

AOS Classification Committee – North and Middle America

Proposal Set 2019-B

12 December 2018

No. Page Title

- | | | |
|----|----|--|
| 01 | 02 | Transfer Orinoco Goose <i>Neochen jubata</i> to <i>Oressochen</i> |
| 02 | 08 | Recognize the parulid genus <i>Leiothlypis</i> |
| 03 | 11 | Change the linear sequence of the Hirundinidae |
| 04 | 16 | Make changes to the English names of hummingbirds in the genus <i>Lampornis</i> : (a) Use mountain-gem for all species of <i>Lampornis</i> , and (b) Delete the hyphen in mountain-gem |
| 05 | 19 | Split Hwamei <i>Garrulax canorus</i> into two species, recognizing <i>G. taewanus</i> |
| 06 | 24 | Split Socorro Parakeet <i>Psittacara brevipes</i> from <i>P. holochlorus</i> |
| 07 | 31 | Merge the storm-petrel genus <i>Oceanodroma</i> into <i>Hydrobates</i> |
| | 33 | External comment on Proposal 2019-B-7 |
| 08 | 36 | Recognize family Leiothrichidae for <i>Leiothrix</i> and <i>Garrulax</i> |
| 09 | 39 | Modify the linear sequence of genera and species in the Passerellidae |
| 10 | 44 | Merge (a) <i>Pselliophorus</i> into <i>Atlapetes</i> , and (b) <i>Melozona</i> into <i>Aimophila</i> |
| 11 | 47 | Separate Gray-faced Petrel <i>Pterodroma gouldi</i> from <i>Pterodroma macroptera</i> |

Transfer Orinoco Goose *Neochen jubata* to *Oressochen***Background:**

This proposal follows SACC Proposal 637, which was based on Bulgarella et al. (2014) as well as unpublished morphological and behavioral evidence. Bulgarella et al. (2014), in a paper on genetic differentiation between island and mainland populations of the two species of *Chloephaga*, also produced a phylogeny of *Chloephaga* and related species based on 636 bp of mtDNA control region sequence; in this phylogeny (see below), one species of *Chloephaga*, Andean Goose *C. melanoptera*, was sister to Orinoco Goose *Neochen jubata* rather than to the remaining species of *Chloephaga*. Proposal 637 recommended either transferring Orinoco Goose *Neochen jubata* to *Chloephaga* or including both in a single genus other than *Chloephaga* (*Neochen* was identified in the proposal, but *C. melanoptera* is the type species of the genus *Oressochen*, and this name has priority over *Neochen*). A third option, transferring *C. melanoptera* to *Oressochen* but maintaining Orinoco Goose in *Neochen*, was not considered. SACC voted to transfer both species to *Oressochen*. Only Orinoco Goose *Neochen jubata* has been recorded in our area, where it is of accidental occurrence.

New Information:

From SACC Proposal 637:

Bulgarella et al. (2014) published a complete phylogeny of *Chloephaga* based on a molecular dataset. They used sequence data from the mitochondrial DNA control region to look at divergence and relationships. No nuclear data were used in the analysis. Although the aim of the paper was to quantify genetic divergence among insular and mainland populations of *Chloephaga* geese, they found an unexpected result relating to *Neochen*. Their results show that *Neochen* and Andean Goose (*Chloephaga melanoptera*) are sister species, and the pair is sister to the rest of *Chloephaga*. Given the lack of nuclear gene sequence data, and the small sample size it is tempting to wait for another paper with a larger dataset to act on this single result. However, I think there are ample reasons to consider that this relationship between *Neochen* and *C. melanoptera* is not only supportable, but in hindsight seemingly obvious.

Andean Goose was always the odd *Chloephaga*: The remaining four species of *Chloephaga* share the same wing pattern, a similar body shape, are strongly aquatic, nest on the ground, and are restricted to lowland temperate regions of the southern cone of the continent. The Andean Goose on the other hand has a different wing pattern in which the dark stripe on the wing does not extend from wing base to primaries. Also, Andean Goose shows white primary coverts contrasting with blackish primaries, whereas in other *Chloephaga* the greater primary coverts are dark, and the alula and lesser primary coverts are a mix of dark and white. The body shape of the Andean Goose is odd in that it holds its neck and nape inflated, giving it a strange head/neck shape. The tertials are broad and bulky, almost forming a bustle on the rear end that is missing from *Chloephaga*. Another difference is that the dark parts on the sitting bird,

mainly on the rear, are iridescent, whereas on *Chloephaga* iridescence is restricted to the dark bar on the greater coverts. Rather than ground nesting, Andean Goose tends to nest on cliffs. Vocally it is divergent from *Chloephaga*, although the difference is not obvious without some attention to the details of the sound.

Structure and Plumage: Both the Andean Goose and the Orinoco Goose share the same odd puffed nape, and neck that is unlike *Chloephaga*. It is a difficult structural shape to describe because I think it is mainly created by the length of the feathers themselves and how they are held erect in most cases, but a quick look at various photos of the species involved shows them well. Both Andean and Orinoco geese can show the structural striping on the neck, as in the unrelated true goose genus *Chen*, but it is not something you see on true *Chloephaga*. Similarly, the broad tertials that form a bustle on the rear parts -- a feature shared with *Neochen*. Iridescence on the tertials as well as upperparts feathering is also shared by Orinoco and Andean geese and is quite different from that of *Chloephaga*. Both the Orinoco and Andean geese show substantial iridescence on the upperparts, including the tertials and lower scapulars and back feathers. This feature unites them and sets them apart from true *Chloephaga*.

Nesting and habitat: The Orinoco Goose is a tree-nesting species, although terrestrial when foraging. They will use a large cavity or broken-off snag as a nest-site. The Andean Goose often nests on cliffs overlooking the water, on a ledge or nook in the cliff. That these are the two species geese that are terrestrial but nest away from flat ground is something that unites the two and separates them from *Chloephaga*. All of these geese are terrestrial, sometimes foraging far from water. The most aquatic is the marine Kelp Goose, whereas the rest graze and are not necessarily found close to water. However, when closer to water, *Chloephaga* retreat to water when alarmed or with chicks. In contrast, in my experience Andean Geese retreat by flying or walking away, but do not tend to swim. In fact, of the hundreds if not thousands of Andean Geese I have observed, I do not recall them swimming. Similarly, Orinoco Goose is not a species that commonly swims, although I am much less experienced with that species.

Distribution: Both the Andean and Orinoco geese are found much farther north than core *Chloephaga*. In fact in range they replace each other, one in the highlands of the Andes, and the other in the lowland savannas east of the Andes. There is little overlap in the distribution of Andean Goose and Upland Goose, but essentially Andean and Orinoco are allopatric with the southern *Chloephaga*. All other *Chloephaga* are sympatric, separating out ecologically. Although most of the species are often found together, the strictly marine Kelp Goose stands out in being found within sight of the other species, but associating usually with the other species due to the habitat difference.

Voice: This needs more study; all of these geese have male whistling calls and female grunting voices. Although in listening to voices on xeno-canto, to me the structure of sounds of Andean and Orinoco geese are more similar to each other than they are to *Chloephaga*.

Chicks: The plumage of downy young is an interesting character. It is particularly interesting given the different habitat and ecology of the species. Both Andean and Orinoco geese have brightly plumaged chicks, essentially black-and-white striped. They have white faces, black crowns and back of neck, and a black patch around the eye and black spot on the ear. Overall, they are remarkably similar. Downy young of the southern *Chloephaga* are variable, bolder striped on Ruddy-headed Goose, but not nearly as contrasting as that of Andean-Orinoco, and not showing the black ear patch. Kelp Goose has greyish white chicks, Upland Goose also dull largely unicolored youngsters but a buff color. Here are some photos to compare:

Andean Goose <https://www.flickr.com/photos/55681839@N07/7678638248/>

Orinoco Goose <https://www.superstock.com/stock-photos-images/4273-12414>

Upland Goose <http://ibc.lynxeds.com/photo/upland-goose-chloephaga-picta/pair-three-small-chicks-swimming>

Ruddy-headed Goose <http://www.surfbirds.com/community-blogs/falklandbirder/2008/11/>

It should be noted that Buckner et al. (2018) recently published a phylogeny that also includes the sister relationship of *N. jubata* and *C. melanoptera*. Although they included complete mitochondrial genomes for several species, the data for *Chloephaga* and *Neochen* appear to be taken entirely from Bulgarella et al. (2014); therefore, their result is based solely on the same control region sequences used in the previous study. Unfortunately, Ottenburghs et al. (2016) did not sample *N. jubata* or any species of *Chloephaga*. Buckner et al. are currently sequencing UCEs for all species of Anseriformes through the OpenWings project.

Livezey's (1997) morphological analysis of the shelducks and sheldgeese was based on skeletal and tracheal characters, and characters related to natal and adult plumages and soft parts. His analysis (see his tree below) placed *C. melanoptera* as sister to all other species of *Chloephaga* (with 85% bootstrap support), and *N. jubata* as sister to *Chloephaga*. The other four species of *Chloephaga* formed a rather tight group, and *C. melanoptera*, although sister to these species, was somewhat distantly related to them. Livezey placed *C. melanoptera* in a separate subgenus (*Oressochen*) from that of the other four species (*Chloephaga*), maintaining *N. jubata* in the separate genus *Neochen*.

Recommendation:

I'm not particularly impressed by the phylogeny based on control region sequences. The support values for the *jubata-melanoptera* sister relationship are strong (90% bootstrap, 0.97 posterior probability) but it would not take much data to change this result. As noted in the SACC proposal, the primary intent of Bulgarella et al. (2014) was to study genetic differentiation between island and mainland populations of two species of *Chloephaga* geese; the phylogeny was strictly a secondary aim, and it suffers as a result. If we were operating independently on this issue, I would much prefer to wait until nuclear data, or at a minimum more mitochondrial data, are available, before making a change. The anecdotal phenotypic data, although interesting, do not really convince me in the way that an analysis of behavioral and

morphological characters would. Moreover, as noted by Vitor Piacentini, SACC did not consider the option of transferring *C. melanoptera* to *Oressochen* while keeping *N. jubata* in *Neochen*.

Nevertheless, there are arguments for accepting the proposal: (1) *N. jubata* is a South American species that is accidental to our area, and we generally go along with SACC's decisions on such species; (2) SACC has already made this change, and it is better to have a unified list than for SACC and NACC to differ; and (3) *Oressochen* has been adopted by Clements/eBird, based on the SACC decision. Although it was accepted by Clements, which typically adopts the decisions of both AOS classification committees, Tom Schulenberg, compiler of the Clements Checklist, personally was not in favor of adopting *Oressochen*. Schulenberg noted that SACC strongly deviated in this case from their policy of relying on published information when assessing a proposal. Moreover, there is precedent for one committee (in this case SACC) not following the other (NACC) for an accidental in which evidence did not greatly favor the original treatment: SACC recognized the genus *Leiothlypis* for the accidental species Tennessee Warbler following NACC's rejection of this genus (but see Proposal 2019-B-2 below). Although in my view the evidence for transferring *N. jubata* to *Oressochen* is not convincing, these other points should be taken into consideration to round out the committee's perspective on this issue.

tree from Livezey (1997):



Figure 1. One of three shortest phylogenetic trees for Tadornini based on 64 morphological characters; the two other variants differed in the relationships among *Chloephaga hybrida*, *C. picta* and *C. poliocephala* + *C. rubriceps*. Characters providing synapomorphic support for each branch are indicated (see Appendices 1 and 2). See text for explanation of the hypothetical ancestor used in rooting.

tree from Bulgarella et al. (2014):

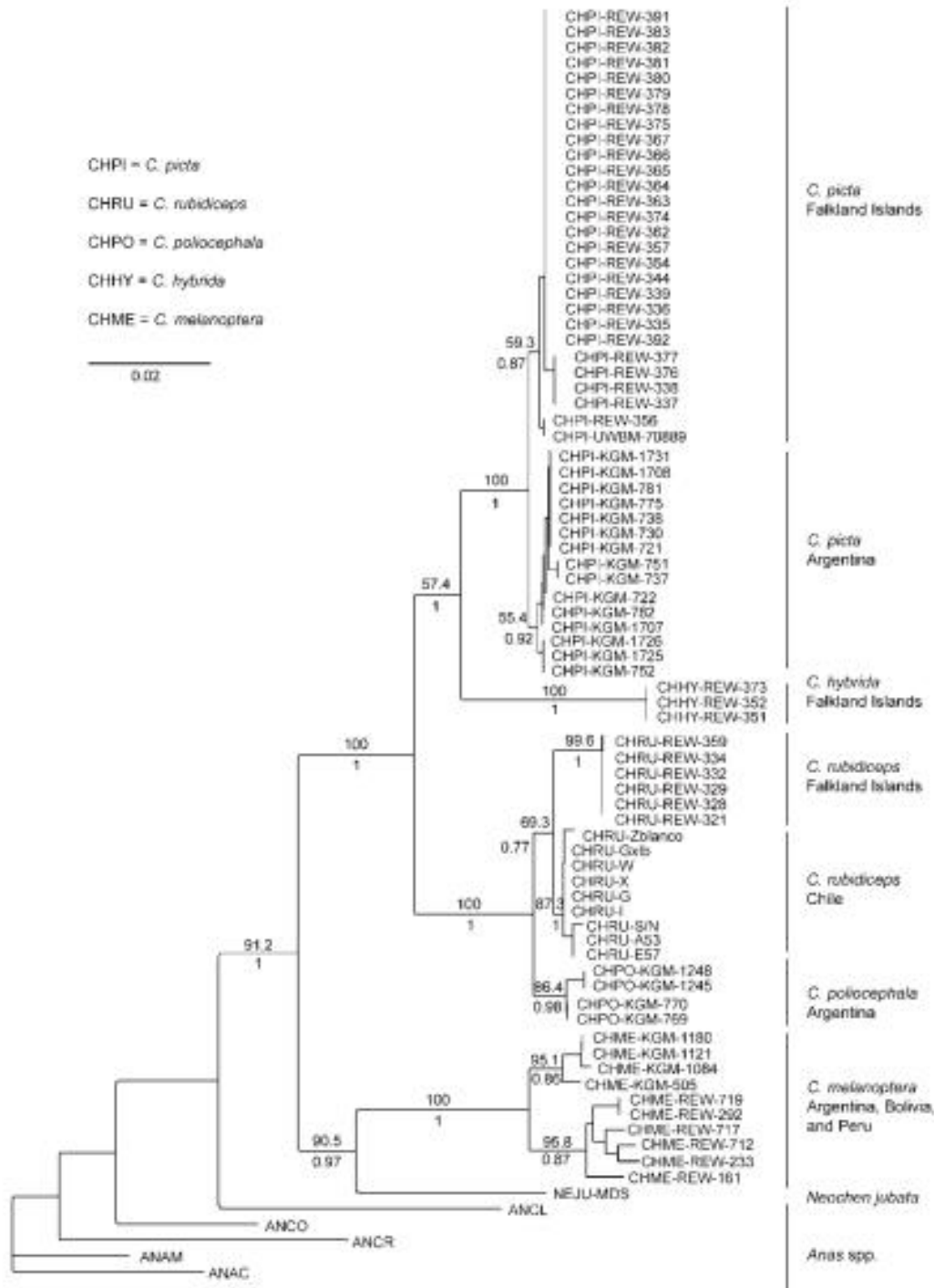


Figure 3. Most likely tree showing the monophyly of *Neochen* and *Chloephaga*. The best-fit model was TVM+I+G with I = 0.6974 and G = 2.3108. Support values above branches correspond to nonparametric bootstrap, and below branches to Bayesian posterior probabilities.

References:

- Bulgarella, M., C. Kopuchian, A. S. Di Giacomo, R. Matus, O. Blank, R. E. Wilson, and K. G. McCracken. 2014. Molecular phylogeny of the South American sheldgeese with implications for conservation of Falkland Islands (Malvinas) and continental populations of the Ruddy-headed Goose *Chloephaga rubidiceps* and Upland Goose *C. picta*. Bird Conservation International 24: 59-71.
- Buckner, J. C., R. Ellingson, D. A. Gold, T. L. Jones, and D. K. Jacobs. 2018. Mitogenomics supports an unexpected taxonomic relationship for the extinct diving duck *Chendytes lawi* and definitively places the extinct Labrador Duck. Molecular Phylogenetics and Evolution 122: 102-109.
- Livezey, B. C. 1997. A phylogenetic analysis of modern sheldgeese and shelducks (Anatidae, Tadornini). Ibis 139: 51-66.
- Ottenburghs, J., H. J. Megens, R. H. Kraus, O. Madsen, P. van Hooft, S. E. van Wieren, R. P. Crooijmans, R. C. Ydenberg, M. A. Groenen, and H. H. Prins. 2016. A tree of geese: A phylogenomic perspective on the evolutionary history of true geese. Molecular Phylogenetics and Evolution 101: 303– 313.

Submitted by: Terry Chesser

Date of Proposal: 29 October 2018

Recognize the parulid genus *Leiothlypis*

Background:

The committee previously considered and rejected a proposal (2009-B-3) to recognize *Leiothlypis* for six species of warblers that we currently classify in the genus *Oreothlypis*. These are the six “dull-colored” species formerly placed in *Vermivora*:

O. peregrina (Tennessee Warbler; the type species)
O. celata (Orange-crowned Warbler)
O. crissalis (Colima Warbler)
O. luciae (Lucy’s Warbler)
O. ruficapilla (Nashville Warbler)
O. virginiae (Virginia’s Warbler)

Oreothlypis also includes two Middle American species formerly placed in *Parula*, *O. gutturalis* (Flame-throated Warbler; the type species) and *O. superciliosa* (Crescent-chested Warbler). As suggested by their former placement in a separate genus, these species differ considerably in phenotype (e.g., plumage, vocalizations) from the other species that we include in *Oreothlypis*.

The transfers of species from *Vermivora* and *Parula* were necessitated by phylogenetic studies indicating that these genera as previously constituted were polyphyletic (see references in Sangster 2008). The most complete study of the Parulidae, although not part of the original proposal, is Lovette et al. (2010). Their well-resolved and highly supported tree showed true *Vermivora* to be sister to a clade consisting of *Mniotilta*, *Protonotaria*, and *Limnothlypis*, and true *Parula* to be embedded in *Setophaga* (formerly *Dendroica*), whereas the species now placed in *Oreothlypis* formed a clade sister to *Catharopeza* + *Setophaga* (see tree below).

The committee considered the *Leiothlypis* proposal prior to the publication of Lovette et al. (2010) and therefore prior to the proposal to completely revise the generic classification of the Parulidae (2010-B-10). That proposal followed the recommendations of Lovette et al. (2010), whose classification reduced the number of genera in the family to 14. Two amendments to this proposal recommended that we retain the phenotypically and phylogenetically distinctive genera *Oporornis*, *Leucopeza*, and *Catharopeza* rather than merging them into *Geothlypis* and *Setophaga*, respectively, and these were passed with the proposal. Probably because we had just considered recognizing *Leiothlypis* the previous year, this issue was not revisited as part of the overhaul of the Parulidae.

This was unfortunate because the situation of *Leiothlypis* is entirely analogous to those of *Oporornis*, *Leucopeza*, and *Catharopeza*. All consist of phenotypically distinctive species long placed in different genera than their proposed conspecifics. Moreover, deep phylogenetic splits separate these genera from their proposed conspecifics, the depth of which are all similar, ranging on the timeline of Lovette et al. (2010) from roughly 0.35 (for the split of *Oporornis* and *Leucopeza* from *Geothlypis* and each other) to 0.40 (for the split of *Leiothlypis* from *Oreothlypis*) to 0.40-0.45 (for the split of *Catharopeza* from *Setophaga*).

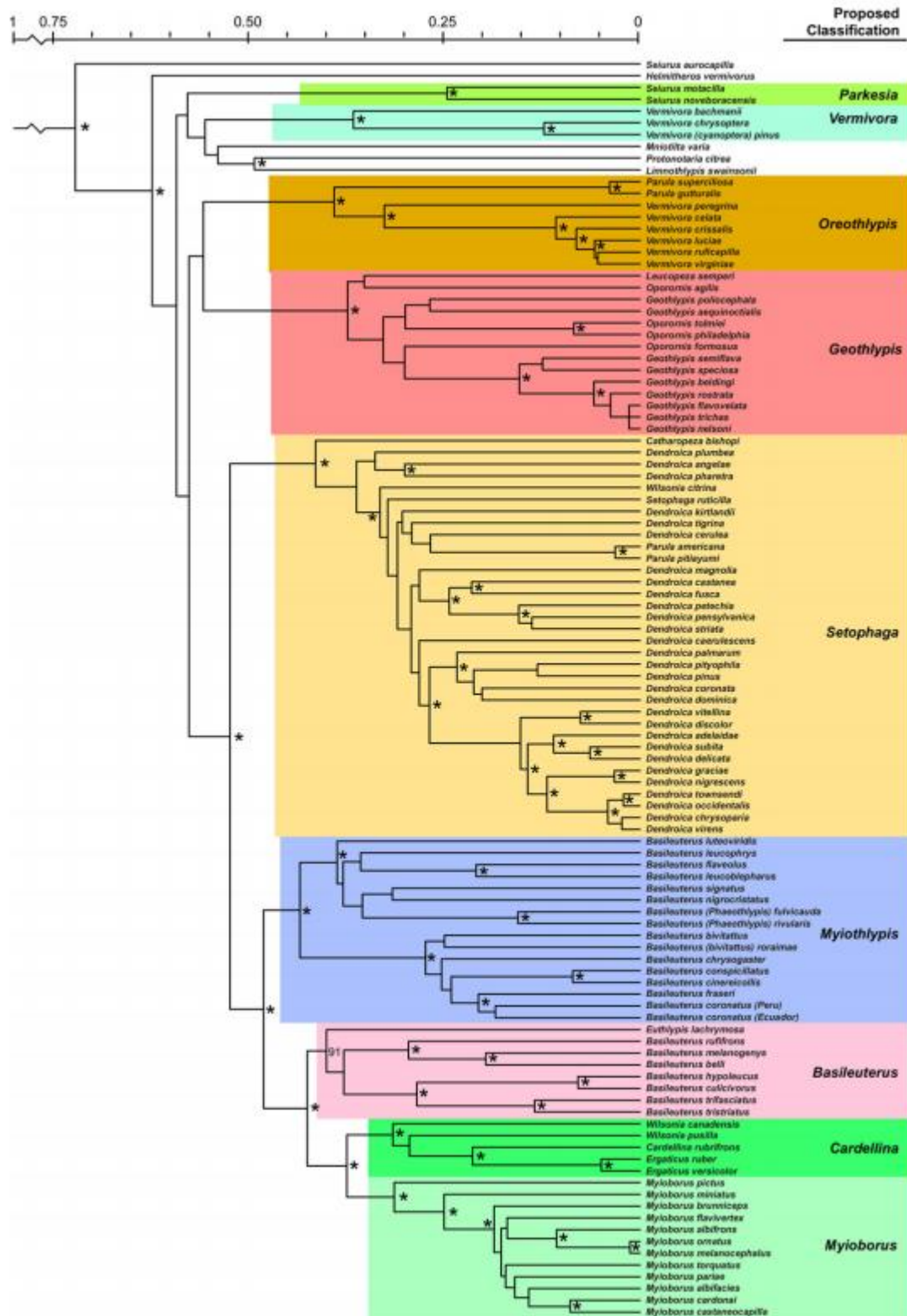


Figure 1. Maximum likelihood tree from Lovette et al (2010) based on analyses of >10,000 bp of nuclear and mitochondrial DNA. The scale at the top was arbitrarily set to 100 time units from the root of the tree.

Recommendation:

I recommend that we recognize *Leiothlypis* for the six species listed above. Most contemporary references, including SACC (which recognized *Leiothlypis* despite the NACC rejection) and the Clements checklist, already recognize *Leiothlypis*.

References:

- Lovette, I. J., J. I. Pérez-Emán, J. P. Sullivan, R. C. Banks, I. Fiorentino, S. Córdoba-Córdoba, M. Echeverry-Galvis, F. K. Barker, K. J. Burns, J. Klicka, S. M. Lanyon, and E. Bermingham. 2010. A comprehensive multilocus phylogeny for the wood-warblers and a revised classification of the Parulidae (Aves). *Molecular Phylogenetics and Evolution* 57:753-770.
- Sangster, G. 2008. A revision of *Vermivora* (Parulidae) with the description of a new genus. *BBOC* 128: 207-211.

Submitted by: Terry Chesser

Date of Proposal: 26 November 2018

Change the linear sequence of the Hirundinidae

Effect on NACC:

This proposal would revise the linear sequence of Hirundinidae to reflect new information regarding evolutionary relationships in the family.

Background:

Swallows in the family Hirundinidae are well studied in terms of their ecology and general biology. However, they are constrained morphologically such that many species appear similar in phenotype, which has made a robust phylogeny elusive for decades. Sheldon et al. (2005) built on phylogenetic inference of Wittingham et al. (2002) to generate a phylogeny that sheds new light on evolutionary relationships within the swallows, which suggested that the linear classification of this group should be revisited.

New information:

Sheldon et al. (2005) sequenced one nuclear locus, β -fibrinogen intron 7 (β fib7), and two mitochondrial gene regions, ND2 and cytochrome b (cytb). Among the 84 species of swallow recognized at the time of the publication, they had β fib7 for 47 species (56%), ND2 for 61 species (73%), and cytb for 74 species (88%), such that 75 species had at least one gene region available for analysis. Eighty-four individuals were included in the analysis in total, and some species included more than one subspecies or individual.

Following DNA sequencing, the authors performed a variety of phylogenetic analyses (Fig. 1; Fig. 2). The resultant phylogenies are generally robust and provide strong support for relationships within the family. Based on a 'ladderized' version of this tree and 'northwest-to-southeast' ordering, I have provided a new linear sequence for the family here.

Table 1: Current linear classification of the Hirundinidae.

Common Name	Scientific Name
Cuban Martin	<i>Progne cryptoleuca</i>
Caribbean Martin	<i>Progne dominicensis</i>
Sinaloa Martin	<i>Progne sinaloae</i>
Gray-breasted Martin	<i>Progne chalybea</i>
Southern Martin	<i>Progne elegans</i>
Brown-chested Martin	<i>Progne tapera</i>
Tree Swallow	<i>Tachycineta bicolor</i>
Mangrove Swallow	<i>Tachycineta albilinea</i>
Golden Swallow	<i>Tachycineta euchrysea</i>
Violet-green Swallow	<i>Tachycineta thalassina</i>

Bahama Swallow	<i>Tachycineta cyaneoviridis</i>
Blue-and-white Swallow	<i>Pygochelidon cyanoleuca</i>
Black-capped Swallow	<i>Atticora pileata</i>
White-thighed Swallow	<i>Atticora tibialis</i>
Northern Rough-winged Swallow	<i>Stelgidopteryx serripennis</i>
Southern Rough-winged Swallow	<i>Stelgidopteryx ruficollis</i>
Bank Swallow	<i>Riparia riparia</i>
Cliff Swallow	<i>Petrochelidon pyrrhonota</i>
Cave Swallow	<i>Petrochelidon fulva</i>
Barn Swallow	<i>Hirundo rustica</i>
Common House-Martin	<i>Delichon urbicum</i>

Table 2: Proposed revision for the linear classification of the Hirundinidae.

Common Name	Scientific Name
Bank Swallow	<i>Riparia riparia</i>
Tree Swallow	<i>Tachycineta bicolor</i>
Bahama Swallow	<i>Tachycineta cyaneoviridis</i>
Violet-green Swallow	<i>Tachycineta thalassina</i>
Golden Swallow	<i>Tachycineta euchrysea</i>
Mangrove Swallow	<i>Tachycineta albilinea</i>
Black-capped Swallow	<i>Atticora pileata</i>
White-thighed Swallow	<i>Atticora tibialis</i>
Blue-and-white Swallow	<i>Pygochelidon cyanoleuca</i>
Northern Rough-winged Swallow	<i>Stelgidopteryx serripennis</i>
Southern Rough-winged Swallow	<i>Stelgidopteryx ruficollis</i>
Sinaloa Martin	<i>Progne sinaloae</i>
Brown-chested Martin	<i>Progne tapera</i>
Caribbean Martin	<i>Progne dominicensis</i>
Cuban Martin	<i>Progne cryptoleuca</i>
Gray-breasted Martin	<i>Progne chalybea</i>
Southern Martin	<i>Progne elegans</i>
Barn Swallow	<i>Hirundo rustica</i>
Common House-Martin	<i>Delichon urbicum</i>
Cliff Swallow	<i>Petrochelidon pyrrhonota</i>
Cave Swallow	<i>Petrochelidon fulva</i>

Recommendation:

I recommend adopting this new linear classification for the Hirundinidae based on new insights regarding evolutionary relationships. **(Note from the Chair:** This sequence of genera differs

considerably from that used by SACC, apparently also based on Sheldon et al. (2005), but it appears to be correct. See the numbers of species handwritten on Fig. 2.)

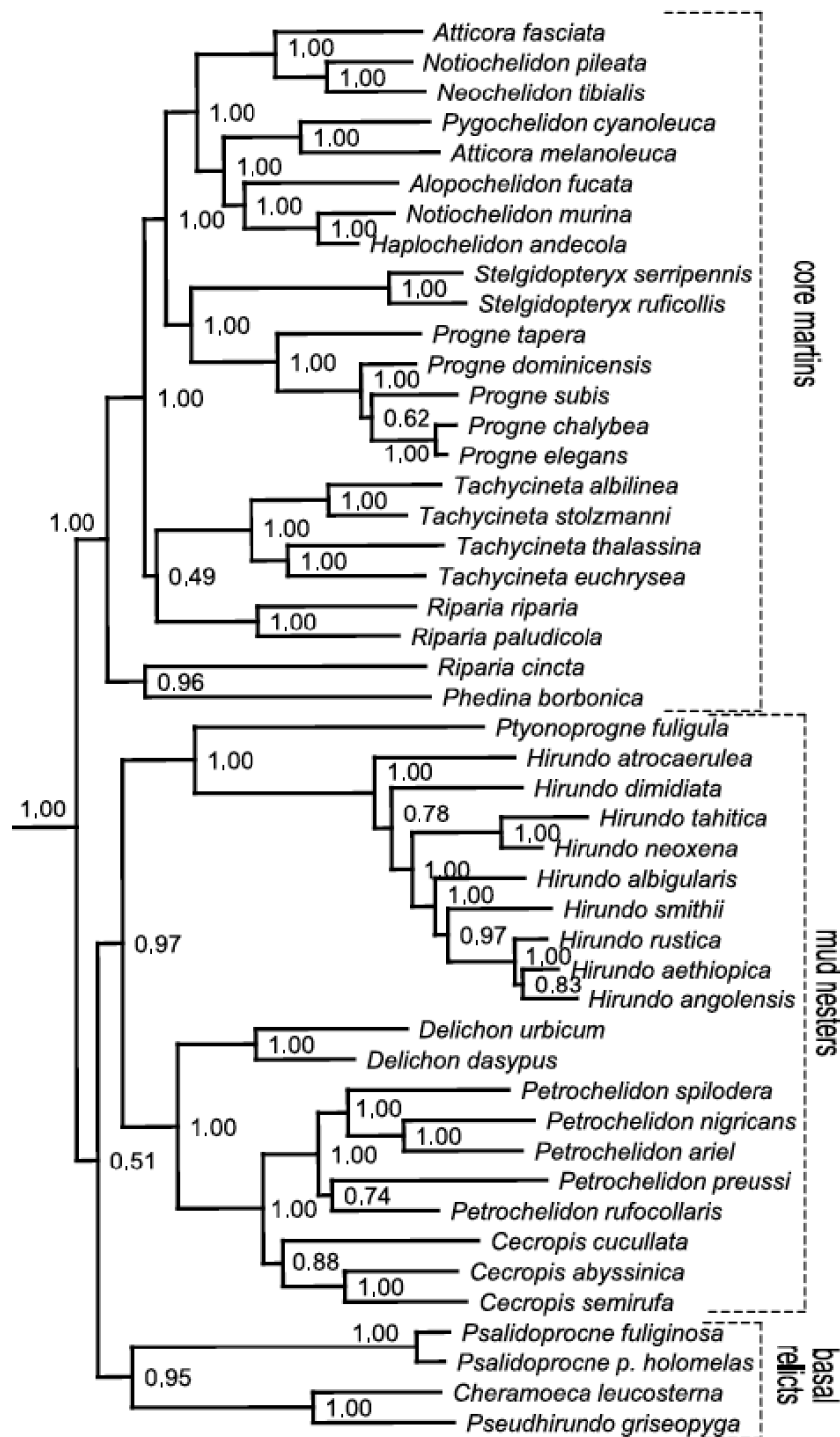


Figure 1. Bayesian consensus tree based on the 47 swallow species for which all three gene regions were sequenced.

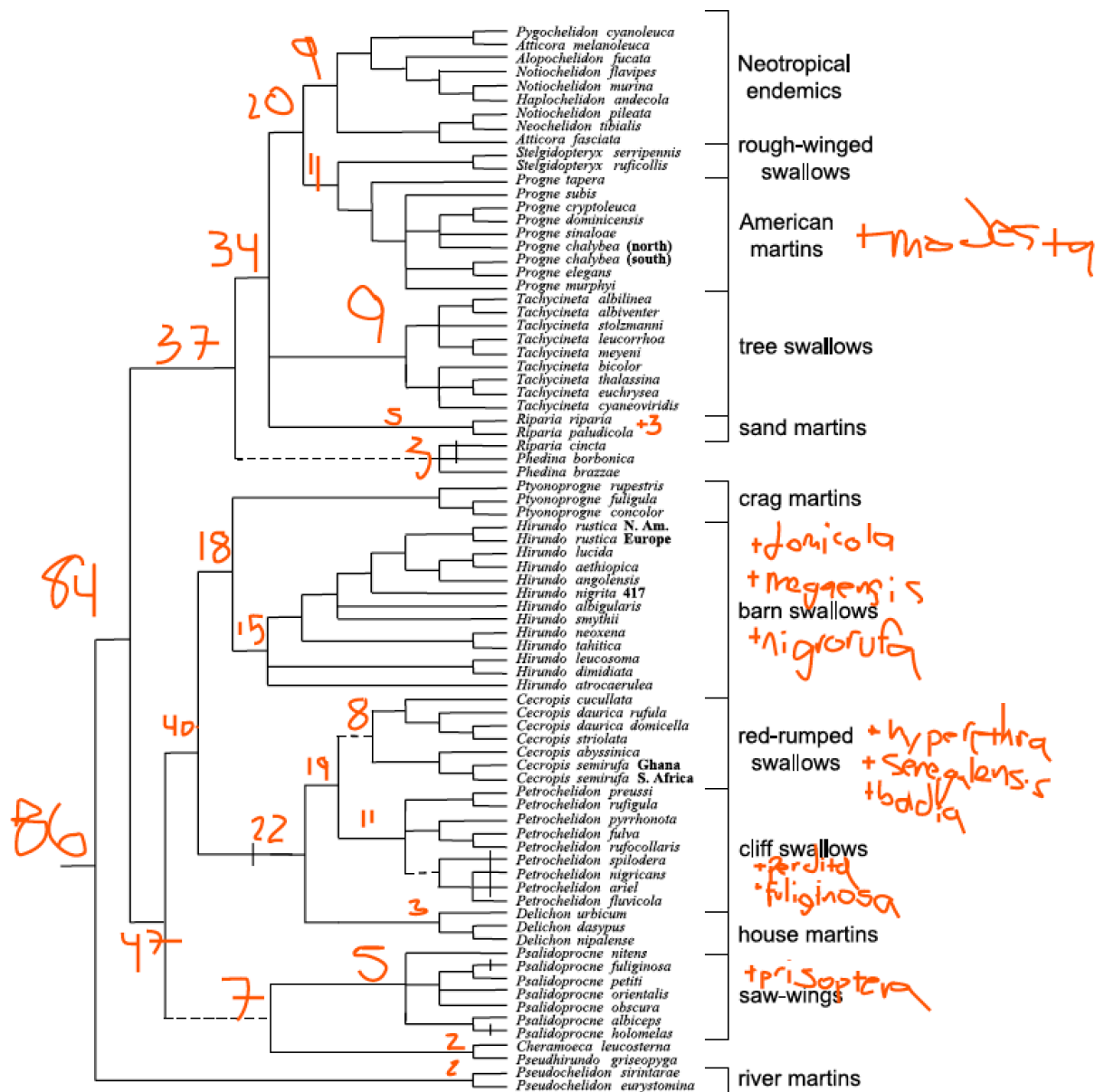


Figure 2. Summary tree of swallow relationships from Sheldon et al. (2005). Dashed lines indicate likely relationships that have not been established unequivocally by the sequence analyses. For the purposes of determining the linear sequence, species not included in the study have been added by hand in the margins, assuming monophyly of genera. Numbers hand-written at the nodes indicate how many daughter species belong to each node.

Literature Cited:

- Sheldon, F. H., Whittingham, L. A., Moyle, R. G., Slikas, B., & Winkler, D. W. (2005). Phylogeny of swallows (Aves: Hirundinidae) estimated from nuclear and mitochondrial DNA sequences. *Molecular Phylogenetics and Evolution*, 35(1), 254–270.
<http://doi.org/10.1016/j.ympev.2004.11.008>
- Whittingham, L. A., Slikas, B., Winkler, D. W., & Sheldon, F. H. (2002). Phylogeny of the Tree Swallow genus, *Tachycineta* (Aves: Hirundinidae), by Bayesian analysis of mitochondrial DNA sequences. *Molecular Phylogenetics and Evolution*, 22(3), 430–441.
<http://doi.org/10.1006/mpev.2001.1073>

Submitted by: Nicholas A. Mason, Museum of Vertebrate Zoology, UC Berkeley; Irby Lovette, Cornell University Museum of Vertebrates, UC Berkeley

Date of proposal: 27 November 2018

Make changes to the English names of hummingbirds in the genus *Lampornis*

a. Use mountain-gem for all species of *Lampornis*

Effect on NACC:

This proposal would change the English names of Amethyst-throated Hummingbird *Lampornis amethystinus* and Blue-throated Hummingbird *Lampornis clemenciae* to Amethyst-throated Mountain-gem and Blue-throated Mountain-gem, respectively.

Background and Rationale:

With at least 347 species of Trochilidae, hummingbird names can be dizzying. Fortunately, there is a lot of creativity in hummingbird names, with probably more interesting and evocative names than for any other family. Also fortunate is that a number of genera have consistent and unique English names and these help birders who may not be fluent in scientific names to understand the traits of each genus. For birders that rely on English names, linkages between genera and English names certainly help them understand relationships between species and learn habits, field marks, calls, and habitat much more easily.

Across the 347 (Clements/eBird Taxonomy v2018, which follows NACC and SACC) species of hummingbirds, there are 113 unique combinations of genus+epithet (e.g., *Lesbia*+Trainbearer, *Phaethornis*+Hermit, *Glaucis*+Hermit, *Amazilia*+Hummingbird, *Amazilia*+Emerald). Thirty-nine genera have English epithets unique to the genus, which makes it easy to keep track. Several other names may be used across small numbers of genera (2-4) and all members of each genus use this name, even though it may not be unique to that genus (e.g., Hermit, Comet, Puffleg, Hillstar, Thornbill, and Sheartail).

- *Coeligena* (11) – 4 Incas and 7 Starfrontlets
- *Discosura* (5) – 1 Coquette and 4 Thorntails
- *Heliodoxa* (9) – Brilliants (8) and one Jewelfront

The remaining names are the most confusing: Emerald (all *Elvira* (2) and *Chlorostilbon* (17), plus about a third of *Amazilia*); Sapphire (all *Chlorestes* (1) and *Chrysuronia* (1), plus 3 *Hylocharis*); Woodstar (all *Calliphlox*, *Chaetocercus*, *Eulidia*, *Microstilbon*, *Myrmia*, *Myrtis*); and, of course, Hummingbird.

Thirty-seven genera use the name hummingbird. Thirty-four of those are genera in which all members are called something-or-other hummingbird, but those genera have few species in them, with the most species-rich genera being *Selasphorus* (7) and *Leucippus* (4). That leaves just three genera — *Amazilia*, *Hylocharis*, and *Lampornis* — in which something named "hummingbird" is mixed up with things named something else.

Amazilia (29) – 21 Hummingbird and 8 Emerald
Hylocharis (8) – 1 Goldentail, 3 Hummingbird, and 4 Sapphire
Lampornis (7) – 2 **Hummingbird** and 5 Mountain-gem

Note that *Amazilia* and *Hylocharis* are both polyphyletic (McGuire et al. 2014) so those genera have some shakeups coming anyway. But *Lampornis* easily can be fixed.

The genus *Lampornis* is monophyletic (e.g., McGuire et al. 2014, which sampled all seven currently recognized species). With just seven species, all of which are distinctively large and have bold facial patterns, *Lampornis* provides a good opportunity to improve English nomenclature for greater clarity.

Green-throated Mountain-gem	<i>Lampornis viridipallens</i>
Green-breasted Mountain-gem	<i>Lampornis sybillae</i>
Amethyst-throated Hummingbird	<i>Lampornis amethystinus</i>
Blue-throated Hummingbird	<i>Lampornis clemenciae</i>
White-bellied Mountain-gem	<i>Lampornis hemileucus</i>
Purple-throated Mountain-gem	<i>Lampornis calolaemus</i>
White-throated Mountain-gem	<i>Lampornis castaneoventris</i>

Only IOC is using the name Blue-throated Mountain-gem, according to [Avibase](#). Similarly, only IOC is using the name Amethyst-throated Mountain-gem ([Avibase](#)). But this does seem like a better name for the following reasons:

- 1) It would make all *Lampornis* use the English name mountain-gem
- 2) It would make all mountain-gems referable to all *Lampornis*
- 3) It would aid public recognition and understanding of the genus *Lampornis*
- 4) It would strengthen the association between *amethystinus* and *clemenciae* and other members of the genus [and, no less importantly, emphasize the distinctions between *clemenciae* and the superficially similar (in the female plumage) Rivoli's Hummingbird *Eugenes fulgens*.]
- 5) It would reduce by two the number of taxa with the fairly unhelpful name "hummingbird"
- 6) It would increase by two the number of species with the evocative and mysterious name "mountain-gem"
- 7) It would reduce by one the number of genera that include the name "hummingbird" with some other English name epithet, leaving only *Hylocharis* and *Amazilia*.
- 8) The new names would create nice symmetry with Green-throated Mountain-gem, Purple-throated Mountain-gem, and White-throated Mountain-gem.

Recommendation:

I recommend a YES vote to strengthen the linkage between the English name epithet and the genus *Lampornis*.

Reference:

McGuire, J.A., C.C. Witt, J.V. Remsen, Jr., A. Corl, D.L. Rabosky, D.L. Altshuler, and R. Dudley. 2014. Molecular phylogenetics and the diversification of hummingbirds. *Current Biology* 24: 910-916. <https://doi.org/10.1016/j.cub.2014.03.016>

b. Delete the hyphen in mountain-gem

We have a lot of hyphens in bird names. When we can get rid of one, it seems worth doing so for brevity and clarity. In this case, there are a few other reasons to eliminate the hyphen.

- a) No other hummingbird monikers carry a hyphen, except racket-tail, which is needed to avoid the awkward, double "t" construction of rackettail. We do not use a hyphen in blossomcrown, sapphrewing, avocetbill, awlbill, trainbearer, goldenthrout, whitetip, helmetcrest, sunangel, or woodnymph. These constructions follow the recommendations of Parkes (1978): "Compound bird names should be spelled as **a single word, unhyphenated**, if ... the second component is a misnomer, either (1) a fanciful nonornithological noun ... EXAMPLES: (1) Woodnymph, Hillstar, Sunangel".
- b) Mountaingem reads perfectly fine, with no confusion in spelling or pronunciation.
- c) This modification would take a small step towards more global consistency. The IOC already uses mountaingem and this small step would help alleviate a tiny bit of inconsistency.

If NACC agrees to this change, the names of the seven species currently named Mountain-gem would become:

Green-throated Mountaingem	<i>Lampornis viridipallens</i>
Green-breasted Mountaingem	<i>Lampornis sybillae</i>
Amethyst-throated Mountaingem	<i>Lampornis amethystinus</i>
Blue-throated Mountaingem	<i>Lampornis clemenciae</i>
White-bellied Mountaingem	<i>Lampornis hemileucus</i>
Purple-throated Mountaingem	<i>Lampornis calolaemus</i>
White-throated Mountaingem	<i>Lampornis castaneoventris</i>

Recommendation:

I recommend a YES vote to simplify the name, eliminate a hyphen, and promote consistency in global nomenclature.

Reference:

Parkes, K.C. 1978. [A guide to forming and capitalizing compound names of birds in English](#). Auk 95: 324-326.

Submitted by: Marshall Iliff

Date of Proposal: 27 November 2018

Split Hwamei *Garrulax canorus* into two species, recognizing *G. taewanus*

Effect on NACC:

This proposal would split the Hwamei (*Garrulax canorus*) into two species, thereby elevating *G. taewanus* to species status and bringing NACC taxonomy in line with most global references. It would also change the English name of *G. canorus*, which is the only one of the two putative taxa that occurs in the NACC area, to Chinese Hwamei.

Background:

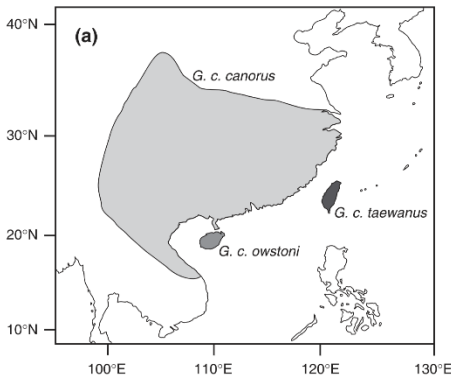


Figure 1: Distribution of subspecies within the *Garrulax canorus* species complex. Taken from Li et al. (2006).

Asian babblers in the family Timaliidae are a widespread, diverse lineage of songbirds that have undergone numerous recent taxonomic revisions at the family, genus, and species level. Hwameis in the genus *Garrulax* are among the most popular caged birds in China and elsewhere in Asia. Three subspecies are currently recognized (Fig. 1).

New Information:

In their treatment of the Asian babblers, Collar (2009) implemented the '7-point' system (Tobias et al. 2010) to assess species limits in many complexes within this lineage. Collar (2009) wrote the following about phenotypic differences between *taewanus* and *canorus*

(see Fig. 2; numbers in parentheses indicate the number of 'points' that each phenotypic difference accumulates):

Collar (2004b) outlined the plumage differences between the taxa *taewanus* and *canorus*, having earlier indicated the candidacy of the split with photographs (Fig. 2; Collar 2003). Race *taewanus* lacks the white brow and broad eye-ring (3), the base colour below and on forehead is pale buff rather than pale rufous (2), and the base colour to the crown and nape is a buffy stone-grey rather than a pale buffy-brown (1); moreover, several website photographs confirm the report by F. Crystal (in litt. 2006) that *taewanus* has 'yellowish skin round the eye', whereas photographs of *canorus* show distinctly (bluish-)greyish skin in this area, offset by the broader white eye-ring (1). Mensurally the two are very close, but with *canorus* having a slightly shorter tail (no score; see Tables 1–2 of Collar (2009)). Tu Hsiao-wei (2003) reported that the song of *taewanus* resembles that of *canorus* but is less complex and more repetitive (1). It is known that the two taxa react to each other's songs, and there is worrying interbreeding of the Taiwan birds with escaped *canorus* that have been imported for singing competitions (L. L. Severinghaus verbally 2003). Nevertheless, a score of 8 permits the separation of *taewanus* at the species level, and I suggest the names Taiwan Hwamei and Chinese Hwamei for the two resultant species.



Figure 2: Photograph from Collar (2003) illustrating phenotypic differences between *G. canorus* (left) and *G. taewanus* (right).

Tu and Severinghaus (2004) examined geographic variation in vocal displays of the mainland *Garrulax canorus* and the island *Garrulax taewanus*. Although the two forms are naturally allopatric, extensive pet trade involving *G. canorus* has resulted in an established population in Taiwan. Tu and Severinghaus (2004) note that hybrids are regularly observed and can be identified by their 'incomplete white eye-ring and eye-line' (Fig. 3). Thus, while reciprocal monophyly in mtDNA suggests that hybridization between the two forms has been infrequent in the past, hybridization has been facilitated by human-mediated movements of *T. canorus* into the range of *T. taewanus*. Tu and Severinghaus (2004) also note differences in the vocal displays of *G. canorus* and *G. taewanus*, stating that songs of the mainland *G. canorus* are more complex and variable. A discriminant function analysis was able to correctly categorize the songs into either taxon 75% of the time (Tu and Severinghaus 2004).



Figure 3: A hybrid Taiwan and Mainland Hwamei captured in the Hualien area of Taiwan (left; photographer, Heng-Wei Hsu). This bird shows a shortened eye-line behind the eye in contrast to that on a Mainland Hwamei (right; photographer, Chieh-Teh Liang). [Caption quoted directly from Tu and Severinghaus (2004).]

Garrulax taewanus and *G. canorus* also exhibit reciprocal monophyly based on mtDNA (Li et al. 2006) and diverged approximately 2.1 mya based on a molecular clock. Furthermore, they are not sister taxa in that *G. c. canorus* is more closely related to *G. c. owstoni* from Hainan (Fig. 4). Li et al. (2006) suggested that reproductive isolation is incomplete between *G. taewanus* and *G. canorus*, largely promoted by the pet trade and movement of *G. canorus* into Taiwan. Nonetheless, Li et al. (2006) proposed that they be treated as separate species based on phenotypic diagnosability and genetic distinctiveness. An additional study by Li et al. (2010) based on microsatellites, a small number of SNPs, and mtDNA, discovered that ~20% of birds sampled in Taiwan were hybrids, including numerous F2 and backcrossed individuals (Fig. 5). Thus, when the two taxa overlap geographically, they seem to hybridize freely and produce fertile offspring capable of interbreeding with each other and either parental form. Li et al. (2010) expressed concern that rampant introgression of *G. canorus* into the genetic background of *G. taewanus* may result in the loss of genetic integrity of the island form if hybridization is allowed to continue unabated.

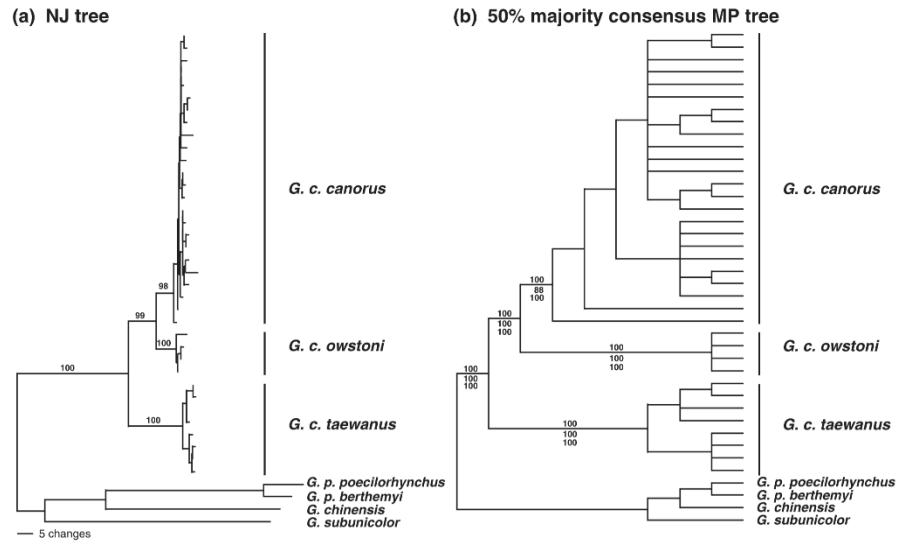


Figure 4: Molecular phylogenies of the Hwamei. A) NJ tree with bootstrap support values for the major clades (b) 50% majority consensus tree of 2808 equally parsimonious trees; numbers indicate percentage consensus (above), and bootstrap values (below) for the maximum-parsimony and maximum-likelihood trees.

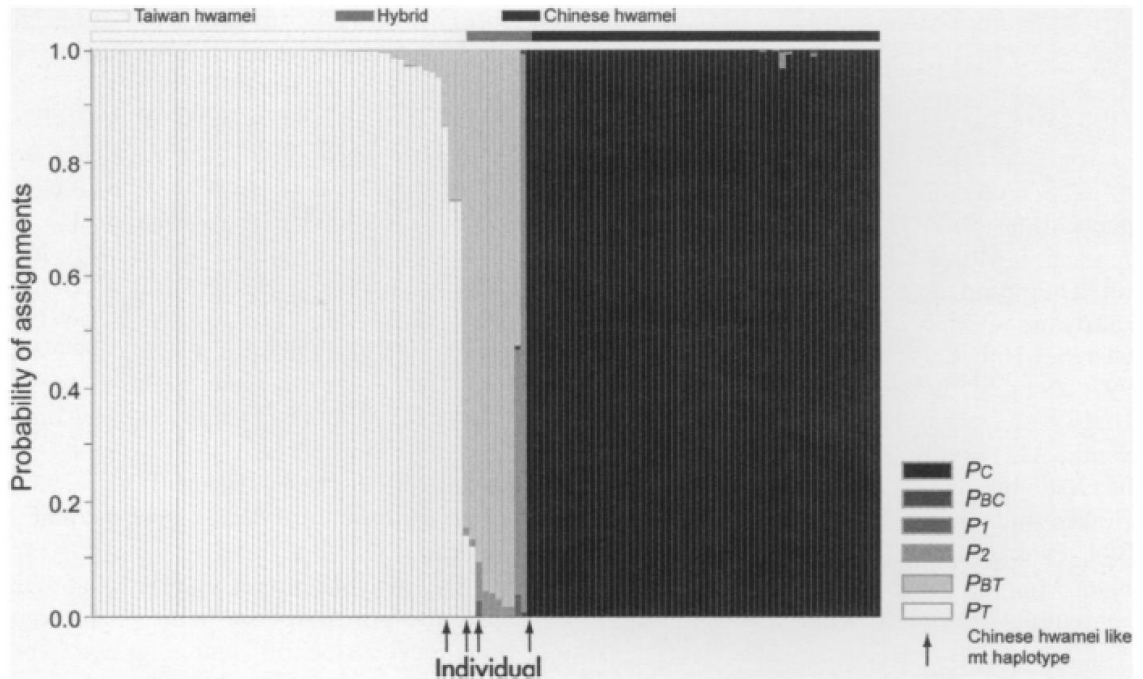


Figure 5: Results from NEWHYBRIDS analysis presented in Li et al. (2010). Each bar represents an individual and the field identification is presented on top. The color of each bar represents probability of assignment to one of 6 hybrid classes. The posterior probability for each individual to be assigned as a Chinese Hwamei (P_T), F1 hybrid (P_1), F2 hybrid (P_2), backcross with a Chinese Hwamei (P_{BC}), or backcross with Taiwan Hwamei (P_{BT}) are labeled in different colors. Arrows indicate the Taiwan Hwamei or hybrid individuals that carried a Chinese Hwamei mitochondrial DNA haplotype.

Recommendation:

Collar (2009) suggested splitting *G. taewanus* and *G. canorus* largely on the basis of qualitative differences in plumage characters observed in photographs, which was also supported by Li et al. (2006) based on reciprocal monophyly in mtDNA. Further studies by Li et al. (2010) indicated extensive hybridization and backcrossing in Taiwan between the two forms, which has been facilitated by human-mediated movements of *G. canorus* into the range of *G. taewanus*. Although the two forms are diagnosable based on plumage and (to a lesser extent) song, they seem to hybridize freely where they occur in Taiwan, and thus do not merit status as separate species based on the BSC. It is worth noting that this taxonomic split has been adopted by the IOC, HBW, and Clements/eBird, but has not been adopted by Howard and Moore. If the split were to be adopted, the proposed common names that are already in use include the Chinese Hwamei (*Garrulax canorus*) and the Taiwan Hwamei (*Garrulax taewanus*).

Literature Cited:

- Collar, N. J. (2003). How many bird species are there in Asia? *Oriental Bird Club Bull*, 38, 20–30.
- Collar, N. J. (2004). Endemic subspecies of Taiwan birds---first impressions. *BirdingASIA*, 2, 34–52.
- Collar, N. J. (2009). A partial revision of the Asian babblers (Timaliidae). *Forktail*, 22, 85–112.
- Li, S.-H., Li, J.-W., Han, L.-X., Yao, C.-T., Shi, H., Lei, F.-M., & Yen, C. (2006). Species delimitation in the Hwamei *Garrulax canorus*. *Ibis*, 148(4), 698–706.
- Li, S. H., Yeung, C., Han, L., Le, M. H., Wang, C., Ding, P., & Yao, C.-T. (2010). Genetic introgression between an introduced babbler, the Chinese hwamei *Leucodioptron c. canorum*, and the endemic Taiwan hwamei *L. taewanus*: a multiple marker systems analysis. *Journal of Avian Biology*, 41, 64–73. <http://doi.org/10.1111/j.1600-048X.2009.04719.x>
- Tobias, J. A., Seddon, N., Spottiswoode, C. N., Pilgrim, J. D., Fishpool, L. D. C., & Collar, N. J. (2010). Quantitative criteria for species delimitation. *Ibis*, 152(4), 724–746. <http://doi.org/10.1111/j.1474-919X.2010.01051.x>
- Tu Hsiao-wei (2003) Geographic variation of Hwamei (*Garrulax canorus*) songs. Master's thesis, Department of Zoology, National Taiwan University, Taipei. [Abstract in Fang, W.-H. (2005) Abstracts of ornithological masters' theses from Taiwan, 1977– 2003. *Forktail* 21: 99–120.]
- Tu, H. W., & Severinghaus, L. (2004). Geographic variation of the highly complex Hwamei (*Garrulax canorus*) songs. *Zoological Studies*, 43(3), 629–640.

Submitted by: Nicholas A. Mason, Museum of Vertebrate Zoology, UC Berkeley; Carla Cicero, Museum of Vertebrate Zoology, UC Berkeley

Date of proposal: 30 November 2018

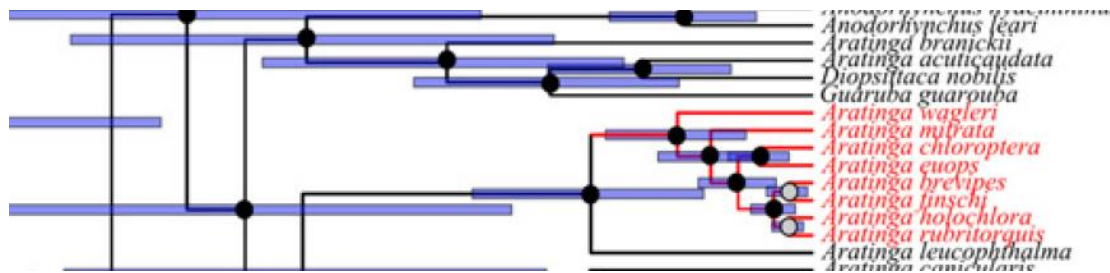
Split Socorro Parakeet *Psittacara brevipes* from *P. holochlorus***Background:**

Parakeets of the recently circumscribed (Remsen et al. 2013) genus *Psittacara* Vigors, 1825 are primarily green, some with red accents mainly on the forehead, and their taxonomy is contentious. The Green Parakeet *Psittacara holochlorus* (Sclater, 1859) of Mesoamerica has long been considered to include the all-green “Socorro Parakeet” *P. h. brevipes* (Lawrence, 1871) and the distinctively plumaged “Red-throated Parakeet” *P. h. rubritorquis* (Sclater, 1887), along with *P. h. brewsteri* (Nelson, 1928), which is evidently very similar to the nominate. Specific status has been recommended for both *brevipes* and *rubritorquis*, for example, by Ridgway (1916), Howell and Webb (1995) and Collar (1997). Collar et al. (2014, 2018) however, using the Tobias criteria, consider only *rubritorquis* specifically distinct. The AOS (AOU 1998) currently recognizes three groups: *holochlorus*, *brevipes*, and *rubritorquis*. In addition, the all-green Pacific Parakeet *Psittacara strenuus* is sometimes considered a subspecies of *P. holochlorus* (e.g., by Collar et al. 2018), from the nominate of which it differs in being notably larger, particularly for bill and feet (Ridgway 1916). The AOS has long treated *strenuus* as a full species, as do e.g. Dickinson and Remsen (2013), on the basis of both *holochlorus* and *strenuus* having been collected at Tapanatepec, Oaxaca, in September 1927, which has been interpreted as indicating sympatry (Bangs & Peters 1928). This evidence of sympatry was considered weak by Howell and Webb (1995) and by Collar et al. (2018), the latter therefore justifying treatment of *strenuus* as a race of *holochlorus*. However, AOU (1998) maintained that “differences are retained in areas of close approach”, implying at least parapatry if not sympatry.

The Socorro Parakeet *P. h. brevipes* was treated as specifically distinct by Ridgway (1916), on account of its larger bill and darker overall coloration than *holochlorus*, as well as differences in relative length of its primaries, the tenth usually being shorter than the seventh. Bangs and Peters (1928) considered that *brevipes* was probably derived from *strenuus* rather than from *holochlorus*, as *brevipes* shares larger bill and feet with the former, although they considered that the different wing formula of *brevipes* is consistent with species status. Howell and Webb (1995) considered that *brevipes* is more divergent from *holochlorus* than is *strenuus*, citing the different wing formula and stating that voice differs notably; they treated *brevipes* as specifically distinct. From the verbal description in Howell and Webb (1995), however, it is difficult to work out just how the voice differs. Navarro-Sigüenza and Peterson (2004) considered *brevipes* an evolutionary species endemic to Socorro Island on the basis of its relatively very large bill and long tail; they also considered *brewsteri* and *rubritorquis* full species.

New information:

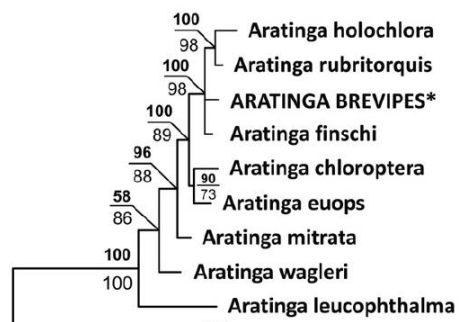
Multiple recent studies have included mtDNA samples of *brevipes* in phylogenies, all producing similar results. In an analysis by Schweizer et al. (2014; screenshot below), the single sample of *brevipes* was sister to Crimson-fronted Parakeet *P. finschi*, with this clade being sister to the clade comprised of *holochlorus* and *rubritorquis*. Urantowka et al. (2014; screenshot below) obtained a similar result using ND2, although the relationship between *brevipes* and *finschi* was unresolved. Martínez-Gómez et al. (2017; screenshots below) analyzed several individuals of *brevipes*, and with the result that for ND2 *brevipes* and *finschi* were sisters, whereas for COI *brevipes* was sister to the clade of *holochlorus* and *rubritorquis*. Unfortunately, neither *P. strenuus* nor *P. h. brewsteri* were included in these genetic analyses.



Relevant part of Fig. 1 of Schweizer et al. (2014), using mtDNA sequences from GenBank.

A. D. Urantowka et al.

Mitochondrial DNA, 2014; 25(5): 365–367



Relevant part of Fig. 1 of Urantowka et al. (2014), using ND2.

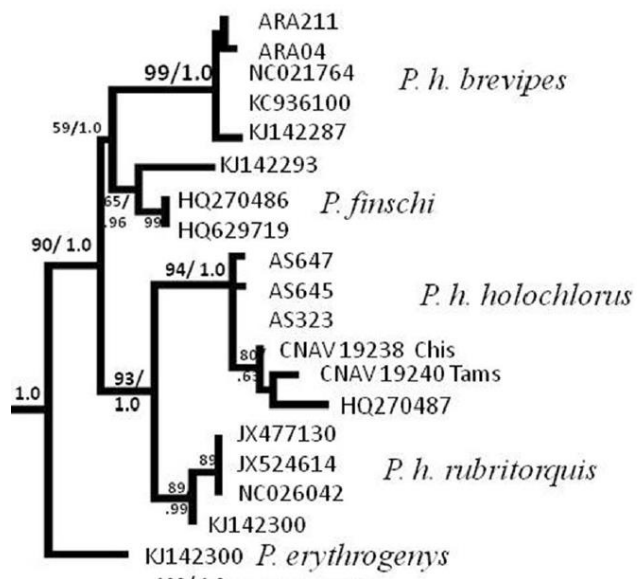


Fig. 2 of Martínez-Gómez et al. (2017); ND2.

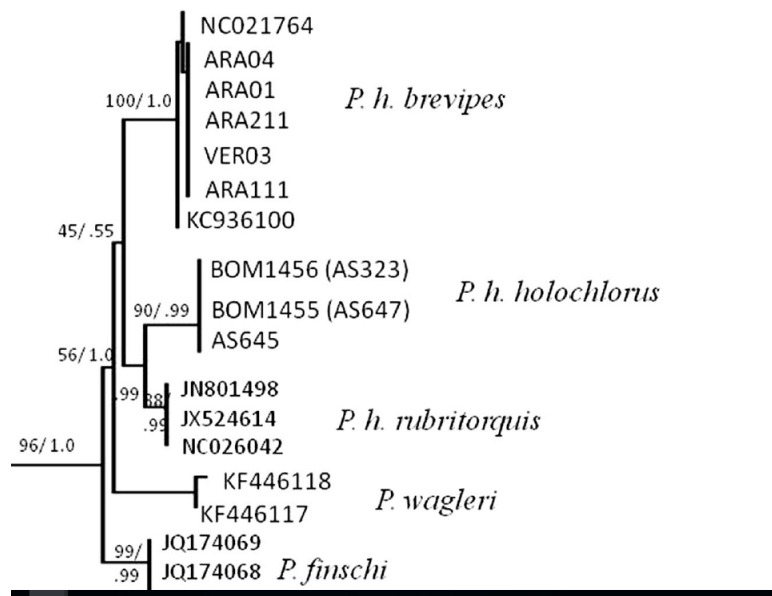
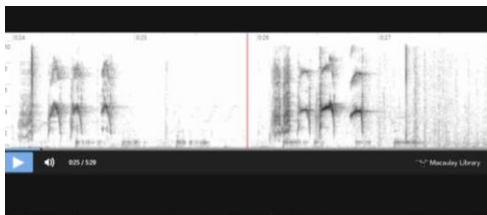
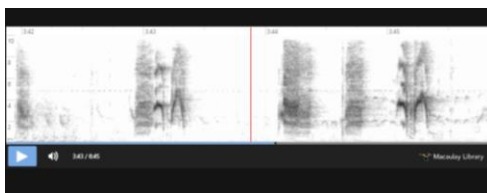


Fig. 3 of Martínez-Gómez et al. (2017), COL.

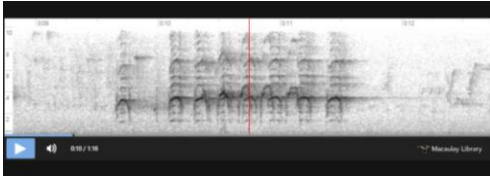
Several sound recordings are now available for *brevipes* from Macaulay Library and xeno-canto, as are larger samples of most of the other taxa. No thorough vocal analysis has been done to my knowledge, but from these recordings I agree with Howell and Webb (1995) that most of them are markedly different than other taxa in the group; many of the calls of *brevipes* are thinner, with few (usually just one) strong harmonics and the fundamental frequency with much the greatest power, and less complex than the common calls of the others, while some other calls of *brevipes* are drier raspy screeches, rather than the full rich screeches common to other group members.



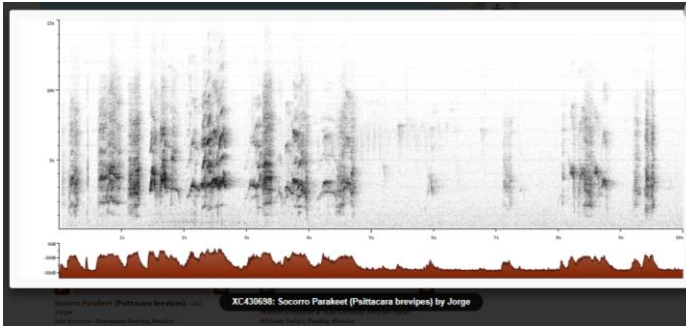
brevipes—LNS 182897, 2 cuts, N. Meza, Socorro



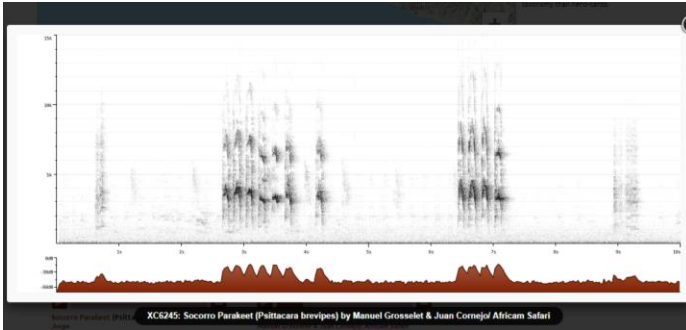
brevipes—LNS 182897, N. Meza, Socorro



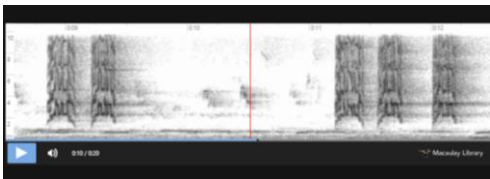
brevipes—LNS 214338, S.N.G. Howell, Socorro



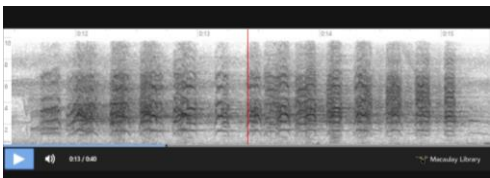
brevipes—XC 430698, Jorge, Socorro



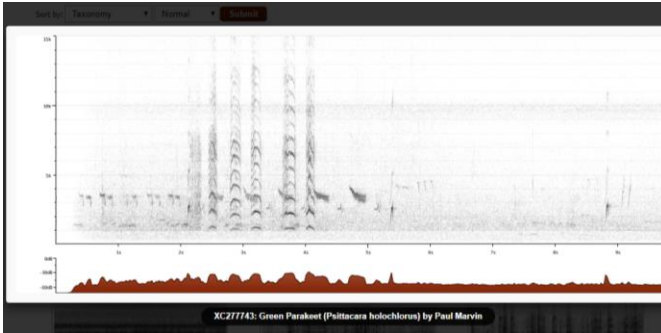
brevipes—XC 6245, M. Grosselet and J. Cornejo, captivity



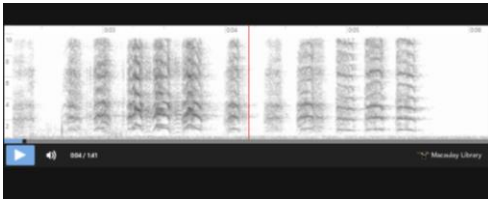
holochlorus—ML 102191791, S. Kiacz, Texas



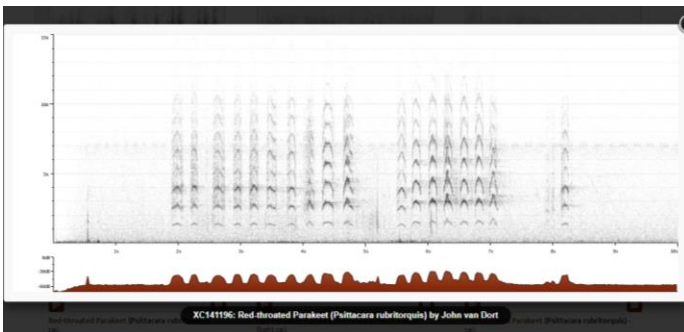
holochlorus—ML 217500, S.N.G.H. Howell, Chiapas



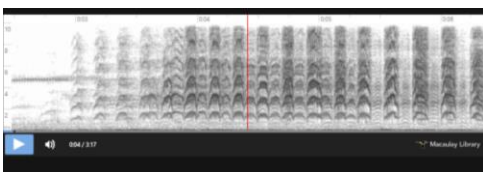
holochlorus—XC 277743, P. Marvin, Texas



rubritorquis—ML 57455911, J. van Dort, Honduras



rubritorquis—XC 141196, J. van Dort, Honduras



rubritorquis—ML 122869941, F. Morazán, Honduras

Although not evident in dried specimens (which I have not examined), iris color in several good-quality photos of *brevipes* is whitish, unlike the dark irides of allied taxa, while its orbital skin is brighter, lighter reddish than in the other taxa; in *holochlorus* the orbital skin is a darker greyish purple, while in *strenuus* it is whitish. These differences have not been properly quantified or even consistently described in the literature, however, and there may be more overlap than I have noted. Martínez-Gómez et al. (2017; screenshots below) showed that *brevipes* occupies unique morphospace due primarily to its longer tail, but it also has a relatively larger bill and shorter wings.

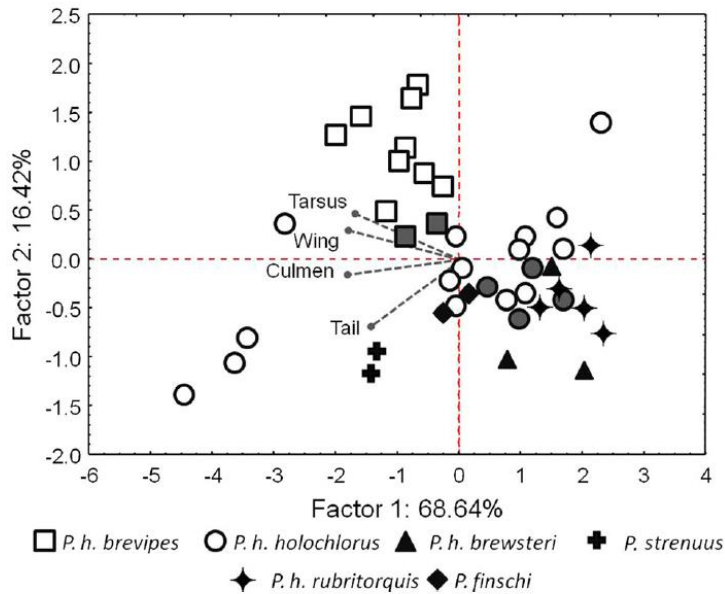
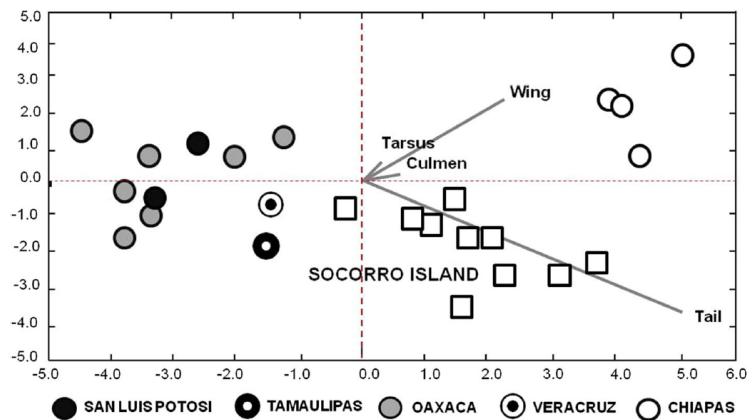


Fig. 4 Principal component analysis of four morphological traits of *Psittacara* species. Gray and black symbols represent scores derived from grand mean values reported by Ridgway (1916) and Nelson (1928)

976

J Ornithol (2017) 158:965–978

Fig. 5 Plot of canonical scores derived from discriminant function analysis of four morphological traits of *Psittacara holochlorus brevipes* (squares) and *P. h. holochlorus* (circles) deposited at CNAV - UNAM



Figs. 4 and 5 from Martínez-Gómez et al. (2017), with *brevipes* represented by squares in a PCA (upper) and DFA (lower).

Subsequent treatments:

Gill and Donsker (2018) recognize *brevipes* and *rubritorquis* as specifically distinct, citing e.g. Martínez-Gómez et al. (2017), among others.

Effect on AOS-CLC area:

If this proposal passes, the AOS would recognize an additional species of *Psittacara*, endemic to Socorro Island. We would need to prepare a new species account for *brevipes* and modify

the existing account for *holochlorus*. This action would also help call attention to the tenuous and evidently deteriorating conservation status of *brevipes*.

Recommendation:

I recommend treatment of *P. brevipes* as a full species, based on the facts that it is evidently not sister to *P. holochlorus*, it is moderately differentiated morphologically, and it is vocally distinct.

Although the fact that *P. strenuus*, suggested to be the source population for *brevipes* (Bangs & Peters 1928), was not included in the genetic analyses may give pause, these two taxa are not particularly similar vocally or morphologically. Likewise, *P. finschi*, to which *brevipes* comes out as sister in multiple analyses, is not especially vocally or morphologically similar to *brevipes*.

A separate proposal should be prepared for splitting *P. rubritorquis*.

Literature Cited:

- American Ornithologists' Union. 1998. Check-list of North American birds. 7th edition. American Ornithologists' Union, Washington, D.C.
- Bangs, O. & J.L. Peters. 1928. A collection of birds from Oaxaca. Bull. M.C.Z. 68:385-404.
- Collar, N.J. 1997. Family Psittacidae (Parrots). In: del Hoyo, J., A.E. Elliott, and J. Sargatal (eds.). Handbook of the birds of the World. Lynx Edicions, Barcelona.
- Collar, N., C.J. Sharpe, & P. Boesman. 2018. Red-throated Parakeet (*Psittacara rubritorquis*). In: del Hoyo, J., A. Elliott, J. Sargatal, D.A. Christie, & E. de Juana (eds.). Handbook of the birds of the World alive. Lynx Edicions, Barcelona (retrieved from <https://www.hbw.com/node/54636> on 3 December 2018).
- del Hoyo, J. & N.J. Collar. 2014. HBW and BirdLife International illustrated checklist of the birds of the world. Volume 1: Non-passerines. Lynx Edicions, Barcelona.
- Dickinson, E.C. & J.V. Remsen Jr. (eds.). 2013. The Howard & Moore complete checklist of the birds of the world. 4th edition, Vol. 1. Aves Press, Eastbourne, U.K.
- Gill, F.B. & D. Donsker (eds.). 2018. IOC World bird list (v8.2). doi:10.14344/IOC.ML.8.2
- Howell, S.N.G. & S. Webb. 1995. A guide to the birds of Mexico and northern Central America. Oxford University Press, Oxford.
- Martínez-Gómez, J.E., N. Matías-Ferrer, & P. Escalante-Pliego. 2017. Phylogeny and taxonomy of the Socorro parakeet (*Psittacara holochlorus brevipes*): recent speciation with minor morphological differentiation. J. Ornithol. 158:965-978.
- Navarro-Sigüenza, A.G. & A.T. Peterson. 2004. An alternative species taxonomy of the birds of Mexico. Biota Neotropica 4:1-32.
- Remsen, J.V., Jr., E.E. Schirtzinger, A. Ferraroni, L.B. Silveira, & T.F. Wright. DNA-sequence data require revision of the parrot genus *Aratinga* (Aves: Psittacidae). Zootaxa 3641:296-300.
- Schweizer, M., S.T. Hertwig, & O. Seehausen. 2014. Diversity versus disparity and the role of ecological opportunity in a continental bird radiation. J. Biogeogr. 41:1301-1312.
- Urantowka, A.D., A.M. Krocak, & T. Strzala. 2014. Complete mitochondrial genome of endangered Socorro Conure (*Aratinga brevipes*)—taxonomic position of the species and its relationship with Green Conure. Mitochondrial DNA 25:365-367.

Submitted by: Pamela C. Rasmussen, Michigan State University

Date of proposal: 3 December 2018

Merge the storm-petrel genus *Oceanodroma* into *Hydrobates*

Background and New Information:

The northern storm-petrels, Hydrobatidae, are currently placed into two genera, *Hydrobates* and *Oceanodroma*. The genus *Hydrobates* includes only a single species, the European Storm Petrel (*Hydrobates pelagicus*), while all other species of northern storm-petrel are placed in the genus *Oceanodroma*. While there are still relatively few studies that look at the phylogenetic relationships of the storm-petrels, recent work has shown that *Oceanodroma* is paraphyletic with respect to *Hydrobates*, with the European Storm-petrel embedded within the larger *Oceanodroma* (Kennedy and Page 2002, Penhallurick and Wink 2004, Robertson *et al.* 2011, Wallace *et al.* 2017). Most studies have found that the European Storm-Petrel is sister to Fork-tailed Storm-Petrel (*O. furcata*) (Robertson *et al.* 2011, Wallace *et al.* 2017; Fig. 1). As a result of the paraphyly of *Oceanodroma*, most taxonomic authorities (e.g., Dickinson and Remsen 2013) have merged the two genera, with *Hydrobates* Boie, 1822, having priority over *Oceanodroma* Reichenbach, 1853.

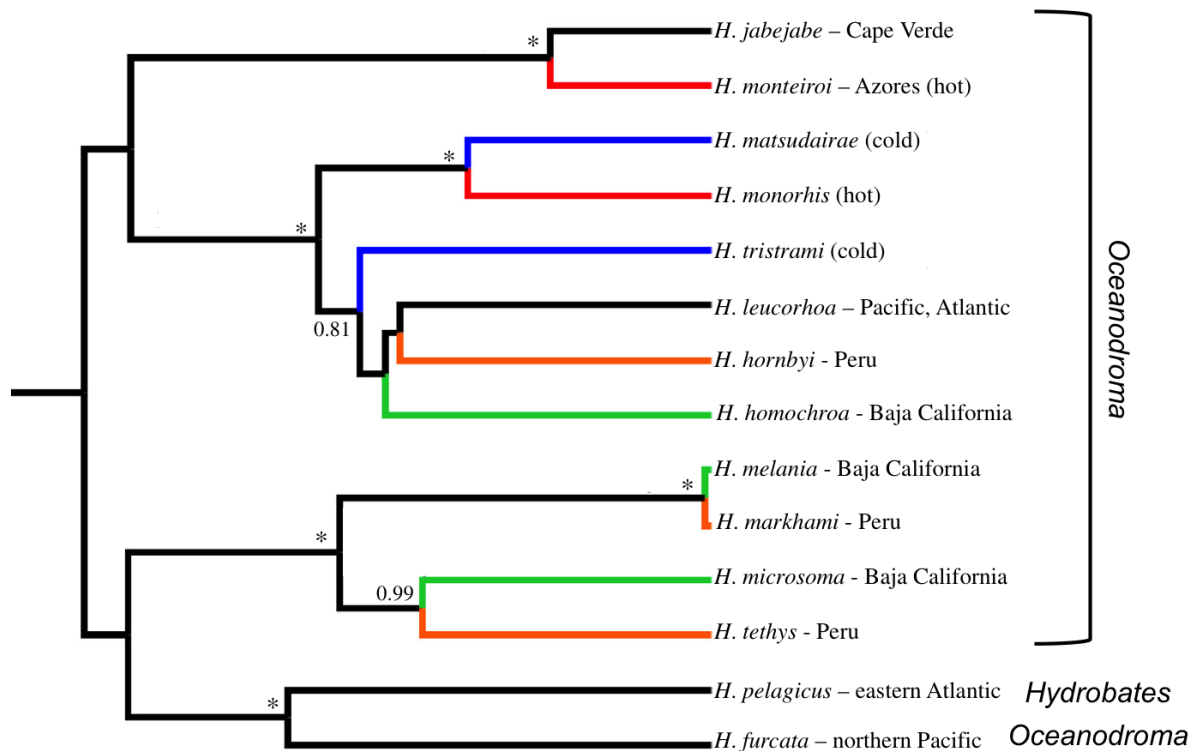


Figure 1. Bayesian phylogeny (based on sequence data from cytochrome-b and 5 nuclear introns), where “*” indicates posterior probabilities of 1.0 and all posterior probabilities above 0.8 are given. Note that *Hydrobates pelagicus* is sister to *Oceanodroma furcata*, which is in turn sister to a clade of New World *Oceanodroma*. This larger clade is in turn sister to the rest of the *Oceanodroma*. Adapted from Wallace *et al.* 2017.

Although the European Storm-Petrel is often found to be sister to Fork-tailed Storm-Petrel, most other relationships within the family are not well resolved, making it difficult to speculate on any well-supported clades within the family (Robertson *et al.* 2011, Wallace *et al.* 2017).

Recommendation:

Based on the findings of several recent molecular phylogenies (Penhallurick and Wink 2004, Robertson *et al.* 2011, Wallace *et al.* 2017), I recommend merging the genus *Oceanodroma* with *Hydrobates*, given that *Oceanodroma* is paraphyletic with respect to *Hydrobates* and that *Hydrobates* has priority. At this time, I propose no change in the linear sequence of the family given the lack of resolution of many relationships. This would result in the following changes to the AOS Checklist:

European Storm-Petrel (*Hydrobates pelagicus*)
Fork-tailed Storm-Petrel (*Hydrobates furcata*)
Ringed Storm-Petrel (*Hydrobates hornbyi*)
Swinhoe's Storm-Petrel (*Hydrobates monorhis*)
Leach's Storm-Petrel (*Hydrobates leucorhoa*)
Townsend's Storm-Petrel (*Hydrobates socorroensis*)
Ainley's Storm-Petrel (*Hydrobates cheimomnestes*)
Ashy Storm-Petrel (*Hydrobates homochroa*)
Band-rumped Storm-Petrel (*Hydrobates castro*)
Wedge-rumped Storm-Petrel (*Hydrobates tethys*)
Black Storm-Petrel (*Hydrobates melania*)
Guadalupe Storm-Petrel (*Hydrobates macrodactyla*)
Markham's Storm-Petrel (*Hydrobates markhami*)
Tristram's Storm-Petrel (*Hydrobates tristrami*)
Least Storm-Petrel (*Hydrobates microsoma*)

References

- Kennedy, M., and R.D.M. Page. 2002. Seabird supertrees: combining partial estimates of Procellariiform phylogeny. *The Auk*, 119: 88-108.
- Penhallurick, J., and M. Wink. 2004. Analysis of the taxonomy and nomenclature of the Procellariiformes based on complete nucleotide sequences of the mitochondrial cytochrome *b* gene. *Emu*, 104:125-147.
- Robertson, B.C., B.M. Stephenson, and S.J. Goldstien. 2011. When rediscovery is not enough: taxonomic uncertainty hinders conservation of a critically endangered bird. *Molecular Phylogenetics and Evolution*, 61: 949-952 .
- Wallace, W.J., J.A. Morris-Pocock, J. González-Solís, P. Quillfeldt, and V.L. Friesen. 2017. A phylogenetic test of sympatric speciation in the Hydrobatinae (Aves: Procellariiformes). *Molecular Phylogenetics and Evolution*, 107:39-47.

Submitted by: Shawn M. Billerman

Date of Proposal: 3 December 2018

Comment on Proposal 2019-A-7

Dear committee members,

I wanted to reach out and make sure you were aware of a potential issue in the data brought forward in the current proposal: Merge the storm-petrel genus *Oceanodroma* into *Hydrobates*. The issue has to do with the placement of *markhami* (Markham's Storm-Petrel) as sister to, and essentially equivalent to Black Storm-Petrel (*melania*) in Wallace et al. 2017. In Table 2 you will see that the divergence between these two species is very small, with "0" being included in the range of divergence possibilities. The problem is that in reality, biologically, and in every way other than both being storm-petrels and all dark, the two are very different. This is an incredibly surprising result!! I am quite sure that the reason for this is that the Peruvian specimen of *markhami* that is used (noted as soft tissue in Table 1) is actually a non-breeding *melania*. *Oceanodroma melania* is very common in Peruvian waters and recently field observers have noted that they can be more common than *markhami* there. This is recent information that is available due to good digital photos, historically it was assumed that *markhami* was the "default" large dark storm petrel in those waters.

As it stands it is likely that no genetic information exists for *markhami*, and its relationships are therefore still unclear. I am willing to bet that it will be in the group that it most closely resembles in flight style, coloration etc, which is with Clade B, the one that includes *leucorrhoa*. If future proposals consider re-arranging the sequence of the storm petrels, and I think there is ample reason to do so with available data, do take into consideration that *markhami* is almost certainly not closely related to *melania*.

Finally, I ask you to consider that merging the entire family into one genus creates a rather uninformative genus! Some of these nodes are thought to be over 11 mya, and there are some clear and well-defined clades within the family. I would suggest that it would be better to separate them out into 4-5 genera to better represent and segment the diversity within the family. For example, the *Halocyptena* genus (*melania*, *tethys*, *microsoma*) shares a distribution in the Eastern Pacific, they also have particularly long tarsi for northern storm petrels, as well as very dark chocolate colored plumage lacking the gray tones (when fresh) of other all dark storm-petrels. Note that white in the rump is not an informative character for storm petrels. The pale ulnar bar on these species is restricted to the greater coverts, while on typical *Oceanodroma* the ulnar bar extends to the bend of the wing and on to the distal median and lesser coverts. The very long legs of *melania*, was distinctive enough that previously it was classified in its own genus (*Loomelania*), I think that *Halocyptena* predates it for the group name, however. I would predict that once other details such as voice can be added to the dataset, the cohesiveness of this genus will become even more clear cut. Similarly, the Band-rumped storm-petrels would make a good genus, one that has a wide distribution in the northern hemisphere and probably contains more species than currently understood. The main clade would remain as *Oceanodroma*, and I would provisionally include *markhami* in there. Finally, the more contentious issue would be if one lumps but *furcata* and *pelagicus* in one genus (*Hydrobates*) or a different genus is chosen for *furcata*. The two are a clade but they are not particularly closely related. In any case, this multi-genus organization would make for a much more informative way to subdivide the family. Creating a one genus family, for a group which is both highly widespread in distribution and holds relatively old lineages does not make much sense.

Submitted by: Alvaro Jaramillo, San Francisco Bay Bird Observatory.

Date: 25 January 2019

Note from the Chair:

Alvaro makes two good points regarding the *Hydrobates* proposal. The first raises the possibility that the *markhami* individual sampled for the Wallace et al. (2017) study may be *melania* instead. Alvaro makes good arguments in support of this, and it certainly looks very suspicious on their tree and in Table 2. I asked ANSP about the ID of the *markhami* tissue used by Wallace et al. but they don't have a voucher for it (presumably it's in Ecuador). This potential misidentification would affect the linear sequence if we were to base a linear sequence on this tree. However, the proposal does not include changes to the linear sequence, presumably because of the lack of support for many of the nodes in their tree, including the deeper nodes. Under these circumstances, I don't think we should make changes to the linear sequence at this time. A complete phylogeny of Procellariiformes, currently in progress, will provide a much better linear sequence.

Alvaro's other point directly questions the proposed lump of all species in the family into a single genus. I agree that this is not ideal, both from a strict information standpoint and from a comparative perspective. The other storm-petrel family, Oceanitidae, which consists of only 7-8 species, is divided into 5 genera, whereas the 15+ species of the Hydrobatidae, which is of similar age and which shows a similar degree of intrafamilial genetic diversity, are currently divided into only 2 genera, now proposed to be reduced to a single genus. Moreover, the Diomedidae, a family with a similar number of species and similar intrafamilial genetic diversity, is generally divided into 4 genera.

Alvaro advocates recognizing *Halocyptena* for *melania*, *tethys*, and *microsoma* (assuming that *markhami* does not belong to this clade) and seems to argue for recognition of 3-4 other genera depending on whether *Oceanodroma* is maintained for *furcata* (note that *furcata* is the type species of *Oceanodroma*, which is not clear in the comment). I agree that there are 4 well-supported clades (p.p = 1.0) that could be recognized as genera, and that *furcata* and *pelagica* could be placed in separate genera. Nevertheless, placement is lacking for *markhami* and, perhaps more importantly, the clade consisting of *castro*, *jabejabe*, and *monteiroi* may not have an available name (*Cymochorea*, *Halocyptera*, and *Hydrobates-Oceanodroma* appear to be available for the other 3 clades). We could recognize different clades than these four, but then we run into problems of a lack of support for the clades.

In my view the most reasonable alternatives, given the potential missing species, the apparent lack of a name for one of the clades, and the lack of nodal support in parts of the Wallace et al. tree, are (1) lumping all species into *Hydrobates*, or (2) maintaining the status quo of *Hydrobates* for *pelagicus* and *Oceanodroma* for our other species until we have more information. I suspect that in the end we will recognize several genera in Hydrobatidae, so perhaps the relevant question is whether we want to transfer 14 species of *Oceanodroma* to

Hydrobates now and then quite possibly transfer most of them to other genera later. Keeping *Oceanodroma* for now would be better in terms of stability but not in terms of a phylogenetically based classification, because we know that *Oceanodroma* is paraphyletic with respect to *Hydrobates*. Of global lists, HBW and Howard & Moore have lumped whereas IOC and Clements have maintained the 2-genus arrangement.

Recognize family Leiothrichidae for *Leiothrix* and *Garrulax*

Background and New Information:

The Babblers (Timaliidae *sensu lato*), an Old World clade of songbirds, have long been a taxonomically challenging group. Before the widespread use of DNA sequence data for understanding phylogenetic relationships, Timaliidae was a very large and extremely diverse family with over 300 species, and was often the family into which taxa with unclear affinities were placed (Collar and Robson 2007). Over the past 15 years, however, a lot of attention has been given to understanding the relationships of the babblers and their place relative to other songbirds (Cibois 2003, Gelang *et al.* 2009, Fregin *et al.* 2012, Moyle *et al.* 2012, Alström *et al.* 2013, Cibois *et al.* 2018, Cai *et al.* 2019).

The babblers and their allies are part of the Sylvioidea radiation of oscine passerines, a primarily Old World radiation of songbirds. Cibois (2003) published the first major phylogenetic study of the babblers, which started to show that many groups once placed in the family were actually closely related to very distant taxa, such as the *Pteruthius* shrike-babblers, which are closely related to the vireos (Vireonidae). Gelang *et al.* (2009), which sampled more genes including nuclear DNA, found very similar patterns within the babblers; they found that the traditional babblers formed four main clades, which included the white-eyes and yuhinas (Zosteropidae). A more comprehensive study (Moyle *et al.* 2012) found strong support for three distinct clades of babblers, which were sister to the white-eyes (Zosteropidae), and adopted the subfamily names proposed by Gelang *et al.* (2009): Timaliinae, Pellorneinae, and Leiothrichinae. Many taxonomic authorities (e.g., Dickinson and Christidis 2014, Winkler *et al.* 2015, Clements *et al.* 2018) have since elevated these three subfamilies to the family level based on the treatment in Fregin *et al.* (2012) and Alström *et al.* (2013). A near-complete phylogeny of the babblers and their allies continues to support the previously identified relationships (although they propose recognizing two additional families, which are not relevant to this proposal; Cai *et al.* 2019).

Of the three newly recognized babbler families, the Timaliidae now includes the tree-babblers and scimitar-babblers, the Pellorneidae includes the ground-babblers, and Leiothrichidae includes, among others, the laughing-thrushes, the “song babblers,” and many African babblers (Moyle *et al.* 2012, Cibois *et al.* 2018, Cai *et al.* 2019, Fig. 1). Three species of babbler have been introduced and have established populations in the AOS checklist region: Greater Necklaced Laughingthrush (*Garrulax pectoralis*), Hwamei (*Garrulax canorus*), and Red-billed Leiothrix (*Leiothrix lutea*), all of which belong to the newly recognized family Leiothrichidae.

Recommendation:

Based on the well-supported phylogenetic studies, as well as the recognition of multiple babbler families by other taxonomic authorities (e.g., Dickinson and Christidis 2014, Clements *et al.* 2018), I recommend following the taxonomic suggestions of Fregin *et al.* (2012) for the laughing-thrushes and leiothrix, also followed by Cibois *et al.* (2018) and Cai *et al.* (2019), and placing the

three babblers found in Hawaii in the family Leiothrichidae. Adopting this change would remove the family Timaliidae from the checklist but would not require any revisions to the linear sequence, as the name Leiothrichidae would simply replace Timaliidae.

Leiothrichidae

Greater Necklaced Laughingthrush (*Garrulax pectoralis*)

Hwamei (*Garrulax canorus*)

Red-billed Leiothrix (*Leiothrix lutea*)

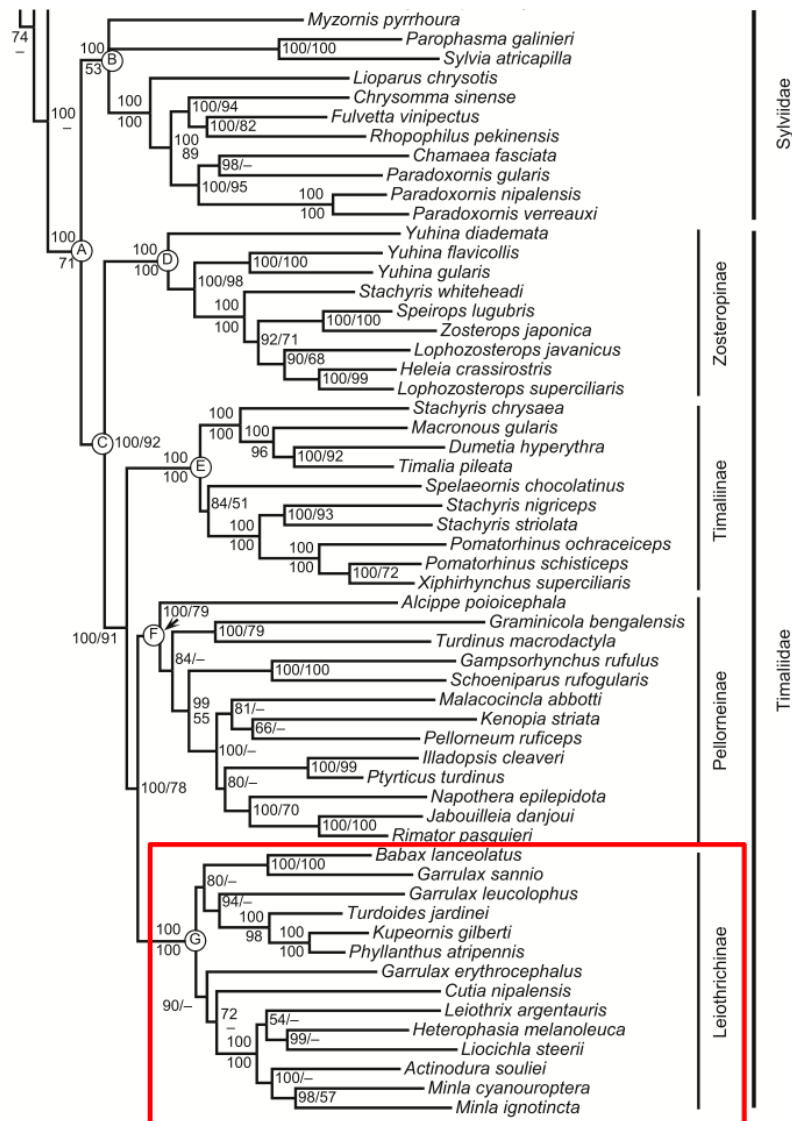


Figure 1. Relationships among babbler families, shown here as subfamilies of a larger Timaliidae. Leiothrichidae is highlighted in red. Adapted from Gelang *et al.* (2009).

References:

Alström, P., U. Olsson, and F. Lei. 2013. A review of the recent advances in the systematics of the avian superfamily Sylvioidea. *Chinese Birds*, 4: 99-131.

- Cai, T., A. Cibois, P. Alström, R.G. Moyle, J.D. Kennedy, S. Shao, R. Zhang, M. Irestedt, P.G.P. Ericson, M. Gelang, Y. Qu, F. Lei, and J. Fjeldså. 2019. Near-complete phylogeny and taxonomic revision of the world's babblers (Aves: Passeriformes). *Molecular Phylogenetics and Evolution*, 130: 346-356.
- Cibois, A. 2003. Mitochondrial DNA phylogeny of babblers (Timaliidae). *The Auk*, 120: 35-54.
- Cibois, A., M. Gelang, P. Alström, E. Pasquet, J. Fjeldså, P.G.P. Ericson, and U. Olsson. 2018. Comprehensive phylogeny of the laughingthrushes and allies (Aves, Leiothrichidae) and a proposal for a revised taxonomy. *Zoologica Scripta*, 47: 428-440.
- Clements, J., T.S. Schulenberg, M.J. Iliff, D. Roberson, T.A. Fredericks, B.L. Sullivan, and C.L. Wood. 2018. The eBird/Clements checklist of birds of the world. v2018. Downloaded from <http://www.birds.cornell.edu/clementschecklist/download/>
- Dickinson, E.C., and L. Christidis. 2014. *The Howard and Moore Complete Checklist of the Birds of the World, 4th Ed., Vol. 2*. Aves Press Limited.
- Fregin, S., M. Haase, U. Olsson, and P. Alström. 2012. New insights into family relationships within the avian superfamily Sylvioidea (Passeriformes) based on seven molecular markers. *BMC Evolutionary Biology*, 12:157.
- Gelang, M., A. Cibois, E. Pasquet, U. Olsson, P. Alström, and P.G.P. Ericson. 2009. Phylogeny of babblers (Aves, Passeriformes): major lineages, family limits and classification. *Zoologica Scripta*, 38: 225-236.
- Moyle, R.G., M.J. Andersen, C.H. Oliveros, F.D. Steinheimer, and S. Reddy. 2012. Phylogeny and biogeography of the core babblers (Aves: Timaliidae). *Systematic Biology*, 61: 631-651.
- Winkler, D.W., S.M. Billerman, and I.J. Lovette. 2015. *Bird Families of the World: An Invitation to the Spectacular Diversity of Birds*. Lynx Edicions, Barcelona.

Submitted by: Shawn M. Billerman

Date of Proposal: 3 December 2018

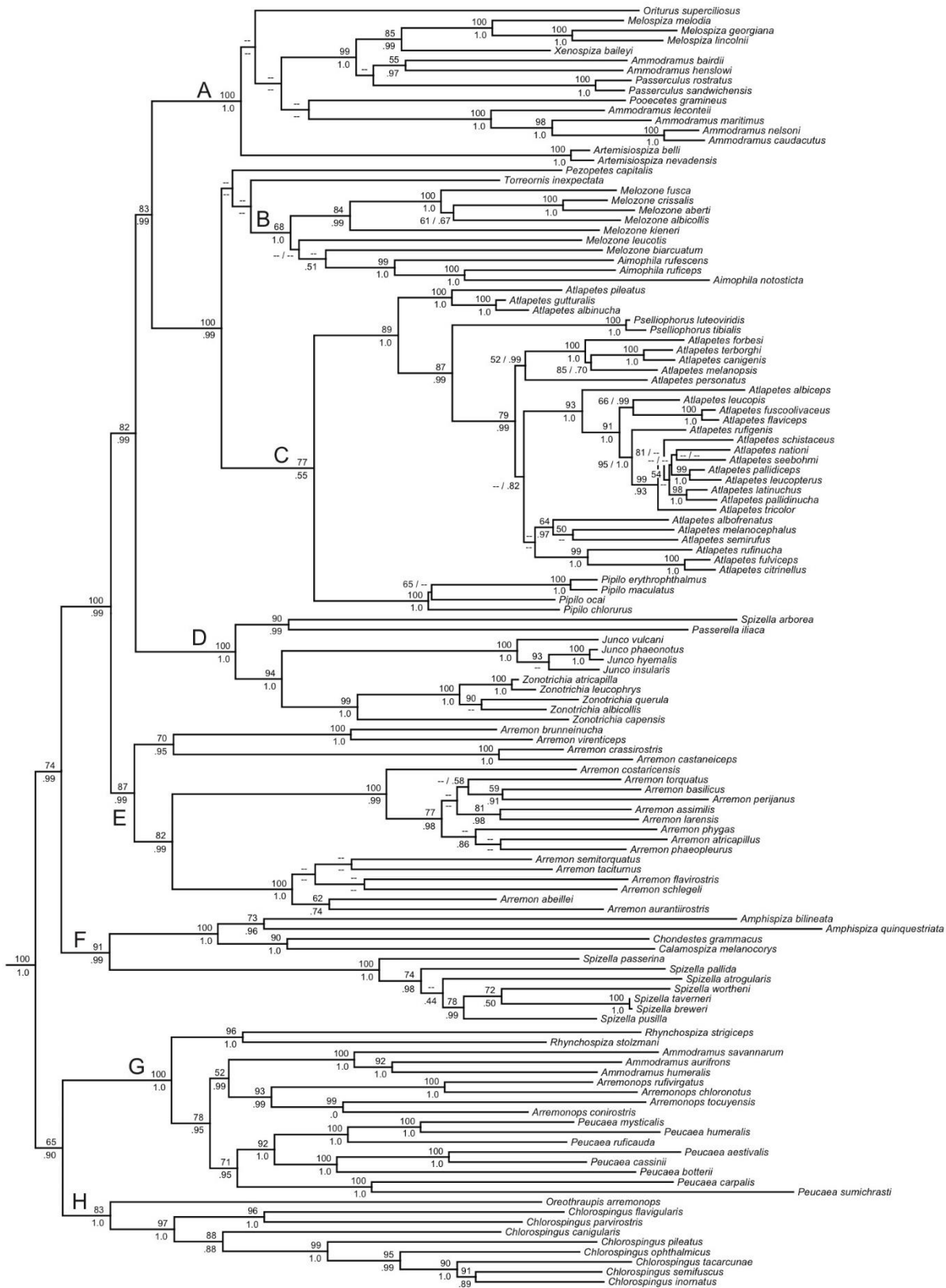
Modify the linear sequence of genera and species in the Passerellidae**Background:**

Recent changes to the Emberizidae *sensu lato* have included splitting the family by recognizing Passerellidae for the New World species (2017-B-6) and splitting the genus *Ammodramus* (2018-C-15). However, we have yet to modify the traditional linear sequence of the Passerellidae, which is largely based on historical momentum. Our current linear sequence of genera, which also reflects recent transfers of taxa both out of and into the family, is:

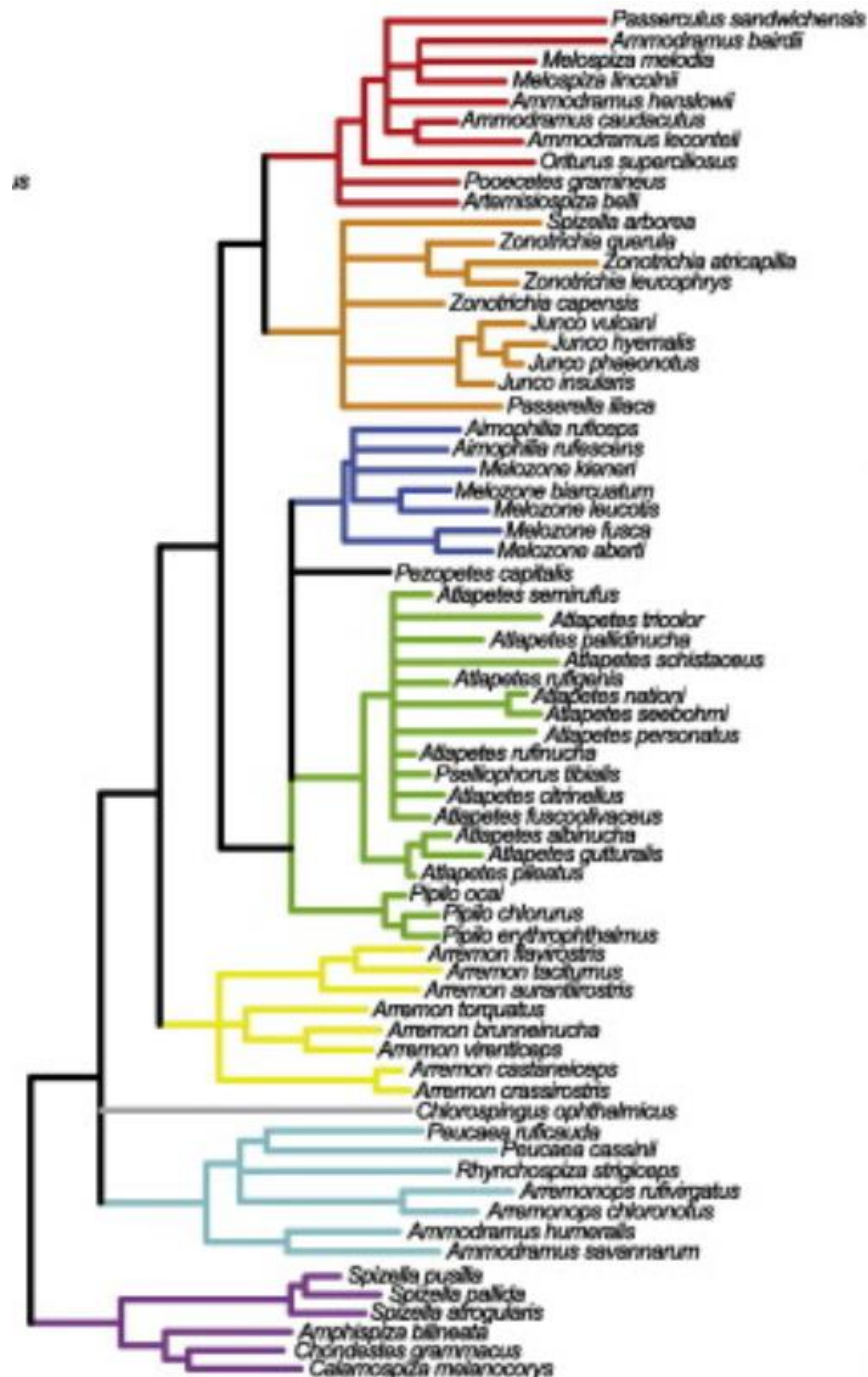
Pselliophorus
Pezopetes
Arremon
Arremonops
Atlapetes
Pipilo
Aimophila
Melospiza
Peucaea
Oriturus
Torreornis
Spizelloides
Spizella
Pooecetes
Chondestes
Amphispiza
Artemisiospiza
Calamospiza
Passerculus
Ammodramus
Centronyx
Ammospiza
Xenospiza
Passerella
Melospiza
Zonotrichia
Junco
Chlorospingus

New Information

Klicka et al. (2014) published a comprehensive phylogeny of the Passerellidae, based on 2184 bp of mtDNA for all 129 species and 5705 bp of nuclear DNA for some 74 of these species. Their mtDNA tree, in which eight main clades are identified by capital letters, is shown below:



Major clades in the nuclear tree (below) are virtually the same as in the mtDNA tree (although note that the relationship between *Atlapetes* and *Pipilo* is not resolved), but the branching pattern among major clades differs. No support values were provided for either this tree or the combined-data tree.



The combined-data tree also recovered similar major clades but relationships among them were unresolved. This result is unsurprising, given the nuclear-mitochondrial conflict at deeper nodes.

SACC Proposal 633 used the mitochondrial tree as the basis for both the sequence of major clades and the sequence of species within major clades. A new linear sequence for our species derived from the mitochondrial tree would be as follows:

<i>Chlorospingus flavigularis</i>	<i>Zonotrichia leucophrys</i>
<i>Chlorospingus canigularis</i>	<i>Zonotrichia atricapilla</i>
<i>Chlorospingus pileatus</i>	<i>Zonotrichia querula</i>
<i>Chlorospingus flavopectus</i>	<i>Zonotrichia albicollis</i>
<i>Chlorospingus tacarcunae</i>	<i>Artemisiospiza nevadensis</i>
<i>Chlorospingus inornatus</i>	<i>Artemisiospiza belli</i>
<i>Peucaea carpalis</i>	<i>Oriturus superciliosus</i>
<i>Peucaea sumichrasti</i>	<i>Pooecetes gramineus</i>
<i>Peucaea ruficauda</i>	<i>Ammospiza leconteii</i>
<i>Peucaea humeralis</i>	<i>Ammospiza maritima</i>
<i>Peucaea mystacalis</i>	<i>Ammospiza nelsoni</i>
<i>Peucaea botterii</i>	<i>Ammospiza caudacuta</i>
<i>Peucaea cassinii</i>	<i>Centronyx bairdii</i>
<i>Peucaea aestivalis</i>	<i>Centronyx henslowii</i>
<i>Ammodramus savannarum</i>	<i>Passerculus sandwichensis</i>
<i>Arremonops rufivirgatus</i>	<i>Xenospiza baileyi</i>
<i>Arremonops chloronotus</i>	<i>Melospiza melodia</i>
<i>Arremonops conirostris</i>	<i>Melospiza lincolni</i>
<i>Amphispiza quinquestriata</i>	<i>Melospiza georgiana</i>
<i>Amphispiza bilineata</i>	<i>Pezopetes capitalis</i>
<i>Chondestes grammacus</i>	<i>Torreornis inexpectata</i>
<i>Calamospiza melanocorys</i>	<i>Melozona kieneri</i>
<i>Spizella passerina</i>	<i>Melozona fusca</i>
<i>Spizella pallida</i>	<i>Melozona albicollis</i>
<i>Spizella atrogularis</i>	<i>Melozona aberti</i>
<i>Spizella pusilla</i>	<i>Melozona crissalis</i>
<i>Spizella breweri</i>	<i>Melozona leucotis</i>
<i>Spizella wortheni</i>	<i>Melozona biarcuata</i>
<i>Arremon costaricensis</i>	<i>Melozona cabanisi</i>
<i>Arremon atricapillus</i>	<i>Aimophila rufescens</i>
<i>Arremon aurantirostris</i>	<i>Aimophila ruficeps</i>
<i>Arremon virenticeps</i>	<i>Aimophila notosticta</i>
<i>Arremon brunneinucha</i>	<i>Pipilo chlorurus</i>
<i>Arremon crassirostris</i>	<i>Pipilo maculatus</i>
<i>Passerella iliaca</i>	<i>Pipilo erythrophthalmus</i>
<i>Spizelloides arborea</i>	<i>Pipilo ocai</i>
<i>Junco vulcani</i>	<i>Atlapetes pileatus</i>
<i>Junco insularis</i>	<i>Atlapetes albinucha</i>
<i>Junco hyemalis</i>	<i>Pselliophorus tibialis</i>
<i>Junco phaeonotus</i>	<i>Pselliophorus luteoviridis</i>
<i>Junco bairdi</i>	

Zonotrichia capensis

In this sequence, *Junco bairdi* and *Melospiza cabanisi*, neither of which was recognized as a species at the time of Klicka et al. (2014) and so went unsampled, follow their former conspecifics *J. phaeonotus* and *M. biarcuata*.

Recommendation:

I recommend that we adopt the new linear sequence as listed above. The mtDNA taxon sampling is comprehensive and the tree generally well supported. Precise relationships of some taxa, e.g., the monotypic genera *Oriturus*, *Pooecetes*, *Pexopetes*, and *Torreornis*, are unclear, but even here their position in or closely related to particular clades receives strong support. Although this new linear sequence is not the last word in this group, as indicated by the differences in topology in the nuclear tree, it at least places closely related taxa in close proximity and breaks up polyphyletic genera such as the former species of *Ammodramus*, and as such is a great improvement over the current linear sequence. An alternative would be to follow the nuclear tree for the linear sequence of major clades and the mtDNA tree for the sequence of species, but the nuclear tree is less well resolved at deeper nodes than is the mtDNA tree. It also seems preferable to follow a single well-sampled and well-resolved tree and to avoid a conflict with SACC on this issue until further data are available.

References:

Klicka, J., F. K. Barker, K. J. Burns, S. M. Lanyon, I. J. Lovette, J. A. Chaves, and R. W. Bryson, Jr. 2014. A comprehensive multilocus assessment of sparrow (Aves: Passerellidae) relationships. *Molecular Phylogenetics and Evolution* 77: 177-182.

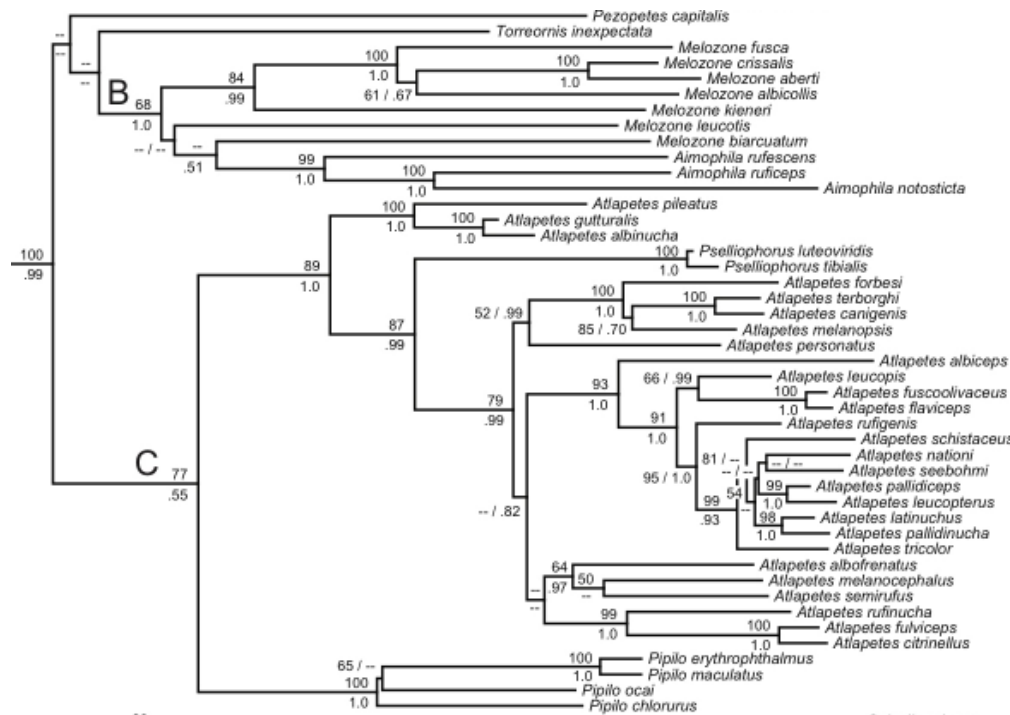
Submitted by: Terry Chesser

Date of Proposal: 6 December 2018

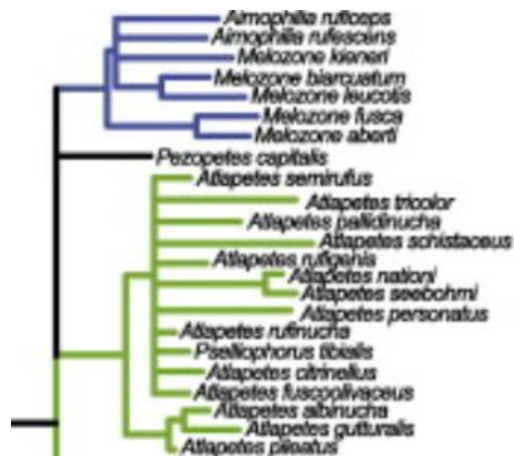
Merge (a) *Pselliophorus* into *Atlapetes*, and (b) *Melozona* into *Aimophila*

Background:

The preceding proposal, which recommended changes to the linear sequence of New World sparrows, ignored the apparent paraphyly of two genera: in the mitochondrial tree of Klicka et al. (2014), *Melozona* is paraphyletic with respect to *Aimophila*, and *Atlapetes* is paraphyletic with respect to *Pselliophorus*:



The nuclear tree has fewer species and provides less resolution, but *Melozona* and *Atlapetes* are again paraphyletic with respect to *Aimophila* and *Pselliophorus*, respectively:



The case of *Pselliophorus* seems straightforward. Support for the mitochondrial clade that includes all species of *Atlapetes* and *Pselliophorus* is strong (89/1.0), and the two species of *Pselliophorus* Ridgway, 1898, can simply be transferred to *Atlapetes* Wagler, 1831.

The case of *Melozona* and *Aimophila* is somewhat more complex. These genera, which constitute Clade B of Klicka et al. (2014), have already been the subject of several recent changes. In the seventh edition of the Checklist (AOU 1998), *Melozona* included only the three then-recognized species of ground-sparrow (*kieneri*, *biarcuatum*, and *leucotis*), whereas *Aimophila* included 12 species. In the 51st Supplement (Chesser et al. 2010), four species of towhees in the genus *Pipilo* (*albicollis*, *fuscus*, *crissalis*, and *aberti*) were transferred to *Melozona*, whereas eight species of *Aimophila* were transferred to *Peucaea* and one species to *Amphispiza*. Moreover, *M. cabanisi* was split from *biarcuata* (*biarcuatum* had been changed to *biarcuata* in the 45th Supplement; Banks et al. 2004) in the 58th Supplement (Chesser et al. 2017). Thus, we currently list eight species in *Melozona* and three species in *Aimophila*.

Support for the mitochondrial *Melozona-Aimophila* clade (Clade B) ranges from only moderate (68% bootstrap) to strong (1.0 posterior probability). Within this clade, the three *Aimophila* species and the four former *Pipilo* species form very strongly supported subclades (99-100%, 1.0), with *kieneri* receiving reasonably strong support as sister to the former *Pipilo* species (84%, 0.99). *Melozona biarcuata* (the type species) is a very poorly supported sister to the *Aimophila* clade, and *M. leucotis* is a very poorly supported sister to the *Aimophila+biarcuata* clade. Regarding the paraphyly of *Melozona* and the possibility that it may not form a clade, Klicka et al. (2014) stated, "More data are required to address this uncertainty. We note, however, that the merging of these two genera would solve this taxonomic problem. In this case, *Aimophila* (Swainson, 1837) would have priority and *Melozona* (Reichenbach, 1850) would be abandoned."

Recommendation:

I recommend that we merge *Pselliophorus* into *Atlapetes*; this seems to be an easy YES vote. Regarding *Melozona* and *Aimophila*, I think we have two reasonable alternatives: (1) accept the merger, or (2) leave these genera as is for now. Klicka et al. (2014) noted that the lack of monophyly could be resolved by transferring all species to *Aimophila*, but the uncertainty of relationships within the *Melozona-Aimophila* clade in both the mitochondrial and nuclear trees, and the lack of strong bootstrap support for monophyly of the clade itself, make this a tougher call. The makeup of these genera has recently been changed, which in my view this could be interpreted in two ways: first, that the status quo lacks historical momentum and so should be more readily changed, or second, that we have already made enough changes to these genera in the face of uncertainty, and that we should leave them as is until more definitive data are available. I slightly favor leaving the genera as is for the moment, and voting NO on part b. Alternatives that would maintain *Aimophila* as currently constituted and place the former *Pipilo* species in their own genus have some appeal but would appear to require the description of several new genera, which should probably be avoided until relationships involving *kieneri*, *leucotis*, *biarcuata*, and *cabanisi* are better resolved.

References:

- AOU. 1998. Check-list of North American Birds. Seventh Edition. AOU, Washington, D.C.
- Banks, R. C., C. Cicero, J. L. Dunn, A. W. Kratter, P. C. Rasmussen, J. V. Remsen, Jr., J. D. Rising, and D. F. Stotz. 2004. Forty-fifth supplement to the American Ornithologists' Union *Check-list of North American Birds*. Auk 121: 985-995.
- Chesser, R. T., R. C. Banks, F. K. Barker, C. Cicero, J. L. Dunn, A. W. Kratter, I. J. Lovette, P. C. Rasmussen, J. V. Remsen, Jr., J. D. Rising, D. F. Stotz, and K. Winker. 2010. Fifty-first supplement to the American Ornithologists' Union *Check-list of North American Birds*. Auk 127: 726-744.
- Chesser, R. T., K. J. Burns, C. Cicero, J. L. Dunn, A. W. Kratter, I. J. Lovette, P. C. Rasmussen, J. V. Remsen, Jr., J. D. Rising, D. F. Stotz, and K. Winker. 2017. Fifty-eighth supplement to the American Ornithological Society's *Check-list of North American Birds*. Auk: Ornithological Advances 134: 751-773.
- Klicka, J., F. K. Barker, K. J. Burns, S. M. Lanyon, I. J. Lovette, J. A. Chaves, and R. W. Bryson, Jr. 2014. A comprehensive multilocus assessment of sparrow (Aves: Passerellidae) relationships. *Molecular Phylogenetics and Evolution* 77: 177-182.

Submitted by: Terry Chesser

Date of Proposal: 7 December 2018

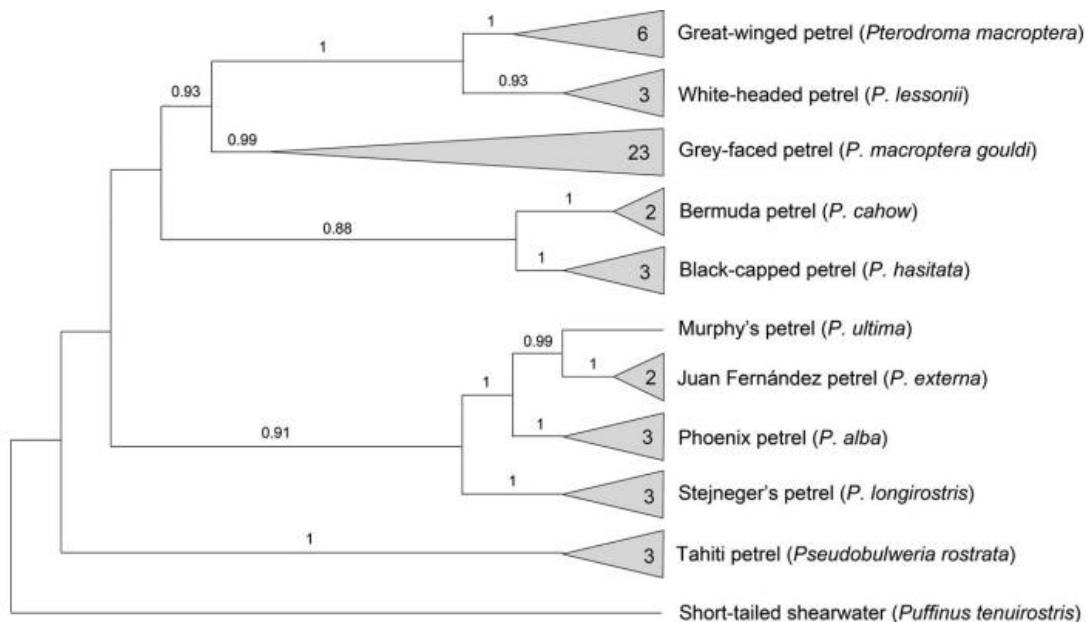
Separate Gray-faced Petrel *Pterodroma gouldi* from *P. macroptera*

Background:

The Great-winged Petrel *Pterodroma macroptera* is a relatively large, dark petrel that we currently treat as a single species with two subspecies: the nominate subspecies breeds on islands in the southern Atlantic and Indian oceans, and subspecies *gouldi* breeds exclusively on islands off the North Island of New Zealand. The latter was described by Hutton in 1869 as *Aestrelata gouldi*, the type specimen having been collected by Gould off Tasmania. Subspecies *gouldi* differs from the all-dark nominate form in the contrasting pale gray feathers on its forehead, chin, and throat, which give it the English name Gray-faced Petrel. The new species was merged into *P. macroptera* by Mathews and Iredale (1913) and was considered a subspecies of *macroptera* by most twentieth century references (e.g., Peters 1931, 1979; Sibley and Monroe 1990). However, some recent sources (e.g., Onley and Scofield 2007, Howell 2012) have once again split *P. gouldi* from *P. macroptera*, based largely on appearance, range, and vocalizations. The species appears on the AOS Checklist based on a small number of records of *gouldi* off the coast of California (Banks et al. 2004).

New Information:

Wood et al. (2017) conducted a comprehensive study, including analyses of plumage, morphometrics, osteology, mtDNA, vocalizations, parasites, and behavior, of the taxonomic status of the Gray-faced Petrel. The genetic analyses, which were performed using BEAST, provided the surprising result that Great-winged Petrel *P. macroptera* is sister to White-headed Petrel *P. lessonii* rather than to Gray-faced Petrel *P. gouldi*. This was indicated in analyses of partial sequences of CO1 that included nine taxa of *Pterodroma*:



Differences in vocalizations were also evident in both sonograms and in analyses of individual components of their vocalizations. Sample sizes for *macroptera* and especially *lessonii* were somewhat small (n=8 and n=4, respectively), but the analyses of Wood et al. (below in their Table 1) indicated that vocalizations of *macroptera* and *lessonii* were much more similar to each other than either was to *gouldi*.

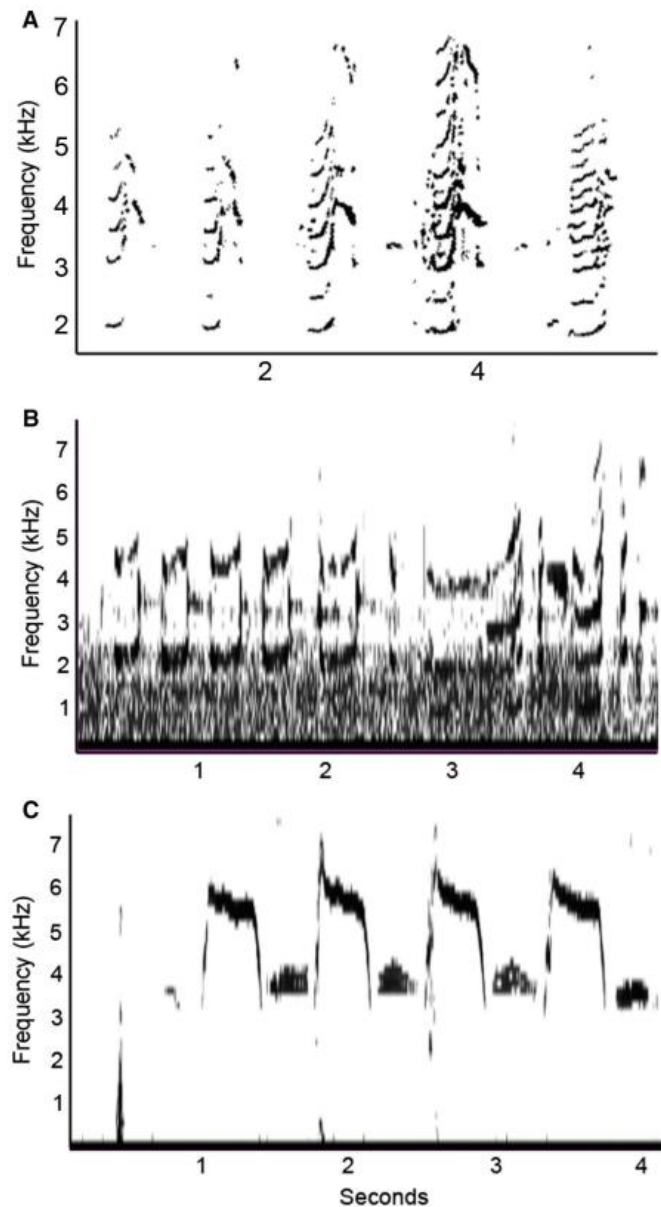


Figure 6. Typical ground vocalizations of: A, great-winged petrel (*Pterodroma macroptera*); B, white-headed petrel (*Pterodroma lessonii*); C, grey-faced petrel (*Pterodroma macroptera gouldi*).

Table 1. Summary statistics (mean $\pm$ SEM) for the 'moan' and 'ti' calls of three large *Pterodroma* petrel taxa.

<i>Pterodroma</i> species	<i>N</i>	Moan note			Ti note			Internote distance (ms)
		Dominant frequency (Hz)	Length (ms)	6 dB bandwidth (Hz)	Dominant frequency (Hz)	6 dB bandwidth (Hz)	Mean harmonic interval (Hz)	
Great-winged petrel (<i>Pterodroma macroptera</i>)	8	622 $\pm$ 12	666 $\pm$ 43	155 $\pm$ 50	3111 $\pm$ 101	1130 $\pm$ 143	401 $\pm$ 13	227 $\pm$ 34
White-headed petrel (<i>Pterodroma lessonii</i>)	4	631 $\pm$ 22	634 $\pm$ 32	162 $\pm$ 59	3101 $\pm$ 98	1044 $\pm$ 134	411 $\pm$ 21	221 $\pm$ 42
Grey-faced petrel (<i>Pterodroma macroptera gouldi</i>)	22	555 $\pm$ 33	720 $\pm$ 27	224 $\pm$ 21	2899 $\pm$ 85	1845 $\pm$ 300	716 $\pm$ 13	134 $\pm$ 48

Information from the scientific literature also revealed differences in life history characteristics between *macroptera* and *gouldi*: *macroptera* lays eggs from mid-May to early June, with hatching in mid-July, whereas *gouldi* lays from mid-June to late July and hatches in August-September, differences that hold among birds breeding at the same latitudes.

Differences in plumage between the dark *macroptera/gouldi* and the White-headed Petrel *P. lessonii*, which has white underparts as well as a white head, are obvious (see below for photos of specimens). However, in at least some morphometric features, *gouldi* and *lessonii* were much more similar to each other than to *macroptera* (see figure below), and the differences in plumage between *macroptera* and *gouldi* exceed those between some other species of *Pterodroma* (Howell 2012).

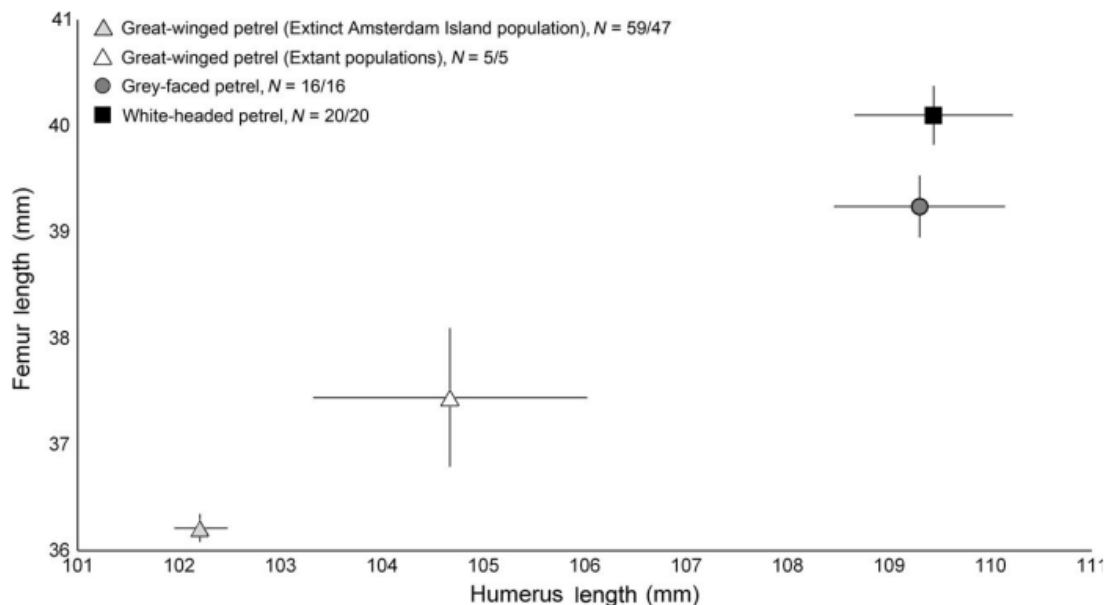
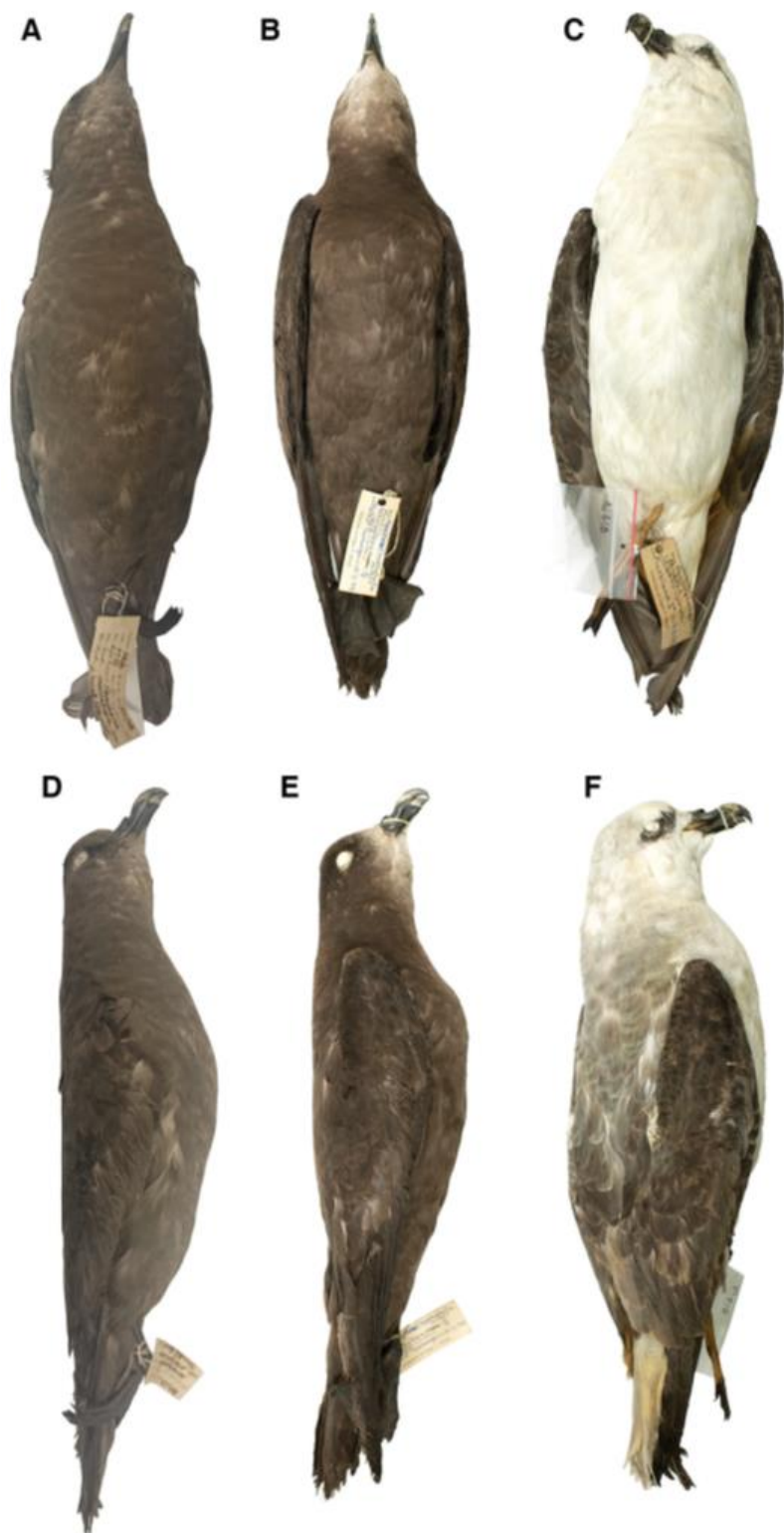


Figure 2. Humerus length vs. femur length in great-winged petrel (*Pterodroma macroptera*), grey-faced petrel (*Pterodroma macroptera gouldi*), and white-headed petrel (*Pterodroma lessonii*) populations. Data shown are means $\pm$ SEM. Number of specimens measured (N) is shown for humeri and femora, respectively. Great-winged petrel measurements are from Worthy & Jouventin (1999), and other measurements are from this study.



Ventral and side views of typical specimens of (from left to right) *P. macroptera macroptera*, *P. macroptera gouldi*, and *P. lessonii*, from Wood et al. (2017).

Recommendation:

I recommend that we split Gray-faced Petrel *P. gouldi* from Great-winged Petrel *P. macroptera*. Several lines of evidence indicate that these taxa are not as closely related as previously thought, but instead have been considered conspecific largely based on similarities in plumage. As Wood et al. (2017) noted, some of this evidence has shortcomings when taken individually (e.g., only mtDNA was sequenced for the genetic study), but cumulatively the data are reasonably robust.

Despite the plumage similarities, numerous characters separate these species, including genetics, vocalizations, and life history. The genetic analyses, although restricted to mtDNA, indicate that the White-headed Petrel *P. lessonii* is the sister taxon to *P. macroptera* and that *P. gouldi* may or may not be sister to the clade of these two species. Vocalizations are important in mate recognition in petrels (McKown 2008), and Wood et al. (2017) suggested that the observed differences are sufficient to prevent interbreeding if these taxa were sympatric. Moreover, morphological differences exceed those between some other species of *Pterodroma*, and phenology of breeding differs between the two taxa, even at the same latitudes.

This proposal would remove *P. macroptera* from the checklist and substitute *P. gouldi*. The English name Gray-faced Petrel (or Grey-faced Petrel) is in general usage for *P. gouldi* and I recommend that we adopt this name.

References:

- Banks, R. C., C. Cicero, J. L. Dunn, A. W. Kratter, P. C. Rasmussen, J. V. Remsen, Jr., J. D. Rising, and D. F. Stotz. 2004. Forty-fifth supplement to the American Ornithologists' Union *Check-list of North American Birds*. Auk 121: 985-995.
- Howell, S. N. G. 2012. Petrels, albatrosses, and storm-petrels of North America: a photographic guide. Princeton Univ. Press, Princeton, NJ.
- Mathews G. M., and T. Iredale. 1913. A reference list of the birds of New Zealand: Part 1. Ibis 55: 201–262.
- McKown, M. M. 2008. Acoustic communication in colonial seabirds: individual, sexual, and species-specific variation in acoustic signals of *Pterodroma* petrels. Unpublished Ph.D. thesis, Univ. North Carolina, Chapel Hill.
- Onley D., and P. Scofield. 2007. Albatrosses, petrels and shearwaters of the world. London: Christopher Helm.
- Sibley, C. G., and B. L. Monroe. 1990. Distribution and taxonomy of birds of the world. Yale Univ. Press, New Haven, CT.
- Wood, J. R., H. A. Lawrence, R. P. Scofield, G. A. Taylor, P. O. Lyver, and D. M. Gleeson. 2017. Morphological, behavioural, and genetic evidence supports reinstatement of full species status for the grey-faced petrel, *Pterodroma macroptera gouldi* (Procellariiformes: Procellariidae). Zoological Journal of the Linnean Society 179: 201-216.

Submitted by: Terry Chesser

Date of Proposal: 10 December 2018