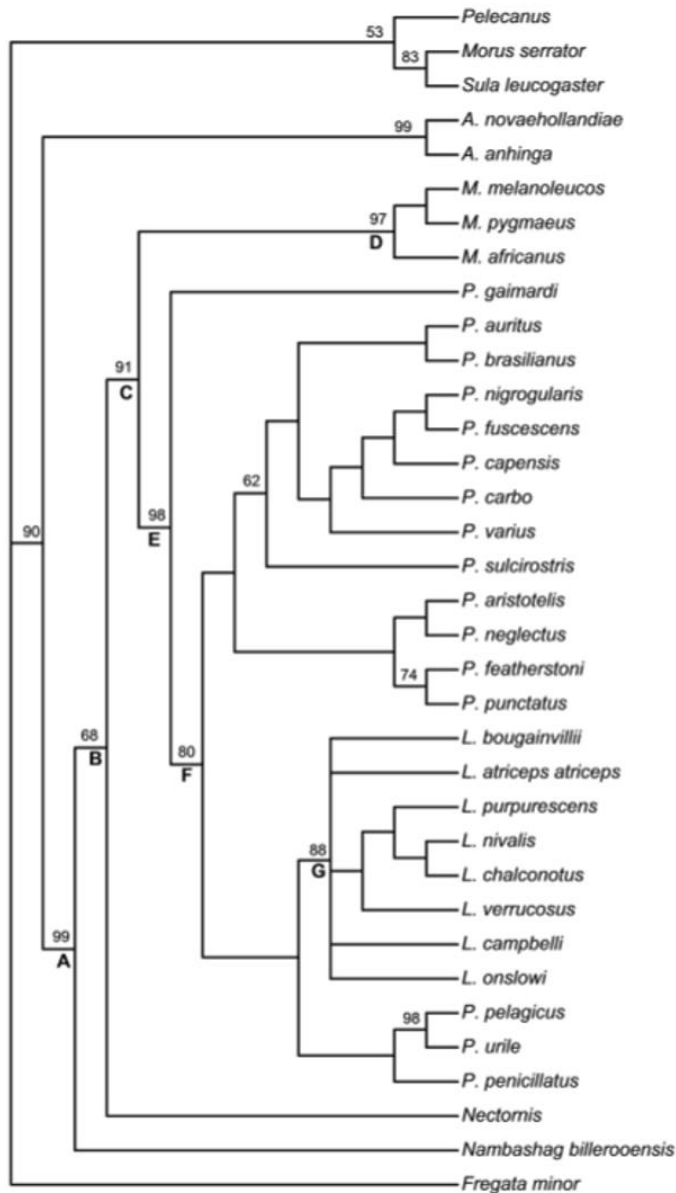


Figure 5 from Worthy (2011).

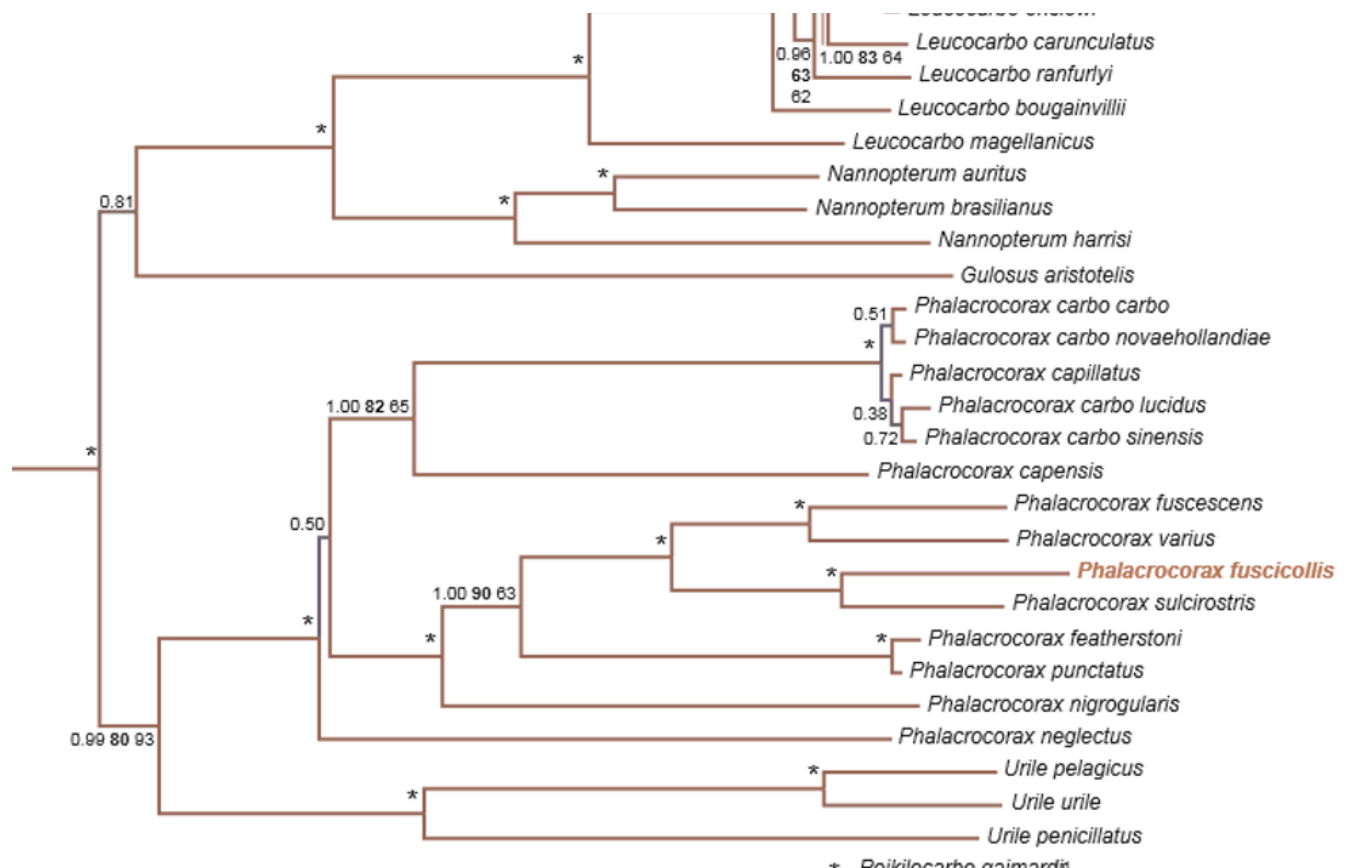


Figure 1 from Kennedy et al. (2019), portion relevant to NACC taxa below.

Effect on AOS-CLC area:

Acceptance of this proposal would result in two very widespread and familiar species long placed in *Phalacrocorax* (*auritus* and *brasiliensis*) being moved to *Nannopterum*, and three other marine Pacific taxa (*penicillatus*, *pelagicus*, and *urile*) being moved to *Urile*. There would be no change to *Phalacrocorax carbo*. No change is needed to English names (though some may be desired, e.g., Pelagic Cormorant), and we have already resequenced NACC-area taxa following Kennedy and Spencer (2014).

Recommendation:

Given the Miocene age of these divergences and the concordance between Worthy's osteological and Kennedy et al.'s genetic phylogenies, at least as far as defining these clades, I recommend that we adopt *Nannopterum* as the genus for *auritus* and *brasiliensis* and *Urile* for the 3-species Pacific clade. Short of maintaining all in *Phalacrocorax*, which I do not recommend considering the great age of the clades, no other treatment agrees well with both datasets and with basic plumage patterns and biogeography.

Please vote on both of the following:

- Recognize *Nannopterum* and transfer *brasiliensis* and *auritus* to this genus; and

- b) Recognize *Urile* and transfer *penicillatus*, *pelagicus*, and *urile* to this genus.

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Submitted by: Pamela C. Rasmussen, Michigan State University

Date of proposal: 30 June 2020

(A) Adopt split of Long-billed Gnatwren *Ramphocaenus melanurus***Description of the problem and new information:**

The Long-billed Gnatwren *Ramphocaenus melanurus* has long been treated as a single widespread, highly polytypic species (Mayr and Cottrell 1964). Now, with the publication of a robust phylogeny of the Polioptilidae (Smith et al. 2018), the most divergent taxa (the *sticturus* group) of the complex have been split (Proposal 790A to SACC, <https://www.museum.lsu.edu/~Remsen/SACCprop790.htm>), based on clear evidence: sympatry of vocally different but morphologically similar taxa that are also deeply diverged genetically (Harvey et al. 2014, Smith et al. 2018). I strongly recommend reading that proposal, as much in it is not summarized here.

The second part of the proposal (790B), to split the northern *rufiventris* group, which includes the subspecies in the NACC region, failed even though historically they had been considered a separate species (see AOU 1983, Phillips 1991), but the case is far less clear and was deemed by most SACC members to require further sampling. There are typical but not absolute vocal differences as well as plumage differences that led to the *rufiventris* group being considered a third potential species group by Sibley and Monroe (1990), as did del Hoyo and Collar (2016), although Dickinson and Christidis (2014) treated the complex as being comprised of two subspecies groups. Clements et al. (2019) and Gill et al. (2020) followed SACC in recognizing the split of Chattering Gnatwren for the E Peruvian to SW Brazilian taxa in the *sticturus* group (including *obscurus*) from Trilling Gnatwren *R. melanurus* (all other races, including the *rufiventris* group).

Effect on AOS-CLC area:

Although the split enacted in 790A involves peripheral southern taxa vs. all others and thus is extralimital to the NACC region, the English names of both daughter species have changed as a result for the SACC area. The forms occurring in the NACC area are part of the species now called Trilling Gnatwren by SACC. However, given that the vast preponderance of the former range of *Ramphocaenus melanurus sensu lato* is occupied by *Ramphocaenus melanurus sensu stricto*, it would be within our guidelines to retain the name Long-billed Gnatwren, and that would have the advantage of stability, especially given the likelihood that the *rufiventris* group may be re-split in the near future. However, we generally follow SACC for groups that are largely in the SACC area.

Other impacts would include needed revision of the **Notes** section and reversing the linear sequence so that *Microbates cinereiventris* follows *Ramphocaenus melanurus*, following our conventions.

Recommendation:

I recommend (with the above reservations) that we follow SACC and (A) adopt the split of *Ramphocaenus melanurus* and (B) adopt the English name Trilling Gnatwren for the taxon group that includes those taxa occurring in the NACC area. I further recommend (C) that we resequence the Ramphocaenini (*sensu* AOU 1983) so that *Ramphocaenus* precedes *Microbates*. Please vote separately for each of these options.

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Submitted by: Pamela C. Rasmussen, Michigan State University

Date of proposal: 13 July 2020

(B) Retain the English name Long-billed Gnatwren for *Ramphocaenus melanurus sensu stricto*

SACC initially voted to replace the English name of *Ramphocaenus melanurus* when splitting it from *R. sticturus*, despite Dan Lane's proposal recommending that the English name be retained for *melanurus sensu stricto* based on this taxon occupying almost all the distribution of *melanurus sensu lato* (and presumably the vast majority of literature on *R. melanurus* referring to this form rather than to the restricted-range *sticturus*). Pam noted this as well in her proposal (2021-A-5) to follow SACC in splitting *melanurus*:

"The forms occurring in the NACC area are part of the species now called Trilling Gnatwren by SACC. However, given that the vast preponderance of the former range of *Ramphocaenus melanurus sensu lato* is occupied by *Ramphocaenus melanurus sensu stricto*, it would be within our guidelines to retain the name Long-billed Gnatwren, and that would have the advantage of stability, especially given the likelihood that the *rufiventris* group may be re-split in the near future. However, we generally follow SACC for groups that are largely in the SACC area."

Most NACC members initially agreed to go along with SACC on the English name, despite its being at odds with our English names policy, but Van recently asked SACC to reconsider their change to Trilling Gnatwren and they have now agreed to retain Long-billed Gnatwren for *R. melanurus* s.s. Now that SACC has changed their vote on this, we also need to vote on retaining the English name Long-billed Gnatwren for *R. melanurus* s.s., a course of action that I strongly recommend.

Submitted by: Terry Chesser

Date of Proposal: 15 April 2021

Change the linear sequence of the gnatcatchers (*Polioptila* spp.)**Description of the problem:**

Our current sequence (Chesser et al. 2019) for gnatcatchers is:

Blue-gray Gnatcatcher *Polioptila caerulea*
Cuban Gnatcatcher *Polioptila lembeyi*
California Gnatcatcher *Polioptila californica*
Black-tailed Gnatcatcher *Polioptila melanura*
Black-capped Gnatcatcher *Polioptila nigriceps*
White-lored Gnatcatcher *Polioptila albiloris*
Yucatan Gnatcatcher *Polioptila albiventris*
Tropical Gnatcatcher *Polioptila plumbea*
Slate-throated Gnatcatcher *Polioptila schistaceigula*

New information:

Smith et al. (2018) produced the first densely-sampled (95-98% of all subspecies) phylogeny of the Polioptilidae using mtDNA and 6 nuclear markers (screenshot below), in which, not surprisingly, the trees produced a very different linear sequence (see tree on next page).

Effect on AOS-CLC area:

Following our conventions for linear sequencing, this would lead to the new sequence:

Slate-throated Gnatcatcher *Polioptila schistaceigula*
Cuban Gnatcatcher *Polioptila lembeyi*
Yucatan Gnatcatcher *Polioptila albiventris*
Tropical Gnatcatcher *Polioptila plumbea* (White-browed *P. bilineata* if proposal passes)
Blue-gray Gnatcatcher *Polioptila caerulea*
Black-tailed Gnatcatcher *Polioptila melanura*
California Gnatcatcher *Polioptila californica*
Black-capped Gnatcatcher *Polioptila nigriceps*
White-lored Gnatcatcher *Polioptila albiloris*

Recommendation:

I recommend that we adopt the new sequence.

Literature Cited:

Chesser, R. T., K. J. Burns, C. Cicero, J. L. Dunn, A. W. Kratter, I. J. Lovette, P. C. Rasmussen, J. V. Remsen, Jr., D. F. Stotz, and K. Winker (2019). Check-list of North American Birds (online). American Ornithological Society. <http://checklist.americanornithology.org/taxa>
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Date of proposal: 14 July 2020

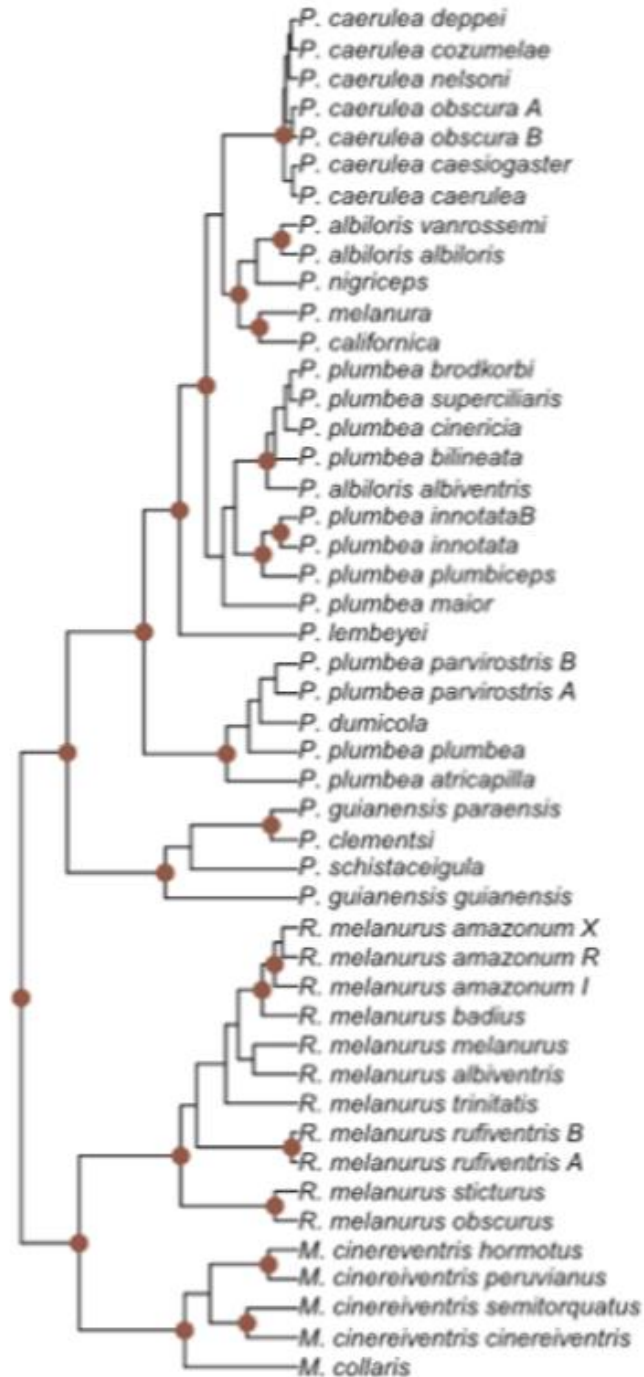


Fig. 1D of Smith et al. (2018), showing their maximum clade credibility tree. Red dots indicate posterior probabilities ≥ 0.95 .

Split Tropical Gnatcatcher *Poliioptila plumbea* into two or more species

Note: This is a joint proposal to be considered concurrently by SACC (proposal number not yet assigned).

Background:

The Tropical Gnatcatcher *Poliioptila plumbea*, as with many widespread and polytypic Neotropical species complexes, has a checkered taxonomic history (see, e.g., Mayr and Cottrell 1964; <https://avibase.bsc-eoc.org/species.jsp?lang=EN&avibaseid=CE922FF7EFA174EE&sec=synonyms>). The nature of variation among gnatcatchers, with the very limited suite of phenotypic characters that may vary seasonally, sexually, and geographically, has meant that plumage-based taxonomies are especially problematic, and that has certainly been true of *P. plumbea*. The two main groups recognized by Sibley and Monroe (1993), Dickinson and Christidis (2013) and del Hoyo and Collar (2016) are the *bilineata* group, occurring from southern Mexico through northwest Peru, and the cis-Andean *plumbea* group, occurring widely in South America. To greatly simplify, the former group has a broad white eyebrow year-round, whereas the latter group lacks this year-round. The races of the *bilineata* group occurring in the NACC region, as recognized by AOU (1957) and subsequent subspecies-level checklists (e.g., Dickinson and Christidis 2013, Gill et al. 2020), are *P. p. brodkorbi* of southern Mexico through northern Costa Rica, *P. p. superciliaris* of north-central Costa Rica to southern Panama or northern Colombia, and *P. p. cinerica* of Coiba Island, Panama. Both the *bilineata* group and the *plumbea* group occur in the SACC region, in some 8–9 races. Zimmer (1942), on the basis of a few northern South American specimens that showed intermediacy between *plumbiceps* and *bilineata*, considered the two main groups to be conspecific. This intermediacy mainly involved tiny, variable amounts of white in the face of some Colombian and Venezuelan specimens, as well as a “perfect transition” between taxa in the amount of white on the outer rectrices.

New information:

In the first densely sampled phylogeny of the Polioptilidae (Smith et al. 2018), multiple cases of polyphyly were uncovered, including the fact that Slate-throated Gnatcatcher *P. schistaceigula* of Panama and northwestern South America was embedded within Guianan Gnatcatcher *P. guianensis*, which has since been resolved with the acceptance of SACC Proposal 751.1 (<https://www.museum.lsu.edu/~Remsen/SACCprop751.htm>) to split *P. guianensis*. No further action with respect to *schistaceigula* is needed by NACC.

Further, and hence the subject of this proposal, *P. plumbea* was found to be polyphyletic, with the taxon from northern Yucatan, then treated as *P. albiloris albiventris*, nested within one of two widely diverged *P. plumbea* clades (see screenshot below from Smith et al. [2018] of the relevant clades) that are highly incongruent with previously recognized group boundaries as outlined above. Instead of all cis-Andean races belonging to the *plumbea* clade, Smith et al. (2018) found that those from central Colombia through the western Guianas are more closely related to the *bilineata* group + *albiventris*. Note that Proposal NACC 2019-C-7 to treat

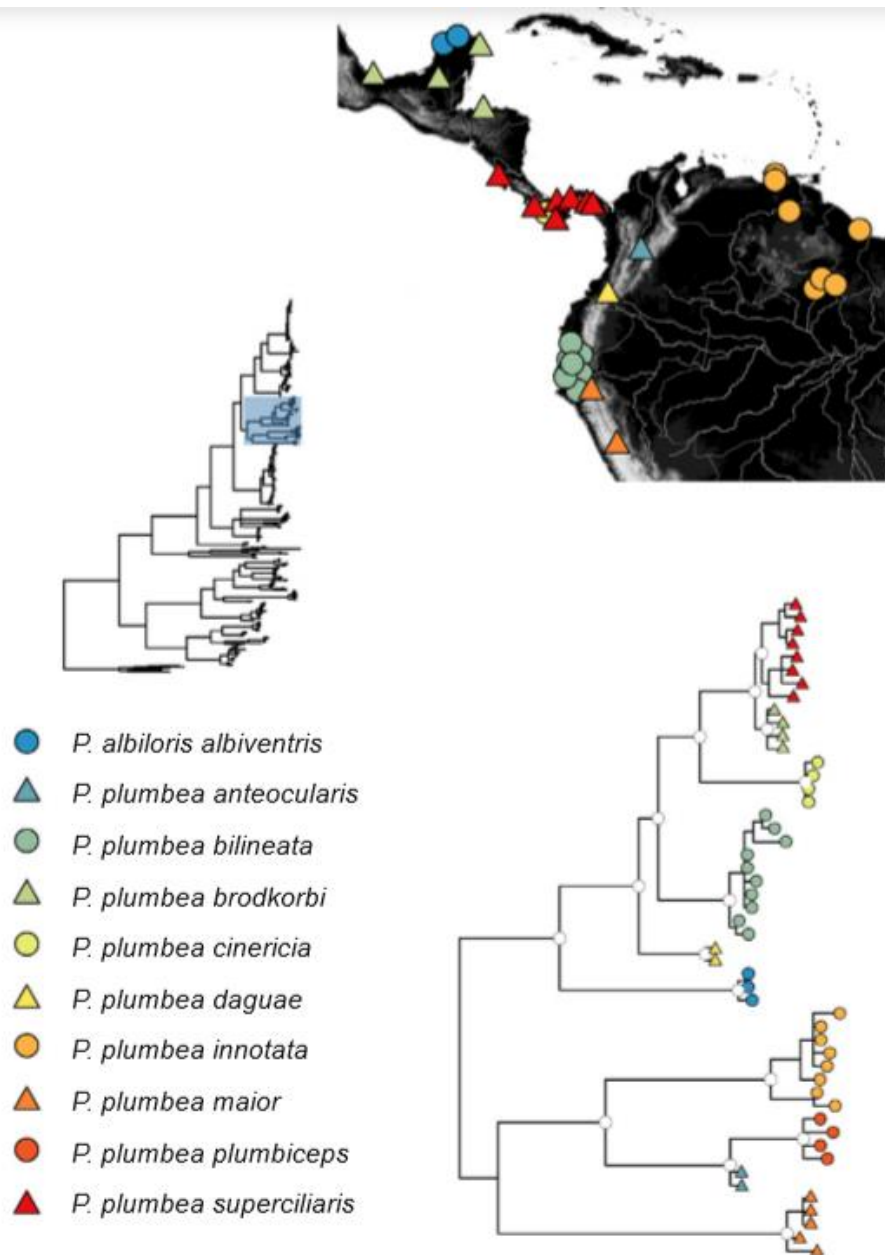


Fig. 4 (part) of Smith et al. (2018). The miniature phylogenies at the top (to the left of each map) show the phylogeny of the family, whereas the larger trees with colored symbols show details of the phylogenies of the two main clades of *P. plumbea* highlighted in blue on the family phylogeny. The white-lored *bilineata* clade, in which all three NACC-region taxa (*brodkorbi*, *superciliaris*, and *cinericia*) occur, is the clade on the upper half of the left phylogeny. SACC-area taxa occur more broadly throughout the phylogeny. Those in the lower half of the left tree are the dark-lored northeastern SA group formerly assumed to be part of the *plumbea* clade; widely allopatric Mara on Valley *maior* (in which females have the white brow) is a rather divergent sister to this clade.

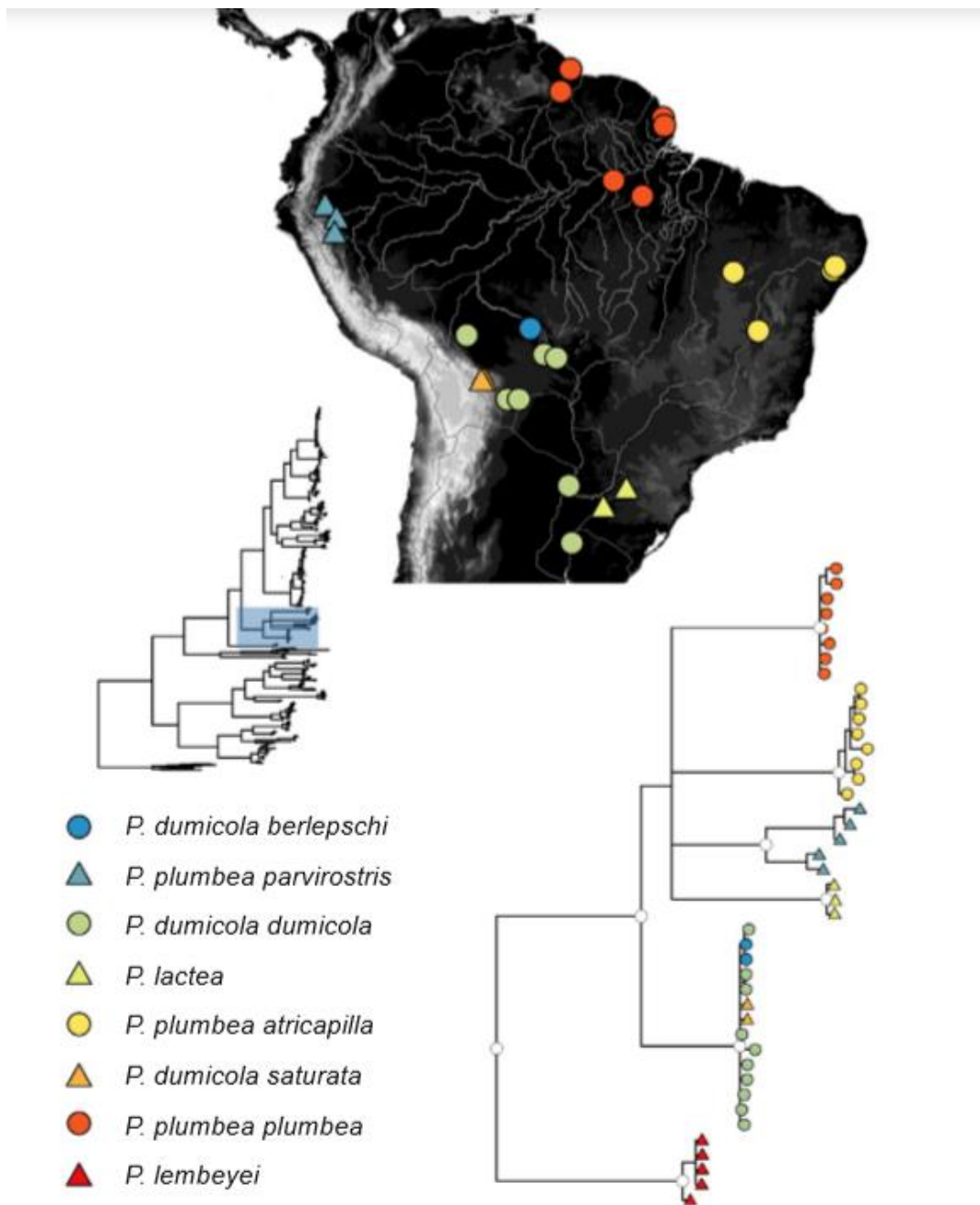


Fig. 4 (part) of Smith et al. (2018). This portion of the phylogeny consists of Cuban Gnatcatcher *P. lembeyei* and *P. dumicola* (lower half) as successive sisters to a polytomy comprised of *P. lactea* + *P. plumbea* (the three races of the nominate group s.s.).

albiventris as a species rather than a subspecies of *P. plumbea* passed, in part in recognition of the apparent inevitability that *P. plumbea* comprises multiple species.

The other group, cis-Andean races from Surinam east and south, the nominate *P. plumbea* group (*plumbea*, *parvirostris*, and *atricapilla*), instead forms a polytomy with Creamy-bellied Gnatcatcher *P. lactea*. The possibility that *lactea* may be a distinctive form of *plumbea* was recognized by Hellmayr (1934). Sister to the *plumbea* s.s. + *lactea* group was Masked Gnatcatcher *P. dumicola* of south-central South America.

Within the Middle American + trans-Andean + *albiventris* + northernmost South American group, Smith et al.'s (2018) molecular phylogeny shows two fairly divergent clades, the *bilineata* clade (which includes the three NACC-area and the northwestern trans-Andean taxa, plus *daguae* of the Cauca Valley, western Colombia) and the northeastern clade (*anteocularis*, *plumbiceps*, and *innotata*) from the upper Magdalena Valley (central Colombia) through Guyana and northern Brazil, hitherto considered part of the nominate group. The sister to the northeastern clade, *maior* of the Marañón Valley (Peru), was treated as a separate species by Hellmayr (1934), as a species group by Sibley and Monroe (1993) and Dickinson and Christidis (2014), and was split by del Hoyo and Collar (2016) based on multiple plumage differences and very different voice; it is also “decidedly larger” (Hellmayr 1934). LePage (2020) lists the *bilineata* group, *albiventer*, and *maior* as separate species from the *plumbea* group, which, however, still includes the *plumbiceps* group of northeastern South America, and therefore is non-congruent with the phylogeny of Smith et al. (2018). del Hoyo et al. (2020, last updated 2017) delineated multiple monotypic groups in the *plumbea* s.s. clade.

Effect on AOS-NACC area:

The more complex issues involving the seemingly parapatric *plumbiceps* and *plumbea* groups fall within the SACC area remit. NACC area taxa all belong to the *bilineata* group, which can hardly remain within *P. plumbea* because of the polyphyly in the phylogeny of Smith et al. (2018). Because *bilineata* (Bonaparte, 1850) is the oldest name in the entire major clade that includes the NACC-area species (including the *plumbiceps* Lawrence, 1865 group), NACC can split this group from the widely diverged *plumbea* (Gmelin, 1788) clade without concern about having to then change the name again soon (unless the proposal to split the two main clades fails in SACC). Nevertheless, this seems an appropriate issue for simultaneous voting by both committees so that the best resolution agreeable to both will result. The fact that NACC already recognizes *albiventris* as specifically distinct should be taken into account in determining which taxa (if any) beyond the Middle American and trans-Andean taxa are included in the *bilineata* group.

Acceptance of this proposal would result in change of the specific epithet of the NACC-area taxa and almost certainly the English name, revisions to the **Distribution** statement, and addition of a **Notes** statement in the *Check-list*.

Effect on SACC area:

The SACC area could gain as many as three species, or potentially suffer a net loss of one species, depending on the outcome of this proposal.

Recommendations:

Please vote on the following issues (see each vote for recommendation and who should vote):

- (A) split the *plumbea* group (*plumbea-parvirostris-atricapillus*) from the remaining taxa (strongly recommended due to polyphyly; **all vote** on this);
- (B) if A passes, adopt the English name White-browed Gnatcatcher for the *bilineata* group, as it is already in use in Sibley and Monroe (1993), HBW/BirdLife, Clements, and elsewhere; however, it is apt only for the Middle American and trans-Andean taxa, if D does not pass (recommended; **all vote** on this);
- (C) if A passes, retain the English name Tropical Gnatcatcher for the *plumbea* group, as it would still represent the most widely-distributed group, is already used in Sibley and Monroe (1993), HBW/BirdLife, Clements, and elsewhere; and good names for gnatcatchers are hard to come by; however, it is likely to cause some confusion with the parent taxon and is apt for most gnatcatchers (recommended; **SACC votes**);
- (D) split the *plumbiceps* group from the *bilineata* group (recommended; **SACC votes**)*;
- (E) split *maior* from the *plumbiceps* group (recommended; **SACC votes**);
- (F) if E passes, adopt the English name Marañon Gnatcatcher for *maior* (recommended; **SACC votes**). Note that Hellmayr (1934) used Greater Gnatcatcher. Either name is apt and distinctive but Marañon has gained currency recently.
- (G) Retain *Polioptila lactea* as a species rather than treating it as conspecific with the *plumbea* group, pending further study (recommended; **SACC votes**). It seems premature to lump this with *plumbea* based on present data and it would be perhaps the most distinctive subspecies of any gnatcatcher if lumped (assuming at least A passes).

*If D passes, a new proposal would be required for the English name of the *plumbiceps* group. Hellmayr (1934) used the names Magdalena Valley Gnatcatcher, Lawrence's Gnatcatcher, and Rio Branco Gnatcatcher for these taxa.

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Submitted by: Pamela C. Rasmussen, Michigan State University

Date of proposal: 16 July 2020

Split *Fregata rothschildi* from Magnificent Frigatebird *F. magnificens*

Note: This issue is also being considered by SACC in their Proposal 872. See SACC votes and comments at <https://www.museum.lsu.edu/~Remsen/SACCprop872.htm>

Background:

The frigatebirds, with their great plumage similarity among comparable ages and sexes, as well as the very different immature stages over a period of several years, have long been the subjects of taxonomic confusion. Few avian groups with so few species can have had so many words, photos, and illustrations dedicated solely (and often futilely) to their identification. Nevertheless, many early authors thought a single species inhabited pantropical oceans, and though several taxa had by then been named, only two species were recognized in the *Catalogue of the Birds in the British Museum* (Ogilvie-Grant 1898). Two forms, a larger and smaller one, were recognized to occur on the Galapagos by Ridgway (1897), but Rothschild and Hartert (1899) believed they intergraded completely and therefore were not worthy even of subspecies status. Mathews (1914), based on study of specimens in the British Museum, recognized that two distinct frigatebird taxa breed in the Galapagos Islands. Among the several new *Fregata* taxa he described from the tropics was *Fregata minor magnificens* Mathews, 1914, which he considered a subspecies of Great Frigatebird *F. minor* (Mathews 1914, 1915). Rothschild (1917) then reconsidered his earlier position and clarified that *magnificens* should be treated as a species rather than as a subspecies of *minor*. Since then, *magnificens* and *minor* have been generally recognized as full species that are mostly allopatric except on the Galapagos, and subsequent authors have generally recognized five species of frigatebird (e.g., Lowe 1924). Two or three subspecies are often recognized for *F. magnificens*, the nominate in the Galapagos, *rothschildi* in most of the rest of the range, and *lowei* for the highly isolated population of the Cape Verde Islands (Swarth 1933, AOU 1957, del Hoyo and Collar 2014). In many other treatments, including most recent ones, however, *magnificens* is treated as monotypic (AOU 1931, Dorst and Mougou 1979, Dickinson and Remsen 2013, Clements et al. 2019, Gill et al. 2020). The AOU (e.g., AOU 1886, 1895, 1910) long recognized just a single regional species, what is now known as the Magnificent Frigatebird *F. magnificens*, but three species are now included in the expanded NACC region (AOU 1983, Chesser et al. 2019), and four in the SACC region (Remsen et al. 2020).

New information:

Hailer et al. (2011) found high levels of gene flow over most of the New World range of *F. magnificens*, including across the Isthmus of Panama, which usually serves as a barrier to seabirds. However, despite predictions based on the extraordinary vagility of frigatebirds, the Galapagos population was found to be strongly genetically differentiated from the other populations (see screenshots below of Figs. 2 and 3 from Hailer et al. 2011). The Galapagos population therefore must have been genetically isolated for at least a few hundred thousand years (Hailer et al. 2011).

Further, in a study of population structure primarily of Atlantic and Caribbean populations, Nuss et al. (2016) found that, although Brazilian and Caribbean populations were genetically isolated from one another, the geographically interposed population from French Guiana (Grand

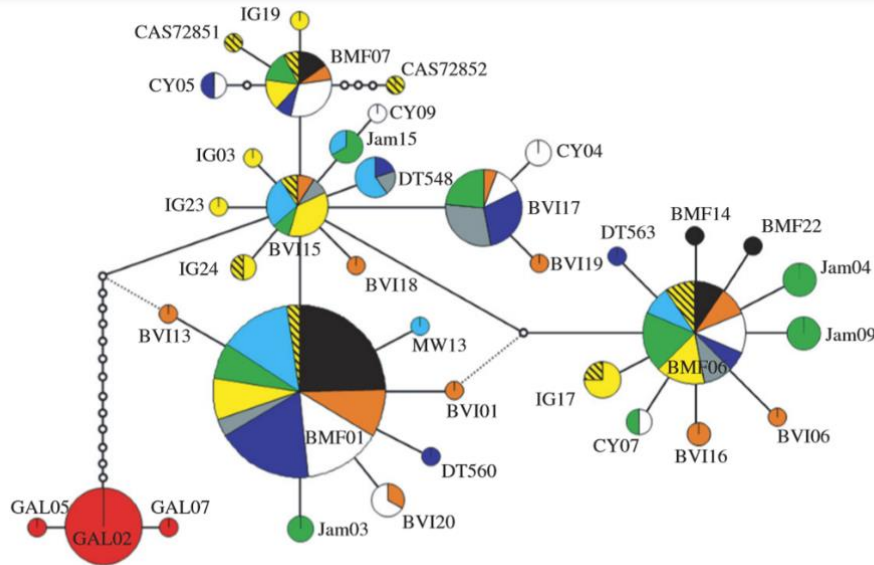


Fig. 2 from Hailer et al. (2011). Parsimony network of mtDNA sequences, Galapagos in red.

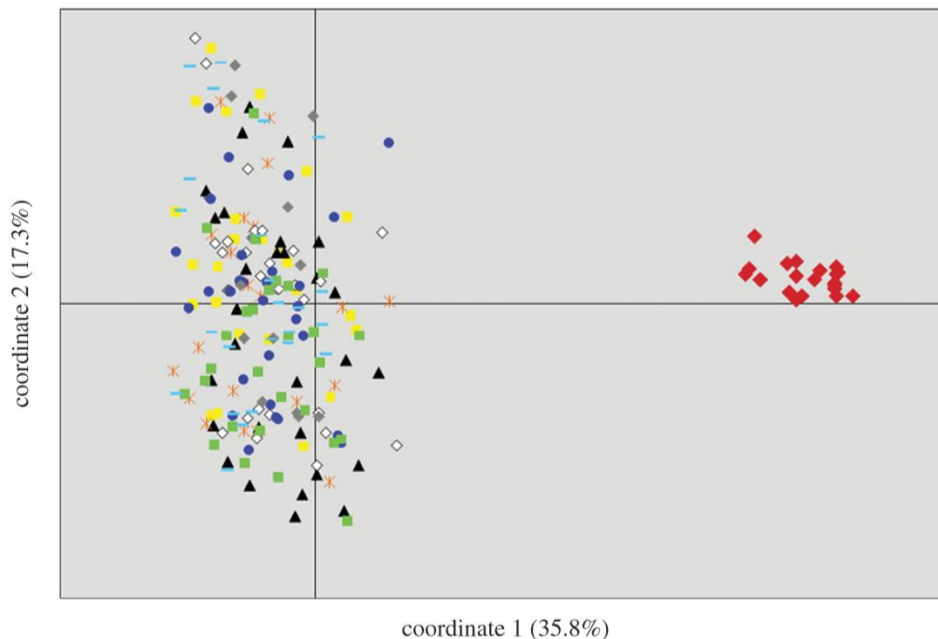


Fig. 3 from Hailer et al. (2011). PCA of microsatellite genotypes, Galapagos in red.

Connétable) shared haplotypes with both regions. As shown by Hailer et al. (2011), the Galapagos population had highly divergent haplotypes (see screenshot of Fig. 2 from Nuss et al. 2016, below). In a study of Mexican *F. magnificens* populations, Rocha-Olivares and González-Jaramillo (2014) found lower levels of gene flow between colonies and especially

between ocean basins than did Hailer et al. (2011), and offered explanations for this discrepancy, including more individuals sampled, more peripheral sampling locations, and greater geographical distances in their more recent study.

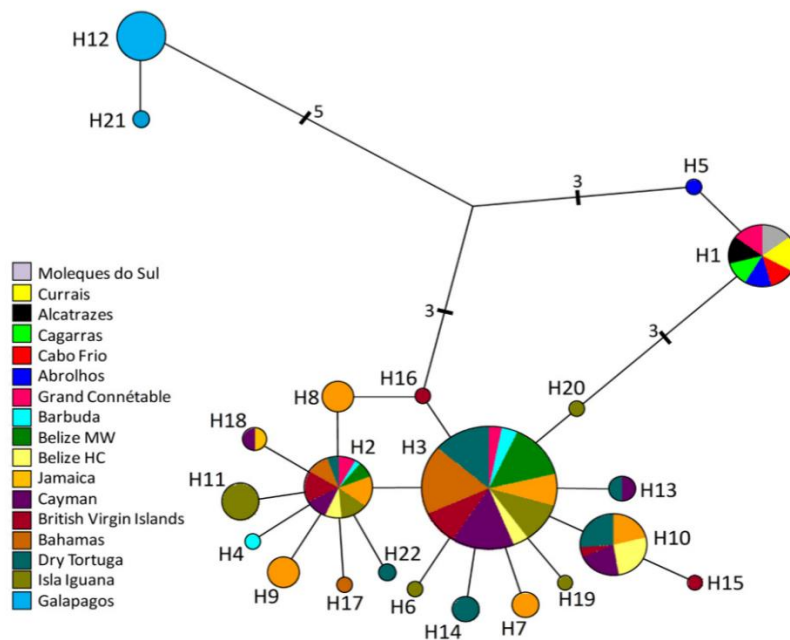


Fig. 2 from Nuss et al. (2016). Median-joining network, mtDNA haplotypes.

Despite the genetic divergence of the Galapagos *F. magnificens* population, the same haemoprotean parasite, *Haemoproteus iwo*, occurs in *F. minor* as well as *F. m. magnificens* from Galapagos and multiple localities within the range of *F. m. rothschildi* (Clade B of Fig. 1 in Levin et al. 2011, see screenshot below). This non-congruence in divergence levels between parasite and host suggests that transfer by hippoboscids flies (e.g. *Olfersia*) may take place between non-breeding frigatebirds at communal roosts, as well as at colonies. There is some movement of non-breeding Galapagos birds to Central America, where dead and/or emaciated birds banded in the Galapagos have been recovered (according to a pers. comm. in Hailer et al. 2011; details not provided). The parasite's lack of divergence may be considered confirmatory of the mixing of frigatebird populations outside of the breeding colonies.

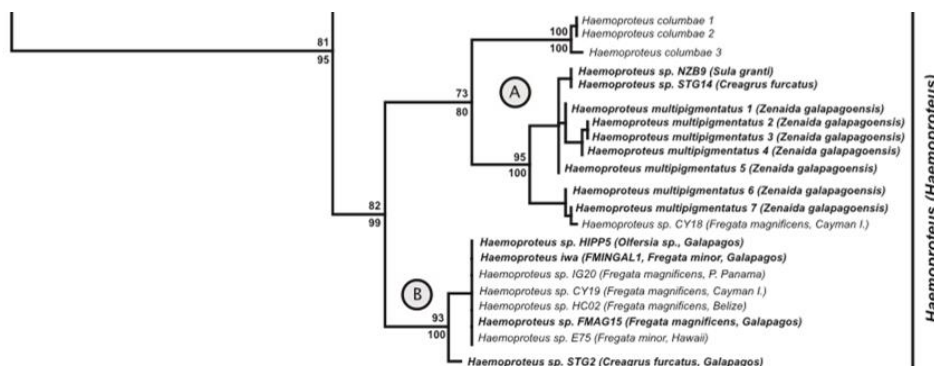


Fig. 1 of Levin et al. (2011). Relevant part of ML tree of haemosporidian cyt b.

Several external measurements of Magnificent Frigatebirds (5 of each sex from the Galapagos, 11 and 16 from non-Galapagos specimens) corroborated that, in wing and inner and outer tail dimensions, and culmen of females, the Galapagos population is significantly larger (Hailer et al. 2011). My informal inspection of many eBird photos (selecting only those in non-foreshortened view) seems to confirm that the tail is relatively longer in Galapagos birds. Otherwise, I cannot see any plumage or soft part color differences and am unaware of any that have been reliably suggested.

The authors of the above studies are in general agreement that sex-biased dispersal (with males exhibiting site-fidelity) and female mate choice for the complex male mating rituals of frigatebirds is most likely to explain the patterns seen, especially the genetic distinctness of the Galapagos population. However, none presented or referenced any data on differences, for example, in display or vocalizations. I located only one online recording from the Galapagos, which did not prove useful, although there must be recordings in compilations and private collections. It seems apparent that isolating mechanisms beyond simple geographical isolation must be operating; otherwise, the Galapagos population would be experiencing gene flow with mainland birds.

The Cape Verde population named *F. m. lowei* has not been included in the above studies, but as of 2012 only one bird of each sex appeared to be present at the former colony (Suarez et al. 2012), due to persecution. These authors indicated their intention to conduct genetic and mensural analyses of the distinctiveness of this virtually extinct population.

Note that Olson (2017) has recently espoused treatment of Lesser Frigatebird *Fregata ariel* as two species, as the form *trinitatis* now restricted to Trindade Island and known from St. Helena by fossils has different proportions (stouter wing and bill) and putative plumage differences in immature stages. There are parallels with the case of Magnificent Frigatebird, but genetic data that would bolster the case for specific status of *trinitatis* appear to be lacking. A proposal (SACC#768, <https://www.museum.lsu.edu/~Remsen/SACCprop768.htm>) to split *trinitatis* was rejected in favor of further evidence.

Effect on AOS-NACC and SACC areas:

If split, the Galapagos population would retain the specific epithet *magnificens*, and thus the widespread frigatebird of the Americas would become *Fregata rothschildi*. There would also obviously be English names issues. In addition, there are evidently records of Galapagos birds from Central America, so details would have to be located for the NACC area, and a new species added for both.

It should be added that, even if this proposal does not pass, this species clearly should not be considered monotypic by global checklist authorities.

Recommendations:

Although it would be ideal if there were behavioral studies and analyses of the courtship display and vocalization repertoire that established the existence of premating isolating mechanisms between Galapagos and mainland birds, these are not available to my knowledge. What we do

know is that there is little if any gene flow, despite movement of at least some non-breeding individuals from the Galapagos to the mainland, which I take to be prima facie evidence that speciation has occurred. Please vote separately for each option.

- a) split *F. m. magnificens*, with the resultant daughter species *F. magnificens* of the Galapagos and *F. rothschildi* in the remainder of the range (whether or not *lowei* of Cape Verde is recognized).

If (a) passes, English name issues arise. Obviously, Magnificent Frigatebird could be retained for the vastly more widespread *rothschildi* but it would no doubt cause confusion, given the retention of *magnificens* by the Galapagos form. (Consider though that we have all learned to live with Great Frigatebird being *Fregata minor*, while Lesser is *F. ariel*.) Another option might be American Frigatebird, but of course Galapagos are part of the Americas. I recommend retention of Magnificent though as being the least disruptive option.

- b) retain the English name Magnificent Frigatebird for *Fregata rothschildi*.

Galapagos Frigatebird would be my suggestion for *F. magnificens* s.s.

- c) adopt the English name Galapagos Frigatebird for *F. magnificens*.

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Submitted by: Pamela C. Rasmussen, Michigan State University

Date of proposal: 20 July 2020

Resurrect *Corthylio* for Ruby-crowned Kinglet**Background:**

The Ruby-crowned Kinglet (*Regulus calendula*) is a small, insectivorous songbird native to North America, with a large range extending from Alaska to Mexico. It breeds in northern coniferous forests of the United States and Canada, but during migration can be encountered in almost any habitat (Swanson et al. 2020). *Regulus calendula* is one of only six species in the small family Regulidae, which includes four representatives in the Old World and two in North America: the Ruby-crowned Kinglet and the Golden-crowned Kinglet (*R. satrapa*, Winkler et al. 2020). All species of the Regulidae are currently placed in a single genus, *Regulus* (Winkler et al. 2020).

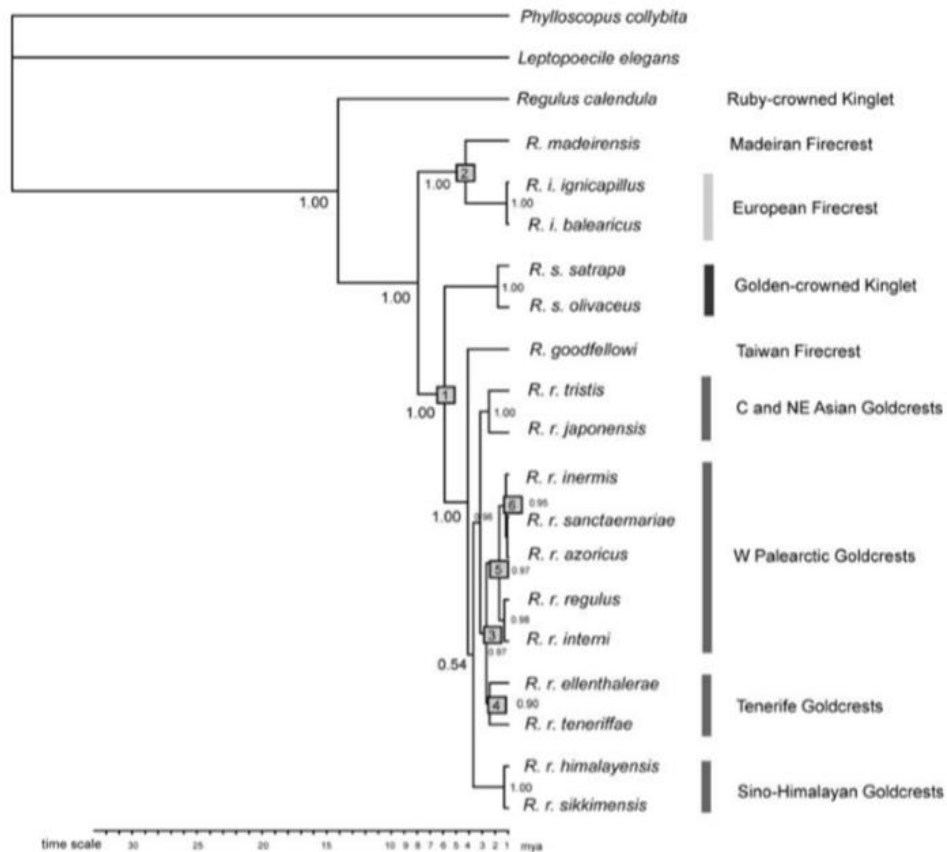
It has long been known that the Ruby-crowned Kinglet is markedly divergent from the other regulids in plumage and other aspects of external anatomy, reflected by the fact that the genus *Corthylio* Cabanis, 1853, was erected for this species. It was, however, treated within *Regulus* in AOU (1886, 1895, 1910). Miller (1915) noted that a well-known defining character of all species of *Regulus* except *calendula* is a single flat feather covering the nares, whereas *R. calendula* has multiple small bristly feathers overlying the nostrils. Further, Miller (1915) documented an additional differentiating character, the shape and reticulation of the pad of the hallux, which is much less distinctive in *R. calendula* than in other species of *Regulus*. This led to the recognition of *Corthylio* in AOU (1931).

Several other authors have since indicated that *R. calendula* is quite distinct from the other species of *Regulus*. Clark (1974) found differences in foot scutes between the two North American kinglets: Golden-crowned Kinglet has three scutes near the distal end of toe IV instead of two as in the Ruby-crowned Kinglet. These differences were hypothesized to relate to increased hanging behavior and greater foot mobility in *R. satrapa* (Clark 1974). Mayr and Short (1970) suggested that the Golden-crowned Kinglet could be more closely related to the Goldcrest (*R. regulus*), and that the Ruby-crowned Kinglet is not closely related to any of the other species of kinglet. Ingold et al. (1988) obtained the first molecular evidence in support of this idea, using protein electrophoresis to show that the genetic distance between the two North American species was similar to distances previously reported between very closely related bird families or between highly divergent genera within the same family. The authors proposed that these two species arose from separate invasions from the Old World (Ingold et al. 1988).

In vocalizations, *R. calendula* is also an outlier within *Regulus* (Becker 1978, Löhrl and Thaler 1980). Using mtDNA, Sturmbauer et al. (1998) and Päckert et al. (2003) found *R. calendula* to be the rather deeply diverged sister to all other regulids. Päckert et al. (2003) mapped song variation on the phylogeny, again showing the divergence of *R. calendula*. Nevertheless, despite Miller's (1915) evidence and the recognition of *Corthylio* in AOU (1931), all kinglets have long been placed in *Regulus* (e.g., AOU 1957, 1983; Mayr and Cottrell 1986, Dickinson and Christidis 2014, Gill et al. 2020), sometimes with *Corthylio* recognized as a subgenus (AOU 1998, Swanson et al. 2020).

New information:

Päckert et al. (2009) produced a slightly more densely sampled mtDNA phylogeny based on sequences of cytb and 16S rRNA, which confirmed *R. calendula* as sister to the other species of *Regulus* (see screenshot of their Figure 3 below).



Given that the divergence of *R. calendula* dates back to about 15 myr, and that it is characterized by well-defined morphological and vocal differences, the reinstatement of *Corthylio* should be considered. This issue has been mentioned but not enacted by any recent major global checklist (Dickinson and Christidis 2014, del Hoyo and Collar 2016, Clements et al. 2019, Gill et al. 2020).

Independent of whether *Corthylio* is again recognized, the linear sequence of the two NACC species should be reversed, such that *calendula* precedes *satrapa*.

On a side note, the Guadalupe race *R. c. obscurus* has been considered a species by some (Miller 1915, AOU 1895) due to its differing coloration, bill, wing, and tarsal proportions, and

wing formula. It is now considered presumably extinct, as recent targeted searches failed to find it (Quintana-Barrios et al. 2006; <https://deadasthedodo.wordpress.com/tag/corthylio-calendula-ssp-obscurus-ridgway/>).

Effect on AOS-CLC area:

Acceptance of this proposal would reinstate the genus *Corthylio* and would reverse the linear sequence of the two species of kinglet. It would have no effect on English names. A separate proposal may be needed to evaluate the specific distinctness of *R. c. obscurus*.

Recommendation:

Arguing against the change are the facts that the Regulidae are a monophyletic group and therefore it is not strictly necessary to treat *calendula* in a different genus, and that such a change would disrupt stability (Brandon and Natalia therefore recommend retaining *calendula* in *Regulus*). Arguing for the change are the facts that the split is relatively ancient and unambiguous, and that *calendula* has multiple morphological and vocal differences from all other regulids (Pam therefore recommends making the change). Please vote separately on each option.

- a) reinstate *Corthylio* for the Ruby-crowned Kinglet, as *Corthylio calendula*.
- b) change the linear sequence of the kinglets, with *calendula* preceding *satrapa*.

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Submitted by: Brandon Woo and Natalia C. García, Cornell University, and Pamela C. Rasmussen, Michigan State University

Date of Proposal: 21 July 2020

Change linear sequence of species in *Chaetura*

Note: This issue is also being considered by SACC in their Proposal 880. See SACC votes and comments at <https://www.museum.lsu.edu/~Remsen/SACCprop880.htm>

Effect on NACC/SACC:

This proposal would alter the current linear sequence of species in *Chaetura* based on new phylogenetic information.

Background:

SACC's current linear sequence for the genus *Chaetura* is as follows (Remsen et al. 2020):

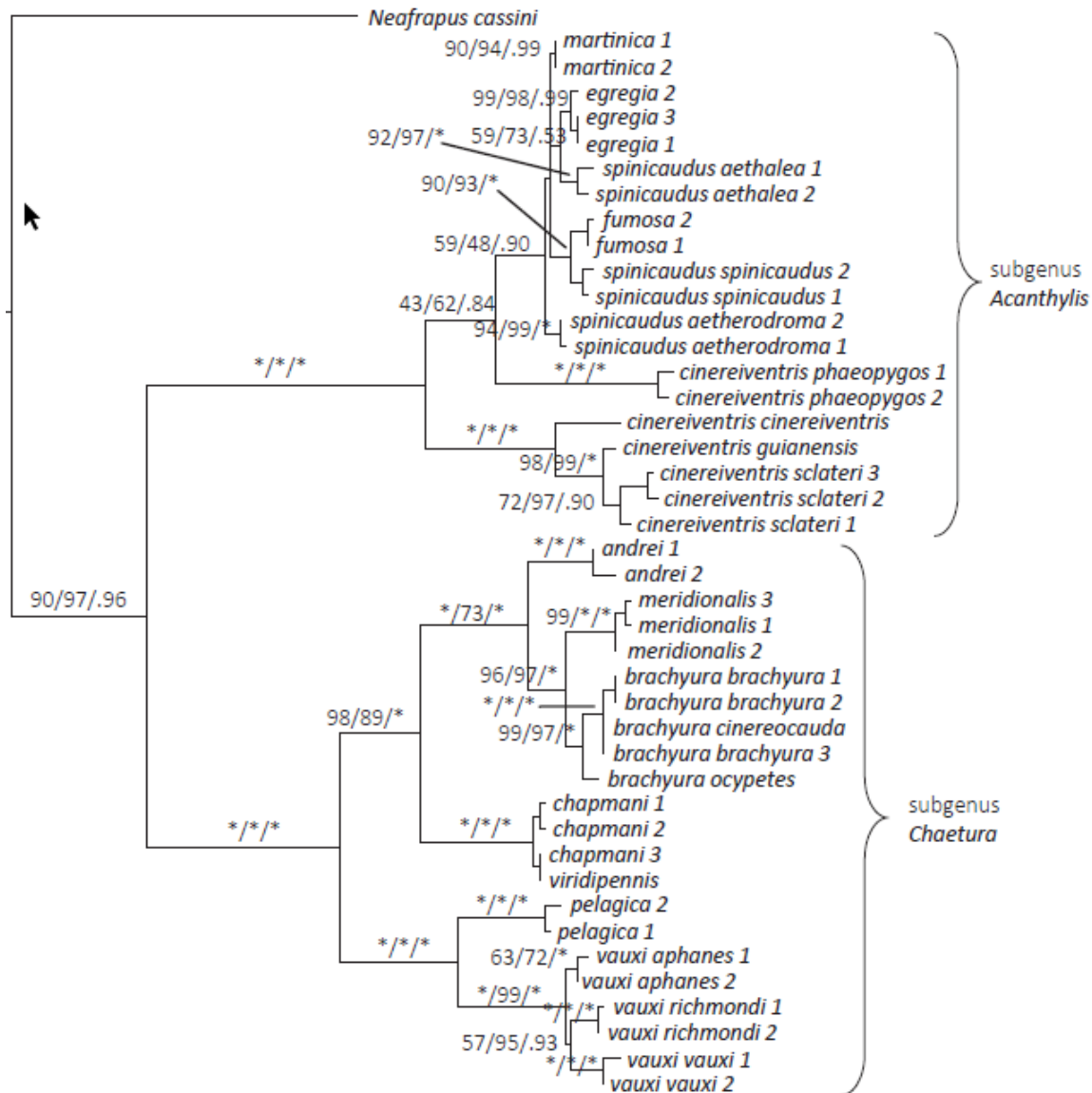
Chaetura spinicaudus
Chaetura cinereiventris
Chaetura egregia
Chaetura vauxi
Chaetura pelagica
Chaetura chapmani
Chaetura meridionalis
Chaetura andrei
Chaetura brachyura

NACC's current linear sequence of *Chaetura* is (Chesser et al. 2020):

Chaetura pelagica
Chaetura vauxi
Chaetura chapmani
Chaetura brachyura
Chaetura meridionalis
Chaetura spinicaudus
Chaetura fumosa
Chaetura cinereiventris
Chaetura martinica

New Information:

Chesser et al. (2018) published a robust phylogeny (below) of the genus *Chaetura* based on combined nuclear and mitochondrial data from all eleven species and 21 of 30 taxa recognized in the genus by Dickinson and Remsen (2013). Their analysis confirmed that the genus is composed of two nearly equally sized subclades that correspond to recognized subgenera (Marin 2000): *Acanthylis* (the gray/pale rumped clade) and *Chaetura* (the brown-rumped clade).



Two species-level revisions of the taxonomy of the genus were mandated by this phylogenetic study, both of which were adopted with the passage of SACC 841 (<https://www.museum.lsu.edu/~Remsen/SACCprop841.htm>). Within the subgenus *Chaetura*, *C. (v.) andrei* was shown to be unrelated to and morphologically distinct from other forms grouped within *C. vauxi*, which led to the recognition of the former as a distinct species, and *C. viridipennis*, formerly treated as a distinct species, was reclassified as a subspecies of *C. chapmani* due to minimal morphological and genetic differentiation.

Resolution of the taxa within the subgenus *Acanthylis* was generally poor, especially for *spinicaudus*, *martinica*, *fumosa* and *egregia*.

Analysis:

(a) Following linear sequencing conventions, the phylogeny of Chesser et al. (2018) can best be represented as follows for the NACC species:

Chaetura cinereiventris
Chaetura spinicaudus
Chaetura fumosa
Chaetura martinica
Chaetura pelagica
Chaetura vauxi
Chaetura chapmani
Chaetura meridionalis
Chaetura brachyura

(b) The phylogeny would be best reflected by a linear sequence of the SACC species as follows:

Chaetura cinereiventris
Chaetura spinicaudus
Chaetura egregia
Chaetura pelagica
Chaetura vauxi
Chaetura chapmani
Chaetura andrei
Chaetura meridionalis
Chaetura brachyura

Recommendation:

We recommend a **YES** vote by NACC members on (a) and a **YES** vote by SACC members on (b). The new sequences better reflect the phylogeny of Chesser et al. (2018) and would bring the two lists into agreement.

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Submitted by: David B. Donsker and Pamela C. Rasmussen

Date of Proposal: 11 August 2020

Reconsider the case to split *Saxicola maurus* and *S. stejnegeri* from Common Stonechat *S. torquatus*

Note: This is an updated and revised version of Proposal 2014-B-11, which was rejected 5-4 in favor of the status quo (no split) vs. a three-way split. We need to reconsider this case because of new evidence indicating sympatry between two of the species groups in the Western Palearctic (Shirihai and Svensson 2018, Loskot and Bakhtadze 2020) and differences in both song and calls (Opaev et al. 2018). Three of four major world lists (Dickinson and Christidis 2014, Clements et al. 2019, and Gill et al. 2020) have now adopted a three- (or more) way split of this extralimital species complex.

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 their 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 *torquatus*. Woog et al. (2008) obtained 915 and 1041 bp sequences of *cytb* and ND2 of 9 taxa of *Saxicola*, five of them normally treated within *S. torquatus*. 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. torquatus* 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)

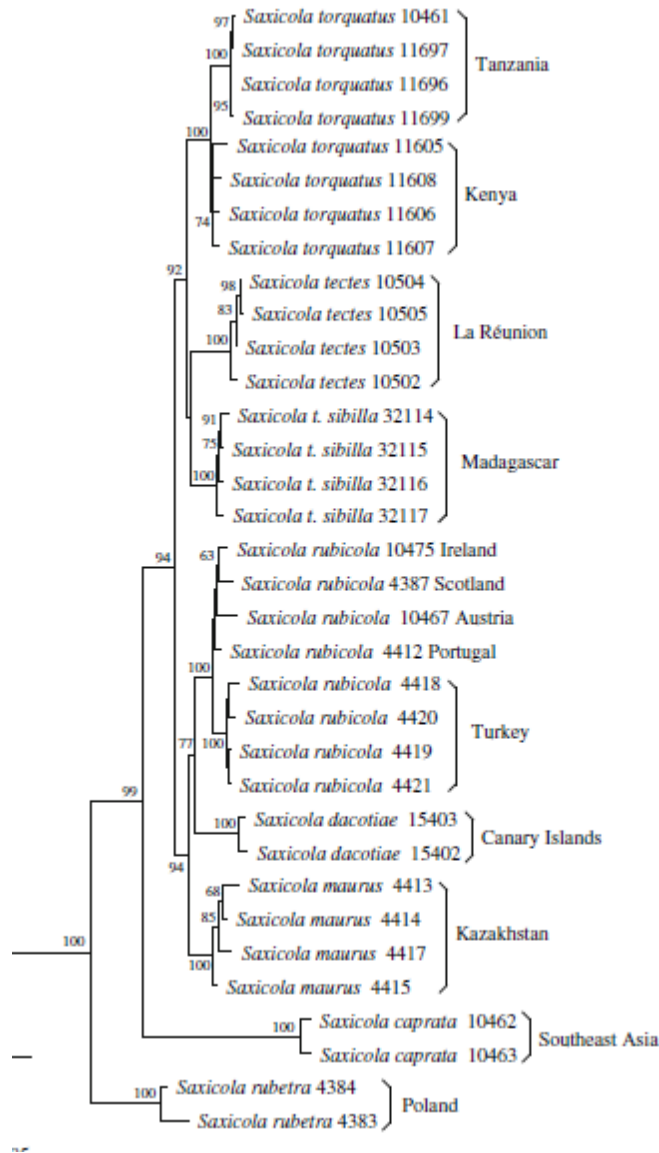
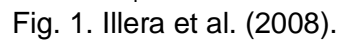


Fig. 2. Woog et al. (2008).



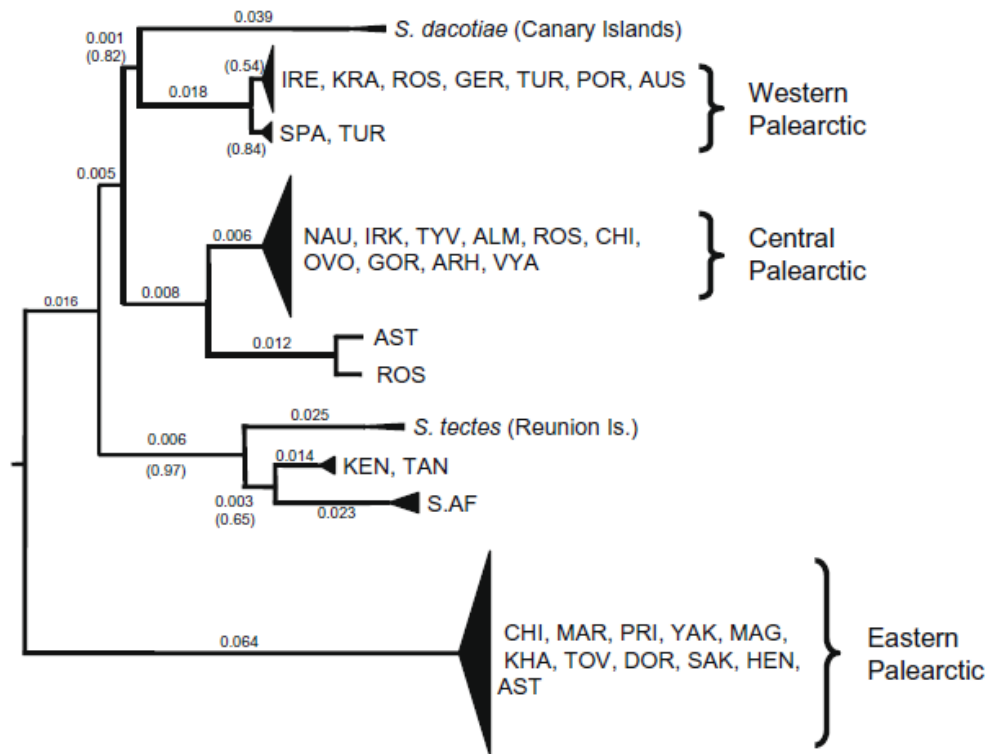


Fig. 2. Zink et al. (2009)

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 full species, and in addition followed Woog et al. (2008) in treating Malagasy birds as a full 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, while *variegatus* preferred more mesic and almost exclusively lowland habitats.

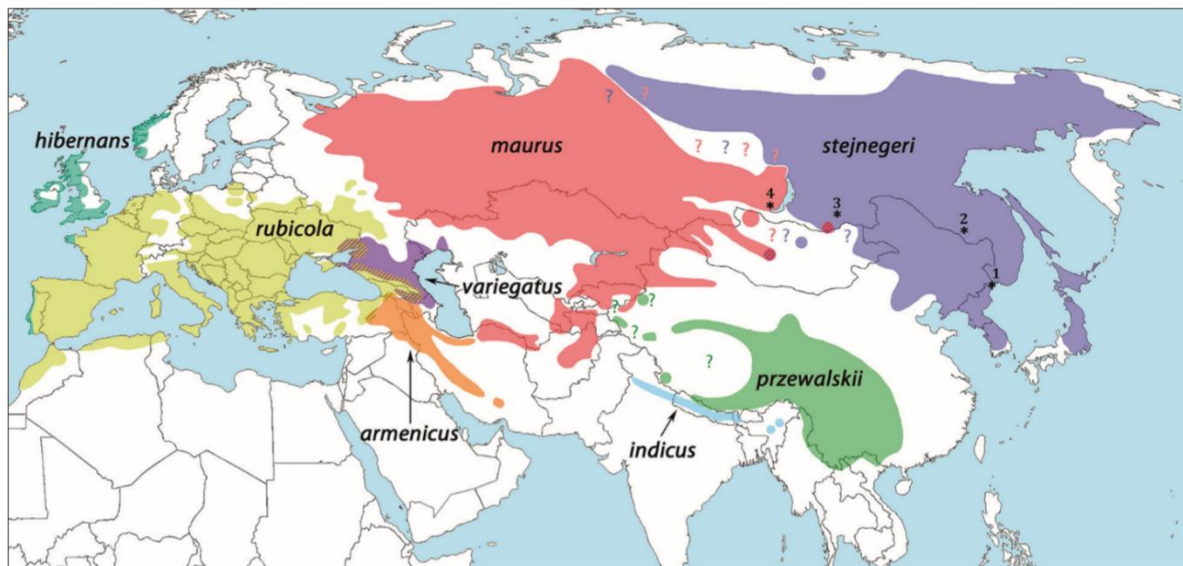


Fig. 1. Breeding ranges of the Eurasian taxa of the *Saxicola torquatus* complex. The hatched areas indicate zones of sympatry or possible sympatry. Numbers indicate the points of field work in Russian Federation: 1 – Khasan, Primorsky Kray, 2 – Khingan State Nature Reserve, Amur Oblast, 3 – Ivano-Arachleisk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

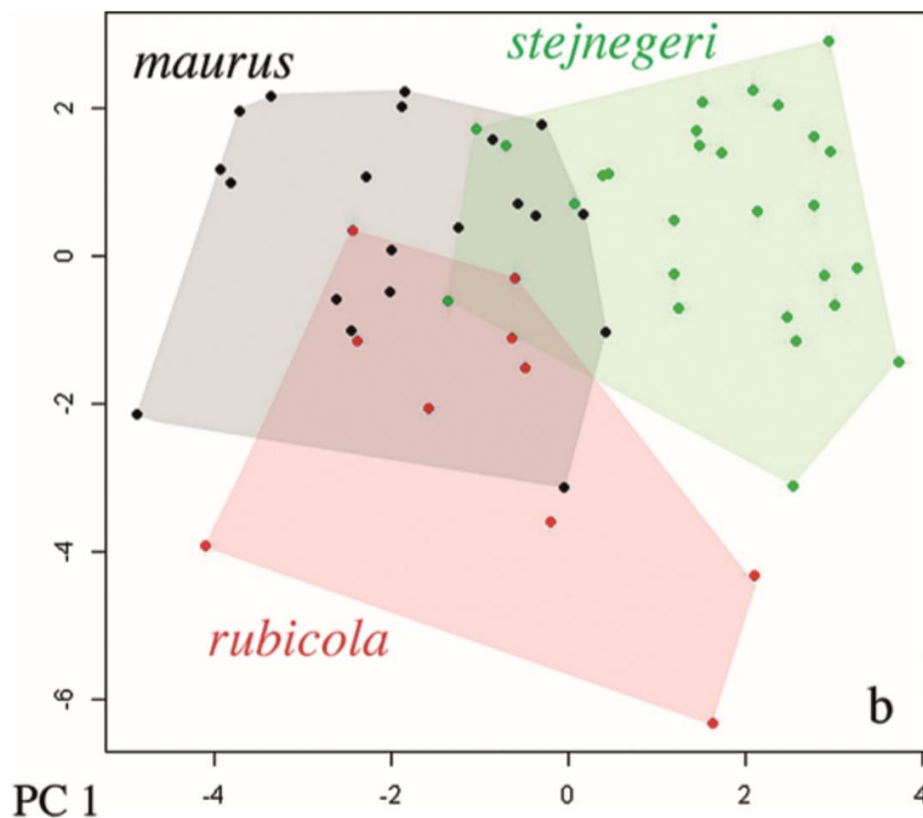


Fig. 2b of Opaev et al. (2018), a PCA of song characteristics.

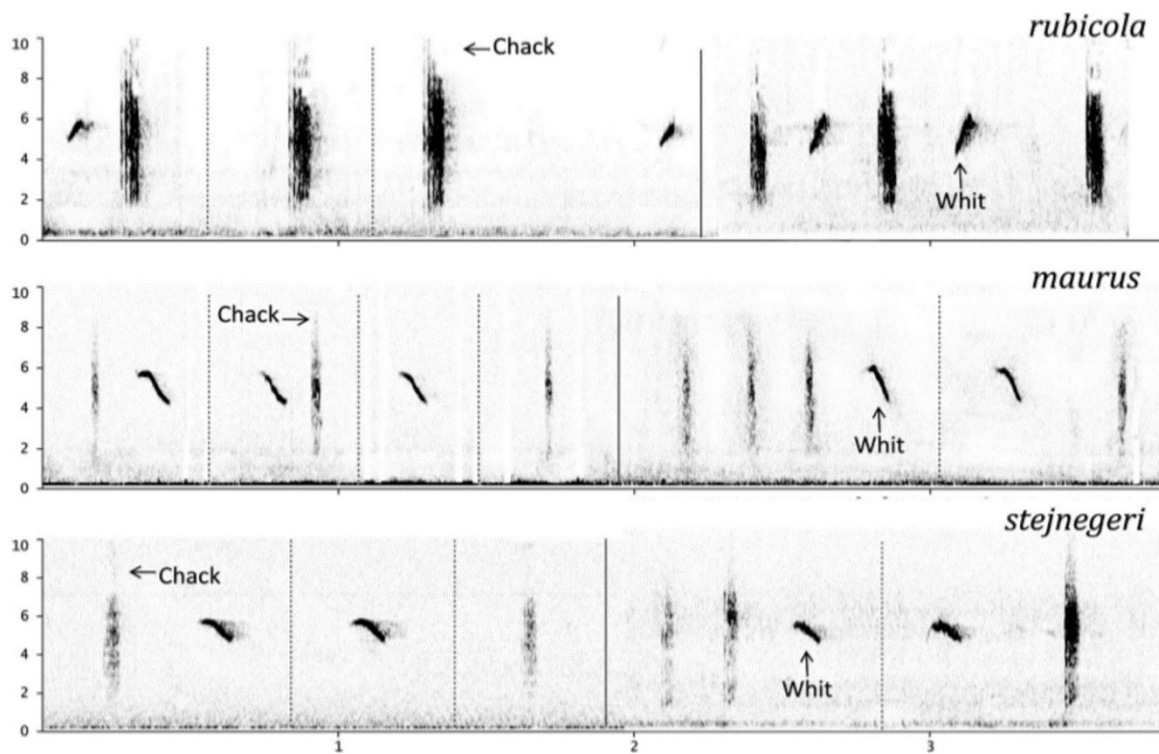


Fig. 5 of Opaev et al. (2018), showing alarm call types of the three Palearctic groups.

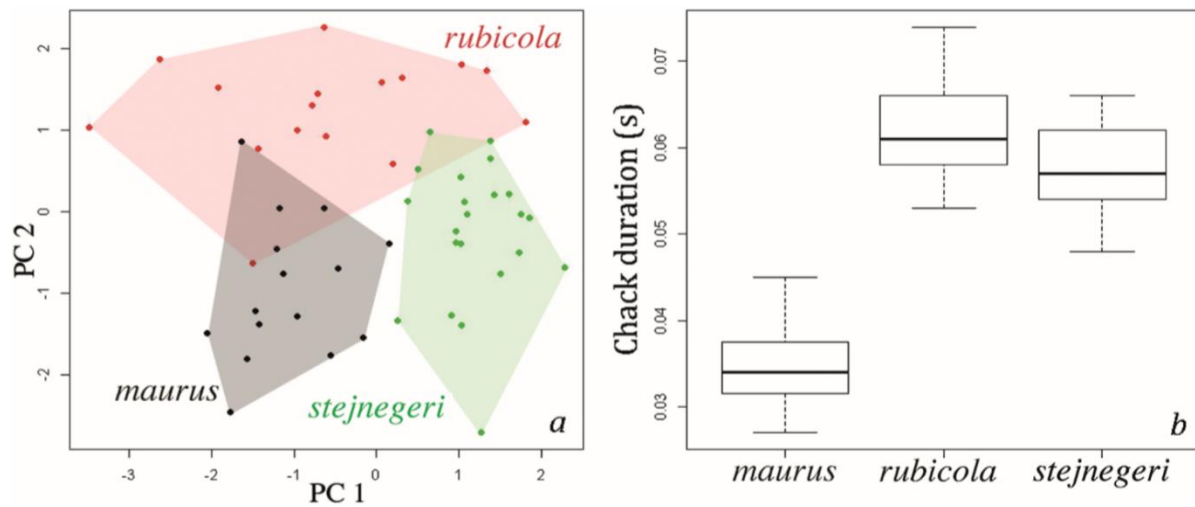


Fig. 6. PCA of four acoustic parameters of whit calls (a) and durations of chack calls (b) of three taxa of the *Saxicola torquatus* complex.

From Opaev et al. (2018).

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 will lead to a name change in the Check-list and a revised account. If we vote to split deeper, removing *stejnegeri* from *maurus*, at least the New Brunswick and perhaps other records will likely be indeterminable (not that this should influence anyone's decision in the slightest).

Recommendation:

The options below represent possible treatments of this taxonomic group. I recommend option c. Please vote YES/NO on each option separately and on English names if voting YES on option b or c.

- a) Make no change, leaving all taxa as part of *Saxicola torquatus* (emendation to specific epithet already accepted in a Supplement on the basis of David and Gosselin 2002). This is untenable, given that sympatry is now clearly established to occur over a considerable area from Russia through Turkey.
- b) Adopt a 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. This would be a conservative approach given the issue with *przewalskii* not being included in any molecular analysis thus far and having priority over *stejnegeri* if lumped. It would also mean that all North American records fit within this single species. It would also follow the interim approach taken by BOU (Sangster et al. 2011). However, it has the disadvantage of not reflecting the deep divergence between *stejnegeri* and all other stonechat taxa as recovered in Zink et al. (2009), and the newly documented vocal differences that include the distinctly different alarm calls of *stejnegeri*.

If option b passes, adopt English names European Stonechat *S. rubicola*, Siberian Stonechat *S. maurus*, and African Stonechat *S. torquatus*, as used in numerous other sources.

- c) Adopt a four-way split between the *maurus* group (Central and South Asian races only), *stejnegeri*, the *rubicola* group, and the *torquatus* group. This, as noted above, ignores *przewalskii* and may lead to further revision when that taxon is included in a future study. It also means that some past NACC-area vagrant records will be unidentifiable. Nevertheless, given the deep divergence between *stejnegeri* and other taxa demonstrated in Zink et al. (2009), the vocal differences documented by Opaev et al. (2018), and the field data by Hellström and Norevik (2014) in which intermediates were not detected in the putative zone of intergradation, this seems the best-supported course of action, and on the basis of these new data I change my recommendation from the 2014 proposal, in which I recommended option b).

If option c passes, adopt English names European Stonechat *S. rubicola*, Siberian Stonechat *S. maurus*, Japanese Stonechat *S. stejnegeri*, and African Stonechat *S. torquatus*, as used in numerous other sources. Note that the English name “Siberian Stonechat” has become widely associated with *maurus*, whether in the restricted sense of Option 3 or the broader sense of Option 2. If Option 3 is adopted, this name is a bit unfortunate since much of Siberia is occupied by what is called in IOC Stejneger’s Stonechat *S. stejnegeri*, although Siberian Stonechat *S. maurus* is widespread in western Siberia. Some other sources (e.g. del Hoyo and Collar 2016) use Japanese Stonechat for *stejnegeri*; I suggest avoiding the creation of newish eponyms.

PS: There is a typo in the Check-list on p. 498: it should say “Winters: [*torquata*] group” rather than “*torguata*”. This may be irrelevant if we accept Option 2 or 3, however, as I assume that text would disappear.

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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

Resurrect *Philodice* as a separate genus from *Calliphlox*

Note: This issue is also being considered by SACC in their Proposal 886. See SACC votes and comments at <https://www.museum.lsu.edu/~Remsen/SACCprop886.htm>

Effect on the AOS Checklist:

This proposal would transfer Magenta-throated Woodstar (*Calliphlox bryantae*) and Purple-throated Woodstar (*C. mitchellii*) to the resurrected genus *Philodice*.

Background:

This proposal is submitted as a complement to NACC proposal 2019-D-14, submitted by Van Remsen, which reinstated *Nesophlox* as the genus for *C. evelynae* and *C. lyrura*. In this proposal we suggest that the revision of *Calliphlox* be extended to resurrect *Philodice* as the genus for *C. bryantae* and *C. mitchellii*.

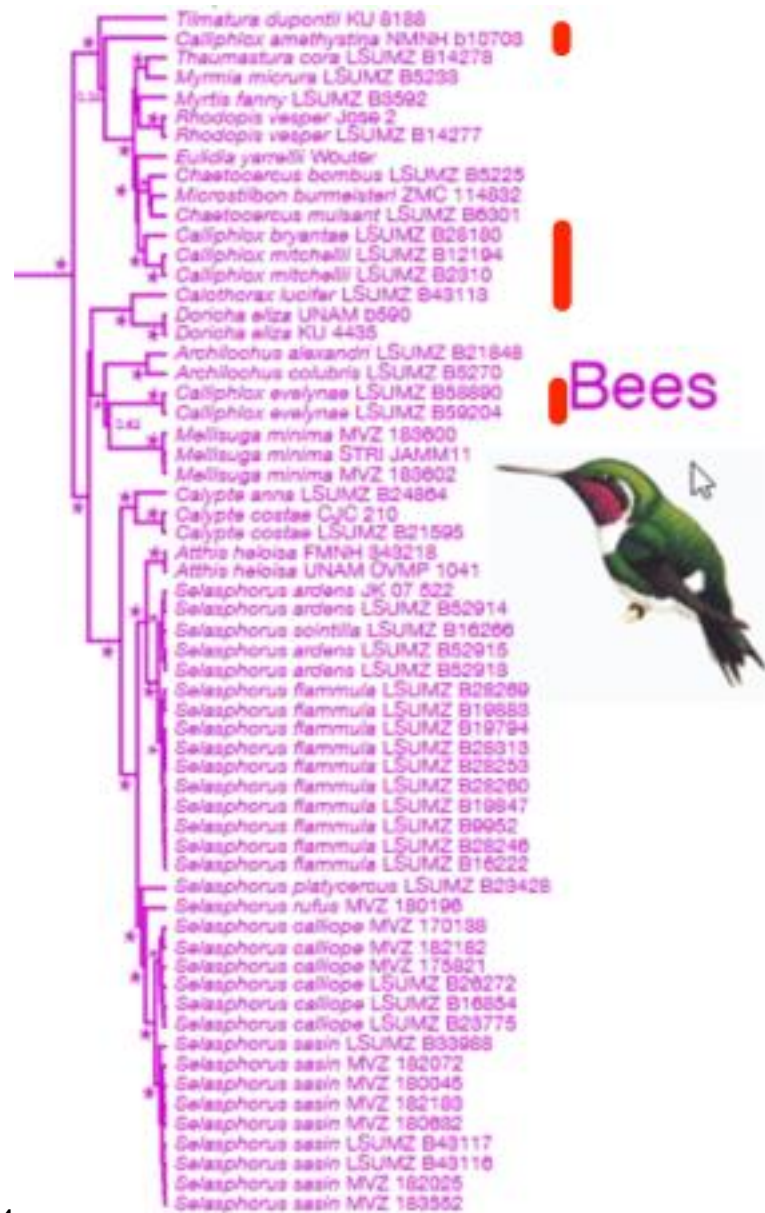
Remsen's proposal outlined the taxonomic history of *Calliphlox*, *Nesophlox* and *Philodice*, which will not be repeated in detail here. Suffice it to say that *Nesophlox* and *Philodice* were frequently subsumed into *Calliphlox* because it was thought that there were insufficient morphological differences between *Nesophlox*, *Philodice* and *Calliphlox* to support generic separation (see also <https://www.museum.lsu.edu/~Remsen/SACCprop164.htm>, which did not pass). Magenta-throated Woodstar and Purple-throated Woodstar have consistently been treated as belonging to *Calliphlox* by the AOU/AOS since Middle American taxa were first included in the sixth edition of the AOU Checklist (1983).

New Information:

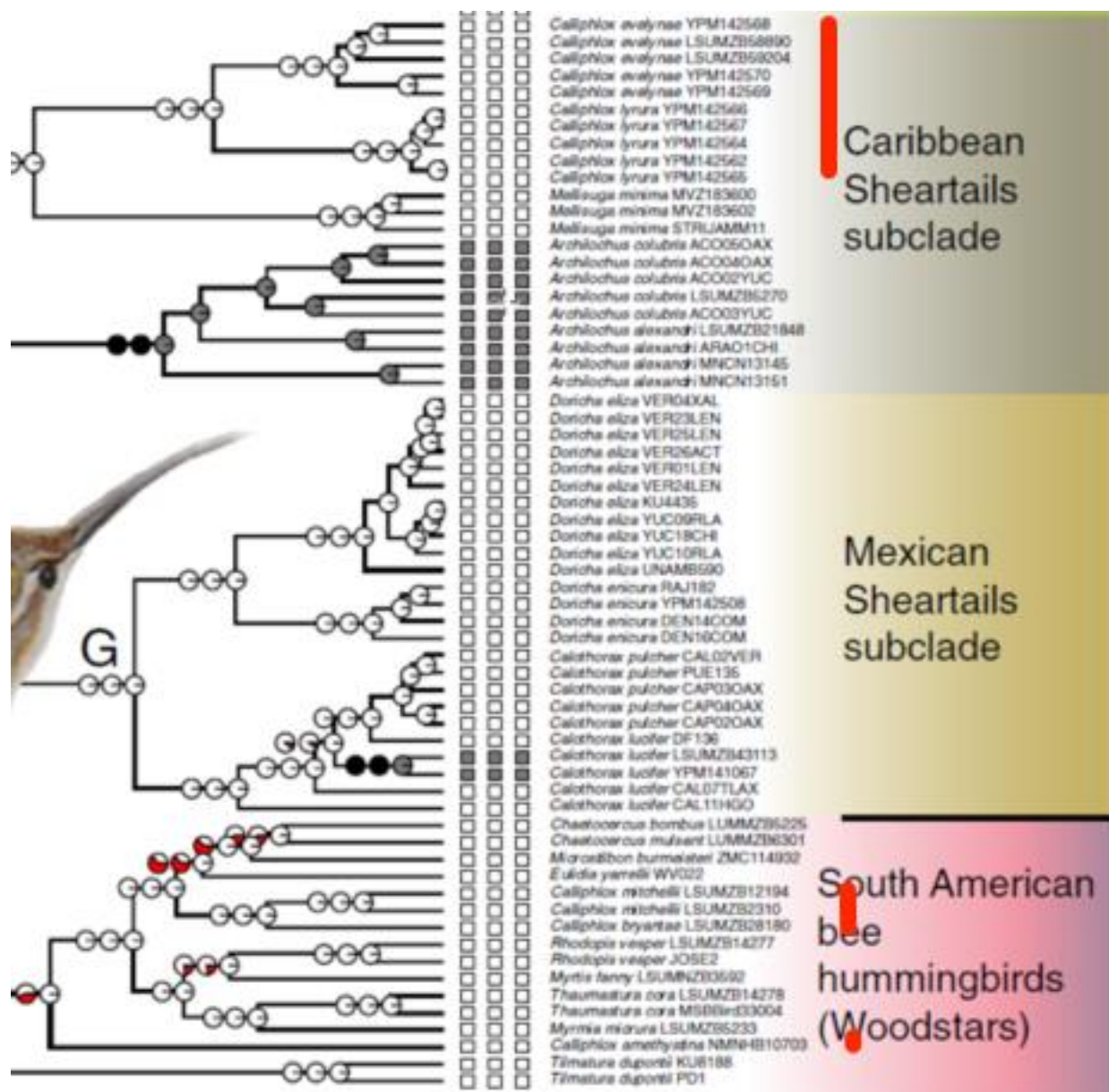
In recent years the family Trochilidae has been the subject of several robust phylogenetic studies. Two of these are specifically relevant to this proposal. As discussed in NACC proposal 2019-D-14, McGuire et al. (2014) examined the entire family and produced a time-calibrated phylogram based on a sampling of 284 hummingbird species representing 101 of the 105 then-recognized genera, using four nuclear and two mitochondrial genes. This resulted in more detailed information on the eight major clades within the family, one of which was composed of the woodstars, sheartails, *Selasphorus*, and relatives and which corresponds to the tribe Mellisugini (or the "bees") (McGuire et al. 2007).

Not discussed in NACC proposal 2019-D-14, however, Licona-Vera & Ornelas (2017) produced a dated multilocus phylogeny restricted to Mellisugini based on a dense sampling of 116 individuals from all 16 recognized genera within the tribe and 32 of the 36 extant species using two mitochondrial and four nuclear genes. Their phylogeny of Mellisugini had a similar topology to that of McGuire et al. (2014) and corroborated the findings of that earlier paper.

The significant portions of both phylogenies are shown below:



McGuire et al. 2014



Licona-Vera & Ornelas (2017)

Both phylogenies demonstrate that *Calliphlox*, as recently treated by the NACC (and the SACC), is polyphyletic. Of its five species, the two Bahama endemics, *C. evelynae* and *C. lyrura*, belong to a completely different subclade (“Caribbean sheartails”) from the other three, which are in the traditional “woodstar” clade. As noted, the NACC recently dealt with this issue by resurrecting the genus *Nesophlox* Ridgway, 1910 for the two Bahamian taxa (NACC 2019-D-14).

To date, both committees have retained the three other species in *Calliphlox*. However, although these three species belong to the same subclade, Amethyst Woodstar *C. amethystina*, the type species for *Calliphlox*, is sister to the remaining taxa within the entire “woodstar” clade and is deeply paraphyletic with respect to the Magenta-throated Woodstar *C. bryantae* and

Purple-throated Woodstar *C. mitchellii*, which are sister species. These latter two species form a distantly related subclade, phylogenetically closer to members of three other genera (*Eulidia*, *Microstilbon*, *Chaetocercus*) than it is to *C. amethystina*. Given their deep phylogenetic divergence, it would seem unlikely that future treatments would consider merging Magenta-throated Woodstar *C. bryantae* and Purple-throated Woodstar *C. mitchellii* with any of those other three genera.

Despite what may have been considered only minor morphological differences in the initial SACC proposal, these phylogenetic findings require that *C. bryantae* and *C. mitchellii* be treated in a separate genus from *C. amethystina*, which as noted is the type species of *Calliphlox*. The genus *Philodice* Mulsant, Verreaux, J & Verreaux, E, 1866 (type *Trochilus mitchellii* Bourcier) is the appropriate available name.

Recommendation:

We strongly recommend a YES vote to this proposal. Note that this treatment has already been adopted by Clements et al. (2019).

Should the proposal pass, we also strongly recommend continuing to use the group name “woodstar” for all. Most members of this clade, which is comprised of several genera, have long been called woodstars, so this would not affect stability.

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Lump McKay's Bunting *Plectrophenax hyperboreus* with Snow Bunting *P. nivalis***Effect on the North American Checklist:**

This proposal would shift the taxonomic rank of *hyperboreus* from species to subspecies, resulting in the loss of one species from the Checklist.

Background:

McKay's Bunting has been treated as a species since the first edition of the AOU checklist (1886), a mere two years after Robert Ridgway (1884) first described it. Ridgway's own doubts about the rank of this taxon are evident from the ambiguous title of his description ("*Description of a new Snow Bunting from Alaska*"), the fact that he begins it with "subsp. ch." (= subspecies characters), and the designation "*Plectrophanes nivalis hyperboreus* Ridgw." written in his own hand on each of the original labels of the four syntypes at the U. S. National Museum (C. Milensky, in litt. 2019). Similarly, most authorities that made explicit study of plumage variation in Holarctic *Plectrophenax* have concluded that *hyperboreus* is merely a subspecies of *nivalis* (Salomonsen 1931, Hellmayr 1938, Vaurie 1959, Portenko 1989). Many other authorities treated it as a subspecies as well (Paynter 1970, Mayr and Short 1970, Cramp et al. 1994), influenced by evidence of extralimital pairings of male McKay's with reported female Snow Buntings at St. Lawrence Island (Sealy 1967, 1969). Its stable taxonomic status within the AOU checklists belies a more skeptical undercurrent, evidenced by statements such as "may be conspecific" (AOU 1998:630) and "recognized plumage differences are no more pronounced than among many passerine subspecies" (Maley and Winker 2007:909), although both AOU (1998) and Maley and Winker (2007) ultimately treated them as separate species.

Snow and McKay's buntings do not display any known prezygotic reproductive isolating mechanisms in behavior or ecology; in fact, there are few if any known differences between the two in these attributes at all (see Lyon and Montgomerie 1995). Their songs are usually described as similar, but *Plectrophenax* song is relatively complex and at least in Snow Buntings subject to regional, individual, and even annual variation (Espmark 1994, Baldo et al. 2014). A rigorous quantification of song between the two has not been conducted, but it would remain to be demonstrated that a detectable difference (if any) would affect mate choice and levels of introgression (i.e., was potentially meaningful evolutionarily and taxonomically). Differences in timing of migration and habitat saturation (Winker et al. 2002, Matsuoka and Johnson 2008) may be acting as isolating mechanisms, but these are likely too porous or too recent to allow or to have resulted in speciation (see below regarding gene flow levels and extralimital breeding). "It is unlikely that effective postzygotic reproductive isolating mechanisms have evolved, and fertile hybrids would be expected" (Maley and Winker 2010:10), and see below regarding intermediate phenotypes that may very well represent intergrades.

Differences in juvenal plumage have been adduced as evidence for species rank (Maley and Winker 2007), but, like the adult plumage, the juvenal plumage is variable, and some individuals are borderline cases (see Figure 2a in Maley and Winker 2007; visual examination of 50+

juvenal plumaged specimens of *Plectrophenax* at UAM). Furthermore, recognition that the Snow Buntings and longspurs constitute their own family (Calcariidae; Chesser et al. 2010) frees them from an expectation that they have a distinctive juvenal plumage as is typical in the family Emberizidae (*sensu lato*) in which they were previously classified. Some evidence suggests those plumages are evolutionarily conserved, a situation that informed the conclusions of that study (Maley and Winker 2007). Graber (1955), in his review of the juvenal plumages of the Emberizidae (as previously constituted), had already pointed out that *Plectrophenax* does not follow those patterns. In the closely related longspurs (*Calcarius*, *Rhynchophanes*), the juvenal plumage is reminiscent of the adult female plumage, as in *Plectrophenax*, and there is no reason to assume the minor differences reflect a deep evolutionary divide.

Snow Buntings are uncommon (at best) during spring migration at St. Matthew Island (Winker et al. 2002), but they are scarce there at other times (see Robinson et al. 2020). For example, in June of 2003, during transect counts of 2,400 McKay's Buntings, zero Snow Buntings were identified and only five (all males) were seen off transect, the latest on 5 June (Matsuoka and Johnson 2008), suggesting that the two forms are nearly allopatric during the breeding season. A gap in regular breeding distribution of at least 264 km, reinforced by a process of heteropatry (migration timing) and philopatry, may be why intergrades are not more common. Snow Buntings have never been documented breeding on St. Matthew Island (Winker et al. 2002, Robinson et al. 2020). The limited evidence for extralimital breeding by McKay's has rarely been accompanied by detailed documentation of the phenotypes involved, but phenotypic McKay's, usually males, are seen in very small numbers, less than annually, during the summer in the Pribilof Islands and on St. Lawrence Island (see Kenyon and Phillips 1965, Sealy 1967, 1969, Kessel and Gibson 1978, Lehman 2019, S. Schuette in litt. 2019, UAM unpublished data). The male McKay's Buntings collected by Spencer Sealy on St. Lawrence Island (University of British Columbia 13274, 13327, and 13328) are typical McKay's.

New information:

The distinctive appearance of male McKay's Buntings has been the driving factor in its taxonomic rank. Recently acquired series of buntings (both *P. hyperboreus* and *P. nivalis townsendi*) from the Bering Sea islands have made clear that plumage variation in both taxa is significant, not related to age, varies continuously between the extremes within a taxon, and that the extremes of one closely approach that of the other (Withrow 2020; Figures 1 and 2 reproduced here, see paper for more photos of intergrades and/or extremes of variation). Intergrades, or birds that appear to be intergrades, appear more frequently than expected between reproductively isolated populations. As a parallel to this situation, in the North Atlantic *P. n. insulae* from Iceland occurs in winter on the British Isles and mainland Europe (see Banks et al. 1991, Winters 2013), but occasionally breeds on Jan Mayen, the Faroe and Shetland islands, and northern Scotland, where some birds are intermediate with nominate *nivalis* (Nethersole-Thompson 1966, Smith 1996, Shirihihi and Svensson 2018). Subspecies *insulae* is distinguished from nominate *nivalis* by being darker in nearly all the same respects that *hyperboreus* is paler and offers an instructive yardstick to which McKay's Bunting may be compared (to my knowledge *insulae* has never been suggested to be of species rank).



Figure 1. Examples of male McKay's Buntings from St. Matthew Island (four at left) and male Snow Buntings from St. Paul Island (four at right), collected in early June and late May respectively. The middle two McKay's are typical; the topmost and bottommost birds represent the pale and dark extremes within birds collected on St. Matthew Island. Similarly, the Snow Buntings represent the breadth of phenotypes collected on St. Paul Island in the Pribilofs.



Figure 2. Examples of female McKay's Buntings from St. Matthew Island (four on left) and female Snow Buntings from St. Paul Island (four on right) collected in early June and late May respectively. The middle two McKay's are typical; the topmost and bottommost birds represent the pale and dark extremes within McKay's.

Initial mtDNA and AFLP-based work on McKay's Bunting (Maley and Winker 2010) detected only small genetic differences. Recent genomic work on the buntings (Winker et al. 2018) found no fixed differences between the species across 3,431 UCE loci, few loci with large allele frequency differences between species, and an overall $F_{ST} = 0.034$, casting serious doubt on the reproductive isolation of McKay's Bunting. Most importantly, this work suggests that levels of long-term gene flow between McKay's and Snow buntings are higher than expected between species (3-5 individuals per generation in each direction), but low overall, probably because of the isolation of McKay's breeding grounds.

Multiple lines of evidence, including plumage patterns, genomic data, and nearly identical life histories all point to McKay's Bunting being a subspecies of Snow Bunting. Its entire breeding range, St. Matthew Island, is fully protected by inclusion in the Alaska Maritime National Wildlife Refuge and it would be protected equivalently under U.S. law as an endemic subspecies.

Recommendation:

I recommend that NACC lump McKay's Bunting with Snow Bunting, treating it as a subspecies of the latter.

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