

AOS Classification Committee – North and Middle America

Proposal Set 2025-A

8 October 2024

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- 02 15 Transfer Pale-eyed Pygmy-Tyrant *Lophotriccus pilaris* to *Atalotriccus*
- 03 18 Revise the taxonomy of the genus *Gygis*: (a) recognize subfamilies Gyginae and Anoinae, and (b) treat *G. candida* and *G. microrhyncha* as separate species from White Tern *G. alba*
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Treat extralimital *Pachyramphus salvini* as a separate species from Black-and-white Becard *P. albogriseus*

Note: This proposal largely follows SACC proposals 955 and 971. Proposal 955 was in turn a reworking of proposal 906 (<https://www.museum.lsu.edu/~Remsen/SACCprop906.htm>) after the publication of more information. Based on proposal 955 (<https://www.museum.lsu.edu/~Remsen/SACCprop955.htm>), SACC voted 8-0 to split *Pachyramphus salvini* from *P. albogriseus*. The suggested English names, however, were rejected, resulting in a second proposal on English names, SACC proposal 971 (<https://www.museum.lsu.edu/~Remsen/SACCprop971.htm>). This proposal resulted in the adoption of Cryptic Becard for *P. salvini* by a vote of 7-1, and retention of Black-and-white Becard for *P. albogriseus*, also by a vote of 7-1. Acceptance of both parts of this proposal will bring the NACC in line with the SACC and world checklists.

Description of the problem:

P. albogriseus has been considered to consist of 5 subspecies: *ornatus* of the highlands of Costa Rica and Panama (and the only subspecies to occur in the NACC area, *coronatus* (Santa Marta), nominate *albogriseus* (Andes of northeastern Colombia, Venezuela), *guayaquilensis* (lowlands of western Ecuador and northwestern Peru), and *salvini* (Andes (southern Colombia to Cuzco, Peru).

Musher and Cracraft (2018) found that *P. albogriseus* was polyphyletic with individuals ascribed to *P. a. guayaquilensis* not being sister to the rest of *P. albogriseus*. Differences in vocalizations have also been described between *guayaquilensis* and *salvini* in Peru (Schulenberg et al. 2007). However, questions remain about the taxonomy (whether *guayaquilensis* is a valid subspecies or is instead part of *salvini*), distribution and potential overlap in northern Peru, and the extent of differences of vocalizations.

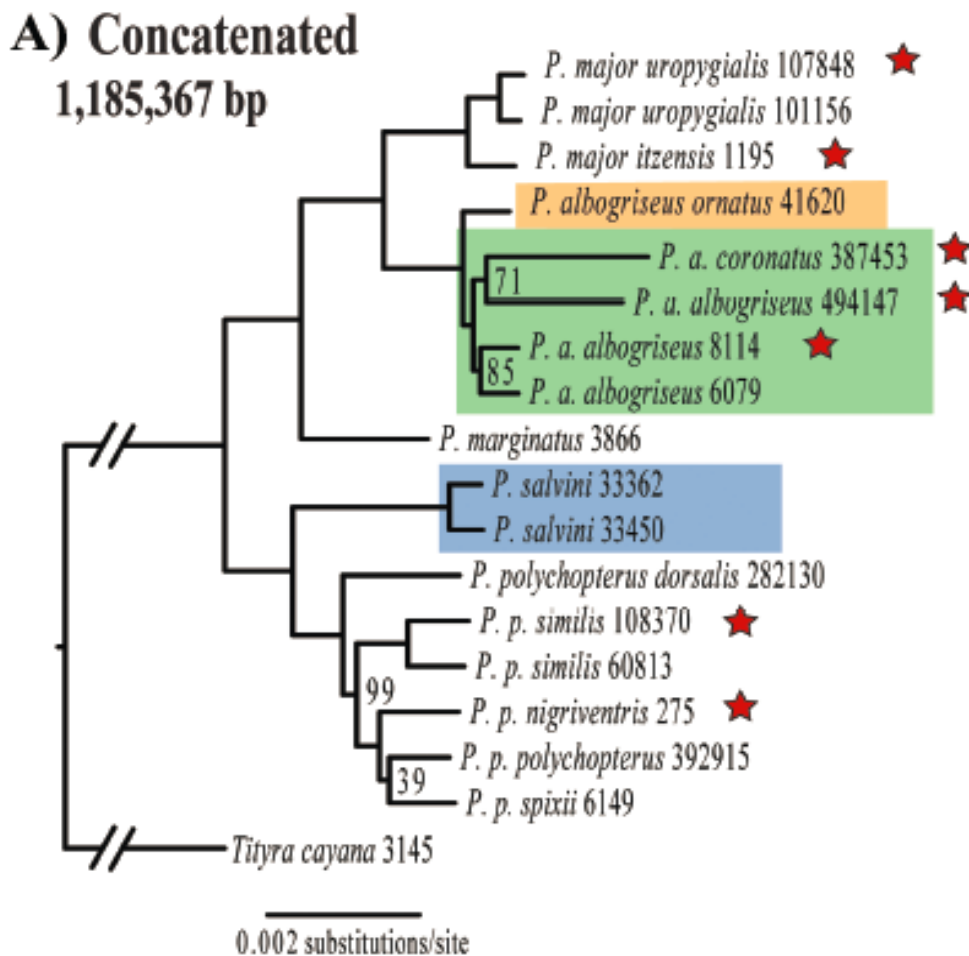
New Information:

Musher et al. (2023) used genetics, morphology, vocalizations, and photographs from the Macaulay Library to clarify the distributions and diagnoses of the two groups within *P. albogriseus* to circumscribe them more precisely. They examined type specimens to ensure a correct nomenclature. They found a fine correlation between vocal, morpho- and genotypes. Surprisingly, they found no less than 13 records of the western form from the east slope, and one record (2 specimens) of the nominate form from the Marañón drainage. The east slope records of the western form were from all months of the year except February and March (the peak breeding season in the west), so it remains possible that the western form is partly migratory and does not breed on the east slope. The two specimens of nominate *P. albogriseus* from the Marañón drainage, however, strongly suggest that the two species breed sympatrically or parapatrically, perhaps occupying different habitats, the western form tolerating drier and

more disturbed habitats, the nominate form perhaps in undisturbed humid forest higher on the slope, this needing further investigation. All 5 specimens from eastern Ecuador that Zimmer (1936) had examined pertained to the western species, whereas the single specimen that Musher had sequenced from eastern Ecuador pertained to nominate *albogriseus*. This led Musher & Cracraft (2018) to apply the name *salvini* to the eastern form, which left only the name *guayaquilensis* available for the western form. A close examination of a large series of specimens, however, including the ten specimens in the type series of *salvini*, showed that the diagnostic characters of *guayaquilensis* are not statistically significant, and that *guayaquilensis* is but a junior synonym of *salvini*. Thus, the correct name for the western form is *P. salvini*.

A more detailed account of the approaches:

Genetics: Seven specimens were sequenced (marked with red stars below) in addition to those sequenced by Musher and Cracraft (2018). The resulting phylogenetic tree based on concatenated nuclear (UCE) data was similar to previous nuclear and mitochondrial trees (Musher & Cracraft 2018, Musher et al. 2019), confirming beyond doubt that *Pachyramphus albogriseus sensu lato* is polyphyletic.



Vocalizations: Two song types were found, consistent with songs described for eastern and western Ecuador (Ridgely & Greenfield 2003) and for eastern and western Peru (Schulenberg et al. 2007); note however that due to nomenclatural confusion, the names to which these vocalizations were ascribed have been mixed (see Proposal 906 and spectrograms below). No specimen with a voice attached was available, but one of the two vocal types was found in Venezuela and Central America, the other in western Ecuador and northwestern Peru, each being areas where only one genotype, one vocal type, and one morphotype had been recorded. Besides song, the two also appear to have different calls. Both vocal types had been recorded in eastern Ecuador and eastern Peru, the eastern type mainly in undisturbed forest, the western type mainly in more open habitat (see spectrograms below).

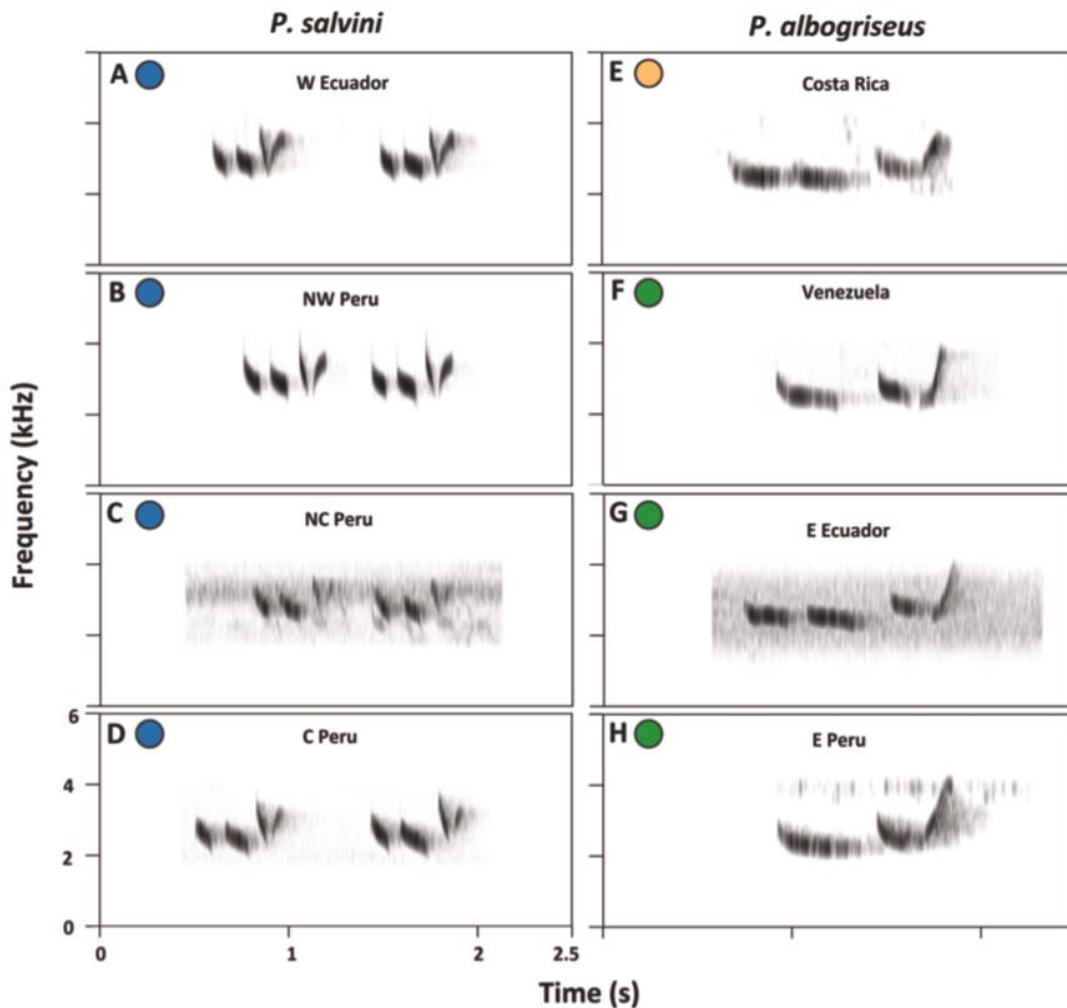


FIGURE 6. Songs of birds formerly included within the Black-and-white Becard *Pachyramphus albogriseus*. (A–D) Slender-billed Becard *P. salvini* (2 song phrases). (E–H) Broad-banded Becard *P. albogriseus* (1 song phrase). (A) Pichincha, Ecuador, 25 August 2012 (XC 108575, A. Spencer). (B) Piura, Peru, 7 July 2015 (XC 297106, R. Gallardy). (C) Cajamarca, Peru, 27 December 2007 (XC 227116, P. Boesman). (D) Huánuco, Peru, 22 May 2010 (XC54569, D. Lane). (E) Puntarenas, Costa Rica, 7 March 2020 (ML 240493071, J. Alvarado). (F) Aragua, Venezuela, 26 May 1969 (ML 62586, P. Schwartz). (G) Napo, Ecuador, September 1995 (XC 264752, P. Coopmans). (H) San Martín, Peru, 22 September 2013 (XC 150850, H. van Oosten). Note the distinctive termination of each phrase.

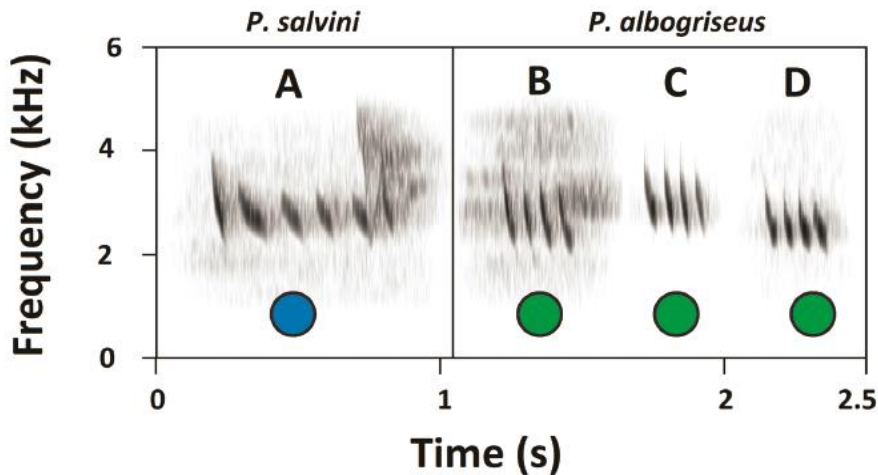


FIGURE 7. Trilled notes of birds formerly included within the Black-and-white Becard *Pachyramphus albogriseus*. **(A)** Slender-billed Becard *P. salvini*. **(B–D)** Broad-banded Becard *P. albogriseus*. **(A)** Guayas, West Ecuador, March 2003 (XC259055, J.V. Moore); **(B)** Aragua, coastal Venezuela, 29 June 1961 (ML62589, P. Schwartz); **(C)** Tungurahua, East Ecuador, 11 September 2011 (XC108656, A. Spencer); **(D)** Huánuco, East Peru, 4 September 1979 (ML17784, V. Emanuel). Note the difference in pace between the two species.

Morphology: Two morphotypes were found. These were consistent with the two genotypes and vocal types. One, *P. albogriseus*, is a large species (average 22 g) with a broad upper wingbar, heavy bill, blackish loreal spot, uniform alula, and faint pale collar; female with a bright chestnut crown surrounded by a broad black band, male with a mostly black upper tail. The other, *P. salvini*, is a smaller species (average 17 g) with a slender bill, relatively narrow upper wingbar, pale-edged alula, no or faint loreal spot, and no pale collar; female with a light brown or dull chestnut crown surrounded by a narrow or no black band, and male with much gray on the upper tail. Only the large species has been recorded in Central America and Venezuela, and only the small species in western Ecuador and northwestern Peru. Both types have been found in eastern Ecuador and eastern Peru, in the Marañón drainage, and possibly in southeastern Colombia. Photographic records are consistent with these morphotypes, adding that the small species also occurs in western Colombia. A comparison of specimens from the Perijá mountains (described as subspecies *coronatus*) with specimens from other parts of Venezuela showed that the diagnostic feature of *coronatus* (the darker crown of the female) does not hold and that *coronatus* should be treated as a junior synonym of *albogriseus*. The Central American form, however, differs from nominate *albogriseus* in a number of respects and should be treated as a valid subspecies: *P. albogriseus ornatus*. To illustrate the differences between these taxa we show specimen comparisons copied from the supplementary data to the paper:



Figure S5. Comparison of a male (top two photos) and female (bottom three photos) syntypes of *P. salvini* (left specimen in each photo) compared to a Peruvian specimen of *P. albogriseus* previously ascribed to *P. a. salvini*, but recognized as *P. a. albogriseus* in this study. The voucher numbers are AMNH 494154 (male *P. salvini* syntype), AMNH 820943 (male *P. albogriseus*), AMNH 494158 (female *P. salvini* syntype), and AMNH 820701 (female *P. albogriseus*). Photos by Lukas J. Musher.



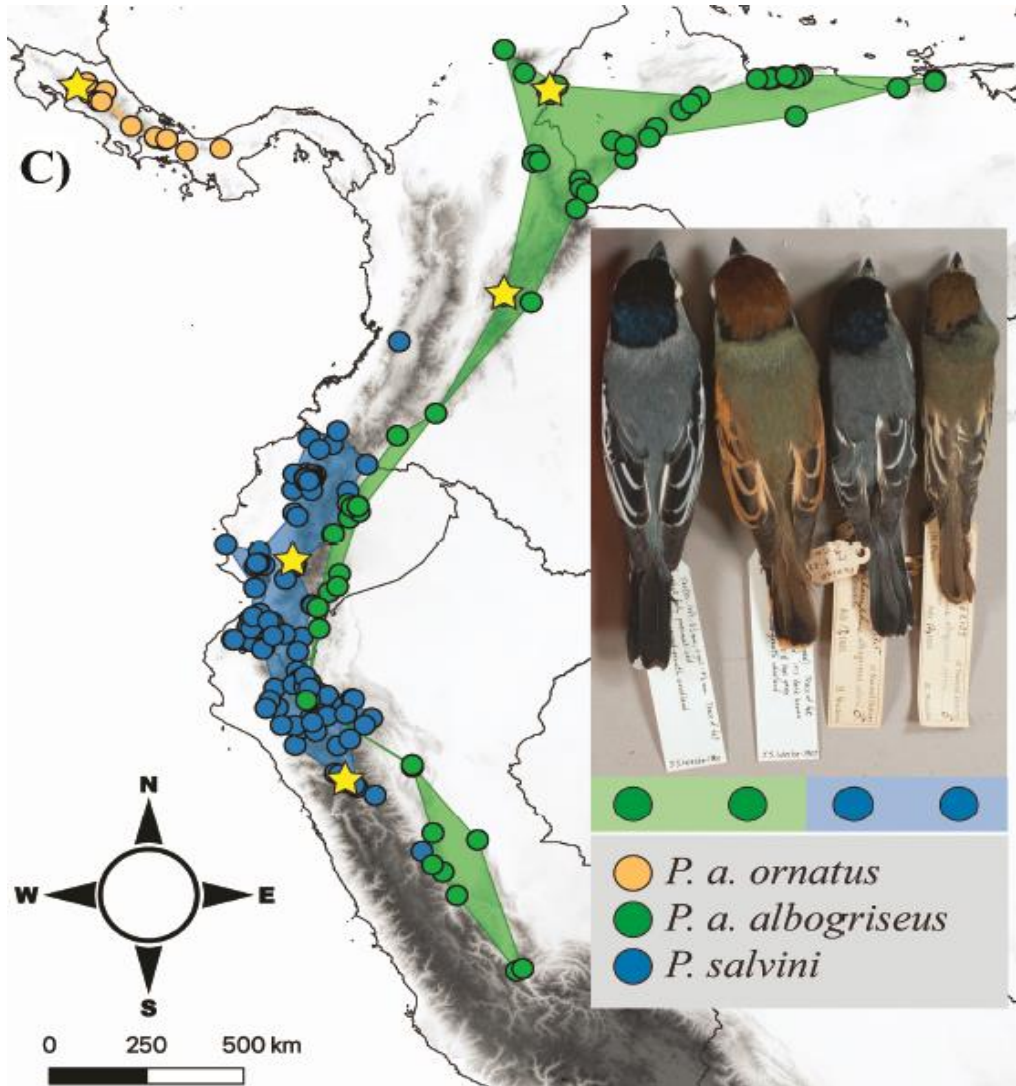
Figure S6. Variation in *P. albogriseus*. The top two photos show males of *P. albogriseus* including (from left to right) *P. a. ornatus* specimens AMNH 390730 and 494162, and *P. a. albogriseus* specimens AMNH 494150, 820943, 820033, and 820266 (the final specimen in this series is an immature male). The bottom photos show females of *P. albogriseus*, including (from left to right) AMNH 390731 (*P. a. ornatus*), 494146, and 821005. Photos by Lukas J. Musher.

Distribution: The integration of genetic, morphological, and vocal data results in the following distributions (type localities are shown by yellow stars, including for the synonymized taxa *guayaquilensis* and *coronatus*):

- *P. albogriseus ornatus*: Humid montane forest of Costa Rica and western Panama (600-1200 m).

- *P. a. albogriseus*: Humid montane forest of Venezuela and northern Colombia south through eastern Ecuador to southern Peru (500-2200 m). Apparently also locally in the Río Marañón drainage ("Lomo Santo" = Loma Santa, Jaen district, 1500 m).

- *P. salvini*: Humid montane and dry deciduous forest in western Colombia, western Ecuador, northwestern Peru, and the Río Marañón drainage. Also, perhaps seasonally only, on the Amazonian slope of southern Colombia (?), eastern Ecuador, and eastern Peru (0-2450 m).



Effect on the AOS-CLC Area:

A split of *P. salvini* would not add a new species to the AOS-CLC area as *P. salvini* is extralimital, but it would result in a new note and a change in the distribution of *P. albogriseus*.

Recommendation:

We recommend splitting *P. salvini* from *P. albogriseus* based on polyphyly when *P. salvini* is included, distinct songs and morphology, and deep genetic divergence.

For English names we recommend the names adopted by SACC: Cryptic Becard for *P. salvini* and Black-and-white Becard for *P. albogriseus*. For more information on English names, see the SACC proposals and discussion at the links posted above.

Literature cited:

- Musher, L. J., and J. Cracraft (2018). Phylogenomics and species delimitation of a complex radiation of Neotropical suboscine birds (*Pachyramphus*). *Molecular Phylogenetics and Evolution* 118:204–221.
- Musher, L. J., M. Ferreira, A. L. Auerbach, and J. Cracraft (2019). Why is Amazonia a 'source' of biodiversity? Climate-mediated dispersal and synchronous speciation across the Andes in an avian group (Tityrinae). *Proceedings of the Royal Society B: Biological Sciences* 286:20182343.
- Musher, L. J., N. K. Krabbe, and J. I. Areta (2023) Underestimated Neotropical diversity: Integrative taxonomy reveals two unrelated look-alike species in a suboscine bird (*Pachyramphus albogriseus*). *Ornithology* 140: 1–17. Online version published 2022: <https://doi.org/10.1093/ornithology/ukac047>.
- Ridgely, R. S., and P. J. Greenfield (2001). *Birds of Ecuador: Status, distribution and taxonomy*. Cornell University Press, Ithaca, NY, USA.
- Schulenberg, T. S., D. F. Stotz, D. F. Lane, J. P. O'Neill, and T. A. Parker III (2007). *Birds of Peru*. Princeton University Press, Princeton, NJ, USA.
- Zimmer, J. T. (1936) Studies of Peruvian birds XXIVL. Notes on *Pachyramphus*, *Platypsaris*, *Tityra* and *Pyroderus*. *American Museum Novitates* 894.

Submitted by: David Vander Pluym, Niels K. Krabbe, Juan I. Areta, and Lukas J. Musher

Date of Proposal: 15 August 2024

Appendix: Comments from the SACC on Proposal 955 (see the links provided above for comments on the subsequent English name proposal, SACC 971):

Comments on Proposal 955:

Comments from Lane: “A) YES. The authors make a compelling case for the species status of *Pachyramphus salvini*, and have done an elegant job of untangling the taxonomic conundrum that has plagued us for so long!

“As for B-D, I am not enamored of their selected names of the daughter species, and vote NO for all. Honestly, those names seem to highlight features that are not immediately obvious (which band is broad?), and do not allow the unaware user to know that the two species had been considered one for so long, nor that they are extremely easily confused! We can argue that the name “Black-and-white” isn’t exactly accurate, as the base color for most of the (male’s) plumage is actually gray, not strictly black and white, but if we can agree that we have lived with it without much chafing, allow me to suggest alternative names. Another way to say “black-and-white” is “pied.” So why not draw attention to the fact that these two species are large and small versions of nearly identical plumage patterns? I would suggest “Greater Pied Becard” for *P. albogriseus* (sensu stricto) and “Lesser Pied Becard” for *P. salvini*. That way, it is clear that they are very similar in appearance (like, e.g., the Yellowlegs), but that size is one of the important characters distinguishing them. Furthermore, these names do not necessarily require sister relationship, as the Yellowlegs case illustrates, but do make clear that the two species have been closely tied for most of their existence.”

Comments from Stiles: “YES. Me gusta la nueva propuesta sobre *Pachyrhamphus salvini* vs. *albogriseus* so YES for my vote! My only doubt is the E-name “Broad-banded” for the latter: to which band does the name refer to?”

Comments from Remsen: “A. YES. I’ve been following this case from the sidelines since my initial proposal (906), and I echo Dan’s comments – outstanding job of working this one out, and indisputable evidence in my opinion for species rank for *salvini*.”

Comments from Gary Rosenberg (voting for Areta on B, C, D): “I agree that the authors have shown using multiple methods that *salvini* should be considered distinct from *albogriseus* - not only is it genetically distinct, but both the vocal, size, and plumage differences support this treatment. I also don’t really like “Broad-banded” for the name for “Black-and-white” - a bit like “Orange-banded” Flycatcher - which I assume refers to the “wing-bars” but have always wondered, as they usually are not orange, and no one really calls wing bars “bands”? I guess there are other English names that use “banded” but it is not always referring to the wing-bars - so not so obvious to the observer. I don’t really like the name Cryptic - as I agree with others that it is not hiding in plain sight from a similar species that it co-occurs with - I think there are enough clear differences now that we are aware of them that the name Cryptic doesn’t really apply. *Salvini* does have a more slender bill - so I am not against that as a common name - although is it really more “slender billed” than other becards? It is when compared to *albogriseus* - but no one is going to see the two together. I like Dan’s idea of “Pied” Becard - so maybe a compromise - Pied and Slender-billed - as opposed to Greater and Lesser Pied Becards? Therefore:”

“B: NO

“C: YES

“D: NO

Comments from Don Roberson (voting for Claramunt): “Like Dan Lane, I vote note “no” on the English name choices.

“As a tiny bit of background, Bret Whitney showed those of us on a Madagascar tour in 1992 a newly discovered species of “warbler” in eastern Madagascar, which I was able to see, listen to, and photograph. It had unique habitat along ridge lines in lowland rainforests, see: Goodman, S.M., Langrand, O. and Whitney, B.M. (1996). A new genus and species of passerine from the eastern rainforest of Madagascar. *Ibis* 138(2): 153-159.

“I thought at the time that “Ridgeline Warbler” would be a good English name; at that time it was thought to be in the Sylviidae before that family got split into a dozen or more. It proved to be in Family Bernieridae. In the meantime, its proposed English name was Cryptic Warbler, and eventually became Cryptic Warbler *Cryptosylvicola randrianasoloi*, and it remains that today. However, it has a distinctive song and was only “cryptic” in the sense that it looked somewhat like a bunch of *Phylloscopus* warblers at first glance.

“Ever since, that English name proved so disappointing to me that — given that it proved to be in an entirely different family than *Phylloscopus*, from which it was supposed to be so “cryptic,” - I’ve thought the English name “Cryptic” should be used with caution.

“The proposed “Slender-billed” and “Broad-banded” are both a bit of a mouthful, and the differences not all that apparent without a lot of background. “Broad-banded” appears to be restrict to the broad v. narrow black band adjacent to the chestnut crown in female, if I understand this correctly. But I don’t understand why it is not proposed as “Slender-billed” versus “Thick-billed,” or “Broad-banded” vs “Slender-banded” for the two taxa, or similar comparative names, which focuses the observer on the same character in each species, rather than two different traits, one of which is only in females? This seems needlessly confusing. With prions there is a Slender-billed and Broad-billed Prion —even if those characters might be hard to determine in the field — but at least it focuses the observer on the bill, not the bill of one and the crown of the other (if a female). So preliminarily a “no” on all these.

“I do like Dan Lane’s proposed Greater Pied and Lesser Pied Becard — which not only gets us to something like “Black-and-white” (the long-standing English name), but a Yellowlegs like comparison.”

“There may be other good potential names, but at this point, I like Greater Pied and Lesser Pied for what is currently up for offer.”

Comments from Donsker (voting for Bonaccorso): “I am reluctant to accept the English names proposed by the authors of this proposal. Rather than trying to select English names that attempt to distinguish these two very similar-appearing species as the authors have valiantly attempted to do, I would suggest that, instead, we consider English names that help to distinguish *P. albogriseus* (s.s.) and *P. salvini* from the three other similar “black-and-white” or “pied” species in the genus *Pachyrhamphus*, i.e., White-winged Becard *P. polychopterus*, Black-capped Becard *P. marginatus*, and, in Central America, Gray-collared Becard *P. major*. “In comparison to those other three ‘black-and-white’ becards, I believe that only *P. albogriseus* and *P. salvini* have uniquely gray or slaty-gray mantles. The mantles of the other three are black. I would propose that the name ‘Gray-backed Becard’ be incorporated into the English names of both species. This unique plumage feature is already reflected in the vernacular German name for *P. albogriseus* (s.l.), which is ‘Graurückenbekarde’.

“My suggestion would be to apply Greater Gray-backed Becard to *P. albogriseus* (s.s.) and Lesser Gray-backed Becard to *P. salvini*. As Dan has already pointed out, using the same basic English term for these two species doesn't necessarily imply a sister relationship any more than it does for the two yellowlegs, the two black-backed gulls or, for that matter, Greater and Lesser Flamingos which aren't even in the same genus. Retaining a similar English name for both species emphasizes their historically confounding similarity.

“Although I think that “pied” becard is actually more suitable for the three becards with black mantles, if gray-backed” becard is unacceptable, I would support Dan's suggestion of Greater and Lesser Pied Becard for the two species. ‘Pied Becard’ would not be a unique application since the French name for *P. albogriseus* (s.l.) is already ‘Bécard pie’.”

Comments from Hilty (voting for Pacheco): “Geez, they have unraveled quite a convoluted puzzle here. And, interesting regarding the songs. This bird is regular in the coastal cordillera of northern Venezuela, and in the Mérida Andes of Venezuela and always seemed quite vocal. However, it seems decidedly scarce (or perhaps not recognized?) in Colombia. At least in my experience, I rarely hear it.

“I don't much care for either name suggested. But, if the name Black-and-white Becard has to go, then Dan Lane's suggested alternatives, Greater and Lesser Pied Becard (eastern and western forms respectively) are better and clearly show originality. As both Dan and Gary pointed out, the name suggested (the name Broad-banded is confusing and unhelpful); and Cryptic really doesn't provide any helpful information.

“I would, however, suggest a slight variation on Dan's names, to make it easier for people to keep the geographical distributions in mind (and this is important with so many new name changes occurring): thus Eastern Pied Becard, and Western Pied Becard. I am aware that there has been some push-back in the past over adding “geographical adjectives” to names, but these are really very helpful for people who English names. The use of “Greater” and “Lesser” in the two names suggests a distinction that I don't think is very obvious at all (at least not in the field, and that is where these English names will be used).”

Comments from Josh Beck (voting for Remsen): ““This is a really cool result, and it shakes up things in a group of similar looking Becards. For better or worse, the name Black-and-white, even if not particularly accurate, and now needing to be retired, was pretty entrenched and well understood; this is not an extremely obscure bird. Looking at possible new English names, while Broad-banded and Slender-billed might be technically correct, I don't feel that they best help a birder / user of English names. They don't provide any way to relate back to the prior name. Based on field experience and having also looked through a good number of photos, I don't think either field mark is particularly easy to interpret in the field. So I follow others in voting NO on B/C/D. I do like Dan's suggestion, and like the idea of “Eastern vs Western” Pied Becard about as well or perhaps a bit better than Greater vs Lesser. In a group of quite similar birds that are all difficult to assign uniquely identifying names to, something that ties back to what they used to be named and that helps distinguish between the two new species does seem helpful and desirable.”

Additional comments from Lane: “I appreciate that my comments on this proposal seem to have resonated with others here, and I am inspired to make a few additional ones on the topic of English names. As several have pointed out “pied” isn’t really all that accurate (at least, not more so than “Black-and-white”... but most English names simply fall short of perfect accuracy, as we all know). I considered “pied” to be a shorter word that still retains the basic meaning. David’s suggestion of “Gray-backed” could work, but males of *Pachyramphus rufus* and some populations of *Pachyramphus major* also share the gray back, so it isn’t as unique as David’s proposal suggested to these two species within the “black-and-white” group of *Pachyramphus*. In addition, the more syllables a name has, the less I like it (harder to spit out when trying to get a group on a bird, for example!). So I’d prefer “pied” over “gray-backed” for succinctness if nothing else. As for Eastern and Western... well, I’d urge a review of the map above. *P. albogriseus* has a representative in Costa Rica and Panama, which is entirely WEST of *P. salvini*’s range. One could see “Eastern” in Costa Rica and “Western” on the eastern slope of the Andes in Peru! In essence, *P. albogriseus* is east, west, north, and south of the distribution of *P. salvini*, so I don’t personally feel using geographic terms really fits well here unless it was something like “Central Pied Becard” and “Peripheral Pied Becard.” Returning to the usefulness of “Greater” and “Lesser” here: yes, it is nearly impossible to judge size of an individual becard in the canopy, but the bill size (in proportion to the head) may prove to be useful in field identification, and *P. albogriseus* has a proportionally larger bill than *P. salvini* (again in a surprising parallel to the yellowlegs!), so to me “Greater” and “Lesser” actually do fit fairly well and could help birders sort out which they are watching while in the field. These remain my first choices, but I am certainly open to seeing what other options are put forth.”

Comments from Areta: “YES. As an author of the work, I would of course vote yes to the recognition of *P. salvini* as separate from *P. albogriseus*, as I did in Proposal #906. Indeed, it was that proposal by Van the one that launched the whole process, which lead to the Musher et al. work that forms the basis of this proposal.”

Comments from Areta on English names: “Regarding the common names, I would like to stress that the whole point of our naming suggestions is to have names aiming to diagnostic features of each taxon. Greater and Lesser perpetuate the myth that one can judge size differences in the field even when lacking comparative views: it is easy to see the size differences of Lesser and Greater yellowlegs when they are side-by-side, but side-by-side comparisons on the same branch of *P. salvini* and *P. albogriseus* would be a miracle. However, they may coexist at least seasonally indicating that being aware of how to distinguish them is key to a better understanding of their distributions, and the only field characters that we were able to consistently assess based on several hundred pictures where the amount of white on the upper wing coverts (i.e., THE band) and the relative bill width. So, to me, even if not perfect, Slender-billed and Broad-banded indicate the two key features that most observers under field conditions will be able to evaluate. Slender-billed is also slender-banded, and Broad-banded is also broad-billed (indeed, Slender-billed is among the most slender-billed *Pachyramphus*). Piece of cake, easy to remember, "easy" to use in the field, and informative. As Dan argued, using Eastern and Western does not work, given the complicated distributions. As for X and Y

Pied Becard, I think there is just too much wording in there, which adds little to their ID, and these are not more pied than other becards. Songs are also diagnostic..."

Comments from Robbins: "YES. A very thorough proposal that made this a straightforward decision. Yes to treating salvini as a separate species.

"Although I don't vote on English names, if I did, I would support Dan's "pied" names!"

Additional comments by Lane: "I recognize that Nacho and all had reasons for the English names they proposed in their paper and this proposal, but I find the reasons Nacho has put forward above to be unsatisfactory. For the average user, it will be unclear that "Slender-billed" and "Broad-banded" are meant to distinguish the two former Black-and-white groups from one another specifically, and *not* from all other Pachyramphus! There are other Pachyramphus (P. versicolor, for example) that are slenderer-billed, and several that have similarly broad upper wingbars. I further have looked at several specimens, and a ream of photos on Macaulay, and concluded that the upper wingbar is not a particularly helpful character to distinguish these two species in the field. Bill size (proportional length with respect to head size, especially) seems to be better and voice better still! As a tour guide who uses English names a lot, and regularly gets questioned by clients about "why did they change the names?" I believe it is best to select names that make clear that these two species are nearly identical -- they are basically large and small copies of one another with very few clear phenotypical characters to separate them. In that vein, Greater and Lesser Pied Becard does manages to convey these several ideas about as well as I can fashion. And as Nacho says that "Slender-billed" also has a "slender band" and "Broad-banded" has a "broad bill"... well "Lesser" has a smaller bill AND band, and "Greater" has a larger bill and band, so these two names seem to better satisfy the issue than the more confusing ones originally proposed. But in the end, this will have to be decided in a separate proposal anyway, methinks."

Comments from Claramunt: "YES. The new study further clarifies the situation."

Comments from Stiles: "YES to split salvini from albogriseus; and I consider Greater and Lesser Pied Becard to be the most digestible E-names."

Comments from Del-Rio: "YES."

Transfer Pale-eyed Pygmy-Tyrant *Lophotriccus pilaris* to *Atalotriccus*

Background:

The NACC is nearly alone in considering the Pale-eyed Pygmy-Tyrant, *Lophotriccus pilaris* (Cabanis, 1847), as part of the genus *Lophotriccus* Berlepsch 1884, rather than in the monotypic *Atalotriccus* Ridgway 1905. The genus of this bird has a long and convoluted history, having bounced around between *Colopterus* Cabanis 1845 (preoccupied) and *Colopteryx* Ridgway 1888, in addition to the two genera mentioned above.

The species is a small, plain, midstory tyrannid, broadly similar to many other species in the genera *Lophotriccus*, *Hemitriccus*, and *Poecilotriccus*, species of which are called Pygmy-Tyrants, Tody-Tyrants, or Tody-Flycatchers. *Lophotriccus pilaris* is found in dry forests of northern South America and reaches our area only in the dry forests of the Pacific slope of west-central Panama.

Because the taxonomy of the group is very convoluted, I have attempted to list below the relevant genera with their author, year of publication, and type species.

Hemitriccus Cabanis & Heine 1859, type *diops*
Oncostoma Sclater, PL 1862, type *cinereigulare*
Lophotriccus Berlepsch 1884, type *pileatus*
Poecilotriccus Berlepsch 1884, type *ruficeps*
Colopteryx Ridgway 1888 [replacement name for *Colopterus*], type *cristatus* = *galeatus*
Atalotriccus Ridgway 1905, type *pilaris*

Perhaps relevant is Ridgway's (1905) description of the genus *Atalotriccus*, although this would be more relevant if there were a comprehensive morphological examination of all taxa in the group, which I don't believe exists.

Atalotriccus gen. nov. (Tyrannidae)

Similar to *Colopteryx* Ridgway (ex *Colopterus* Cabanis, preoccupied), but head without crest, four, instead of three, outer primaries greatly reduced in size (the reduction excessive and the feathers very narrow and acuminate instead of normal in form), and bill much narrower.

Type, *Colopterus pilaris* Cabanis = *Atalotriccus pilaris*.

It is unclear to me what the circumscription of *Colopteryx* was at the time of Ridgway's writing, so I'm not sure what species he was comparing to *pilaris*, but it was probably only the type species *Lophotriccus galeatus*. Ridgway (1907) did not appear to include species other than *galeatus* in *Colopteryx*, which he indicated was extralimital to North and Middle America.

New Information:

Harvey et al. (2020) found that *L. pilaris* fell squarely in the middle of a large and highly polyphyletic clade of small tyrannids, with members of the current genera *Lophotriccus*, *Hemitriccus*, *Poecilatriccus*, and *Oncostoma* all interdigitated. In the most extreme example, *Hemitriccus* shows up in 6 different clades in the tree! All of this is a recipe for a nomenclatural headache, and SACC has not yet addressed the matter in a comprehensive way, which I believe is because they are waiting on a forthcoming publication that will explicitly address the nomenclature and taxonomy of this group in light of the phylogeny of Harvey et al. (2020). That phylogeny is shown below. The key take-away from this tree is that *pilaris* sits on a somewhat long branch, among a clade comprised of taxa in the current genera *Lophotriccus*, *Hemitriccus*, and *Oncostoma*, and perhaps *Poecilatriccus* depending how expansively the clade is defined. Most nodes are fully supported, including all nodes subtending *pilaris*.

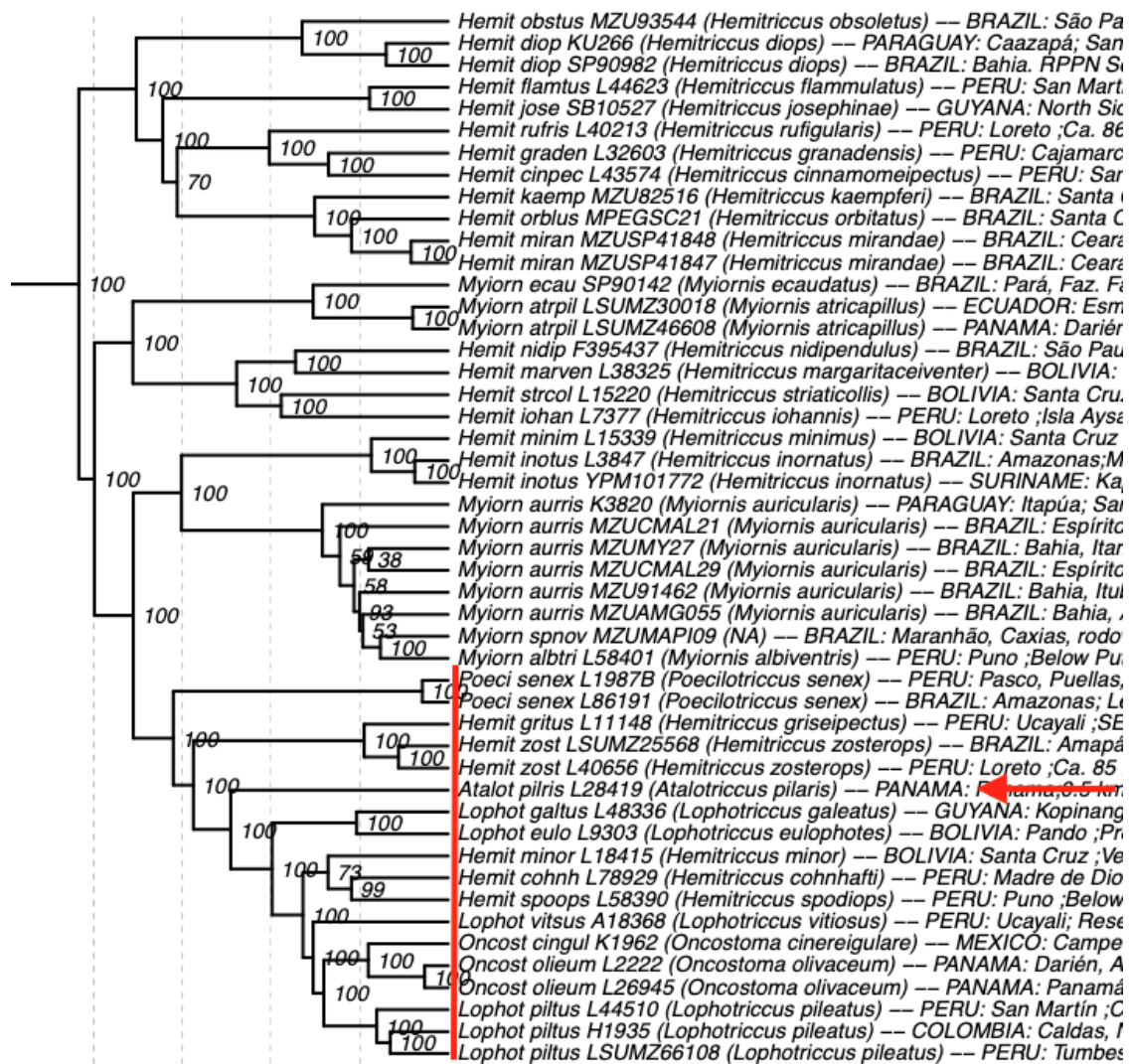


Figure 1. A portion of the suboscine phylogeny from Harvey et al. (2020). *Lophotriccus pilaris* is indicated with a red arrow, under the name *Atalotriccus pilaris*. The vertical red line denotes what (to my eye) seems a fairly cohesive clade. See text for details.

Effect on AOS-CLC area:

Transferring *pilaris* to *Atalotriccus* would result in a name change from *Lophotriccus pilaris* to *Atalotriccus pilaris*.

Recommendation:

This is a tough one, with two alternatives that are both, in my opinion, entirely reasonable. The first would be to transfer *pilaris* to *Atalotriccus* to align with basically all global lists, which nearly uniformly recognize the genus for *pilaris*.

However, based on the phylogeny of Harvey et al. (2020), we know that the taxonomy of the broader *Lophotriccus/Hemitriccus/Oncostoma/Poecilotriccus/Myiornis* clade is in dire need of comprehensive revision. It may be more prudent to wait until that happens, and then transfer *pilaris* to whichever genus is used for the broader clade that *pilaris* is embedded within. In my cursory assessment, I believe that would be *Oncostoma*. Or, if *Lophotriccus* is restricted to just *galeatus* and *eulophotes*, then *Atalotriccus* could be retained for *pilaris*. As for morphology, the species in the clade that I've defined in the tree above (using the red vertical line) are of course fairly heterogenous given that they're currently in 4-5 different genera. However, they do share many similarities, with many having pale eyes, blurry streaks below, and short trilled vocalizations.

Of course, it doesn't hurt to transfer *pilaris* to *Atalotriccus* now, and then move it to whichever genus it goes with after the taxonomic revision (whenever that happens). I should also note that the linear sequence in our list does not align with the phylogeny of Harvey et al. (2020), but it does align with that of Clements for *pilaris* vs. its close relatives, so I'm inclined to make no changes to the linear sequence until the genus-level changes to the broader clade are resolved.

Please vote on the following:

- Transfer *Lophotriccus pilaris* to *Atalotriccus*

I tentatively recommend a **YES** on this proposal.

Literature Cited:

- Harvey, M.G., et al. 2020. The evolution of a tropical biodiversity hotspot. *Science* 370,1343-1348. DOI:10.1126/science.aaz6970
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Submitted by: Oscar Johnson

Date of proposal: 30 August 2024

Revise the taxonomy of the genus *Gygis*: (a) recognize subfamilies Gyginae and Anoinae, and (b) treat *G. candida* and *G. microrhyncha* as separate species from White Tern *G. alba*

Note: Pratt's (2020) paper, which is the primary basis for this proposal, was to have been co-authored by Storrs L. Olson, but the Covid-19 pandemic and resultant lockdown of the research divisions of the Smithsonian Institution prevented him from retrieving his notes on *Gygis* in time, and Pratt's paper was published only with some information cited as *pers. comm.* from Olson. Not long afterwards, Olson unfortunately fell ill and died. In June 2022, with the invitation and assistance of Helen James, Pratt located Olson's *Gygis* file in the Bird Division of the USNM and took custody of it at the institution's request. Surprisingly (Olson had not mentioned it), the folder contained not only the expected data forms and correspondence, but also a nearly finished 6-page typed draft, prepared in April 1994, of a paper about species limits in *Gygis*. In an accompanying letter to the late Claudia Wilds, Olson stated his intention to submit the paper as soon as possible but for unknown reasons he never did so. The manuscript includes handwritten notations in red made by Wilds along with a letter from her with additional relevant comments. Copies of the ms plus Wilds's letter are attached herewith (as Appendices 1 and 2). Combined, they provide two pre-molecular "voices from the grave" in support of the taxonomy proposed herein. Although we cite Olson's (ms) findings where they supplement other results, we urge the committee to read his entire original manuscript for the insights it contains, including a summary of Olson's detailed analysis of specimens in the American Museum of Natural History (from the Whitney South Sea Expedition) and the Smithsonian Institution (from the Pacific Ocean Biological Survey, POSB). The actual handwritten measurements accompanied the Olson ms and can be supplied on request. Olson was quite prescient of genetic research that later confirmed his suggestions regarding the classification of *Gygis* and *Anous*.

This proposal consists of two parts, which can be voted on separately.

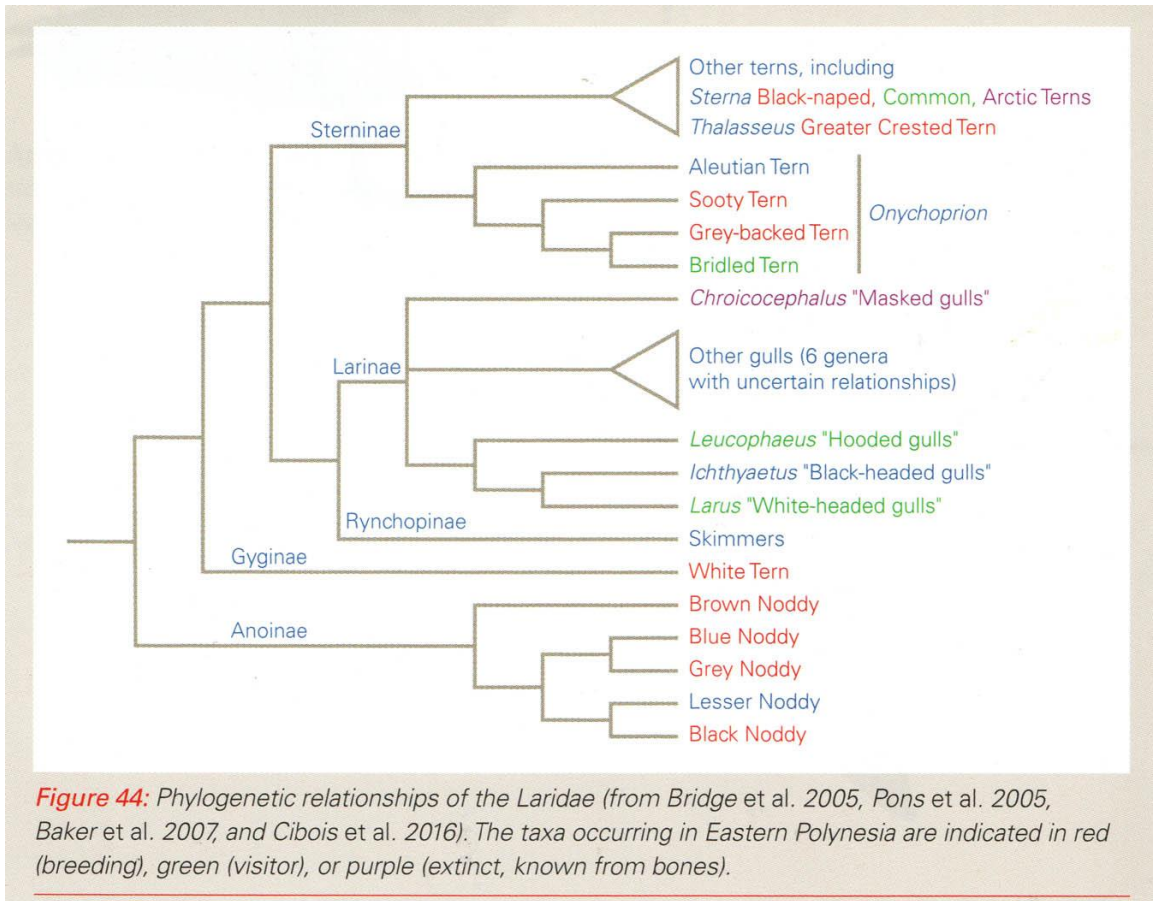
(a) Recognize subfamilies Gyginae and Anoinae

Background:

AOS (AOU 1998) currently classifies *Gygis* and *Anous* among the terns (Laridae: Sterninae).

New information:

Although fine branching details may differ, nearly all recent studies (Bridge et al. 2005, Pons et al. 2005, Baker et al. 2007, Cracraft 2013, Thibault and Cibois 2017, Černý and Natale 2022) and world checklists (HBW and Birdlife International 2022, Boyd 2024) have recognized Gyginae and Anoinae as co-equal subfamilies with Rhynchopinae, Larinae, and Sterninae within Laridae. Olson (ms) anticipated this arrangement based on osteological and other morphological criteria. Thibault and Cibois (2017:246) produced a unified phylogeny based on four studies that produced identical basal branching patterns (a remarkable fact in and of itself):



Černý and Natale (2022) differed in showing Rhynchopinae in the most basal position and Gyginae and Anoinae as sister groups (but with a divergence well before that of the other subfamilies) but also regarded the five lineages as of equal subfamilial rank. Gill et al. (2024) place the noddies and *Gygis* in a basal position among typical terns but do not designate subfamilies. Boyd (2024) uniquely recognized Sternidae (terns including Sterninae and Gyginae) and Laridae (gulls including Larinae and Anoinae). Clearly, Howell and Zufelt's (2019) and Harrison et al.'s (2021) use of the term "white noddies" for *Gygis* is no longer acceptable.

(b) Treat *G. candida* and *G. microrhyncha* as separate species from White Tern *G. alba*

Background:

American Ornithologists' Union (1998 and Supplements) lists the genus *Gygis* as comprising the single species *G. alba* with subspecies groups *alba*, *candida*, and *microrhyncha*. The differences of the form *leucopes* (Holyoak and Thibault 1974) were considered "minor" by Thibault and Cibois (2017) and they disregarded it, as do we. Subsequent authors have variously recognized one (Harrison et al. 2021), two (Pratt et al. 1987, del Hoyo and Collar 2014, Boyd 2024) or three (Olson 2005, Steadman 2006, Howell and Zufelt 2019, Pratt 2020, HBW and Birdlife International 2022) biological species within *Gygis*. Yeung et al. (2009), supplemented by Thibault and Cibois (2017), used mitochondrial genes to conclude that only

one undifferentiated taxon of *Gygis* occurs in the Pacific Ocean, but Thomas et al. (2004) and Černý and Natale (2022) split *G. microrhyncha* (neither study included *alba*). For a discussion of discordance among molecular findings and between molecular and phenotypic data see Pratt (2020).

New Information:

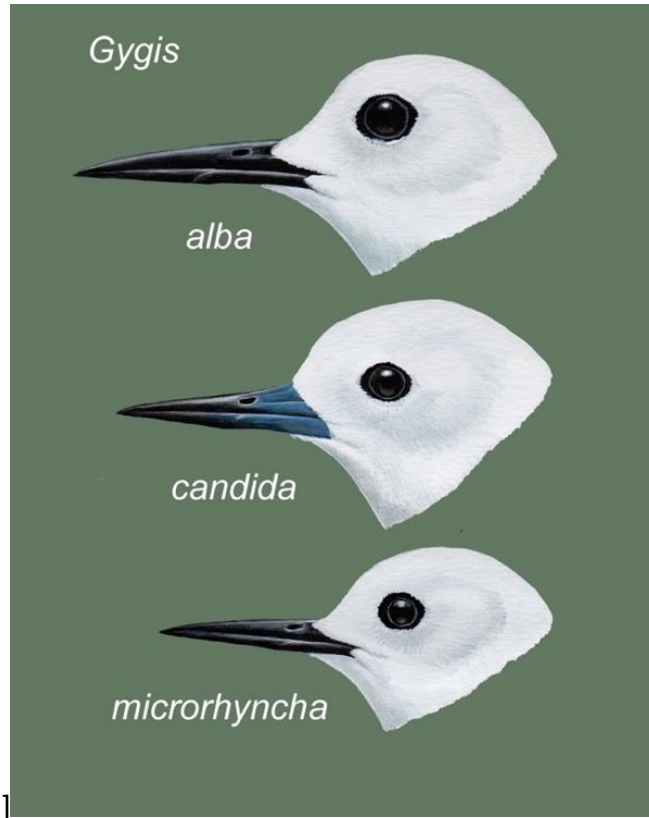
ARCHAEOLOGY. Subfossil bones reveal that *candida* and *microrhyncha* were sympatric in prehuman times over a ca. 9,000 km swath of the tropical Pacific from Tinian in the Marianas to Easter Island. Here is the relevant text from Steadman (2006:400):

well. On the other hand, fossils portray large contractions (>1000 km) in breeding range since human arrival for the terns *Procelsterna cerulea* and *G. microrhyncha*. The former occurs in prehistoric sites on three islands in the Marianas (Table 15-4), 2500 km west of the nearest breeding population in the Marshall Islands. A sighting of *P. cerulea* off the west coast of Thailand (Eller 1989) hints that modern range extensions are also possible. *Gygis microrhyncha* is restricted today to the Marquesas but its bones have been found in prehistoric sites on Mangaia (2200 km SW), Easter Island (3300 km SE), 'Uiha, Ha'afeva, and 'Eua in Tonga (3600 km SW), and Tinian in the Marianas (8900 km W; Tables 15-2 to 15-4). *Gygis microrhyncha* was sympatric with *G. candida* (Figure 15-12) on these islands, thus reinforcing the distinctiveness of these two species (Pratt et al. 1987:186-187), which many authors have regarded as conspecific.

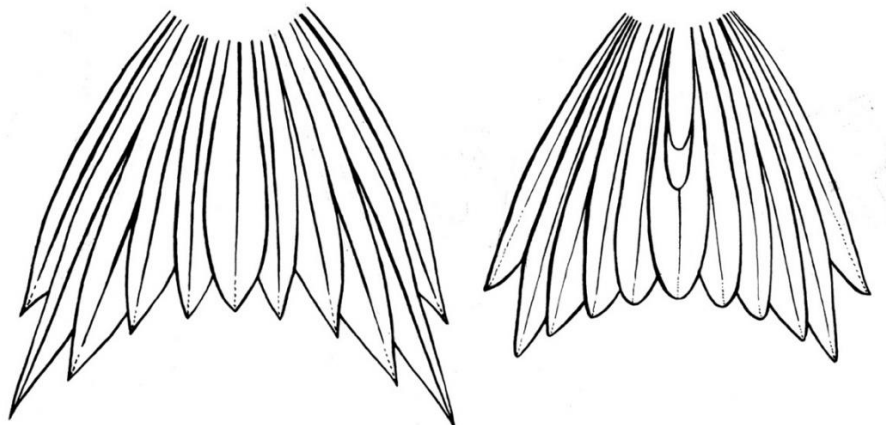
This fact alone establishes that these two taxa are separate species under the BSC. Thibault and Cibois (2017) suggested that Steadman (2006) merely divided a continuum of size at some arbitrary point and called larger specimens *candida* and smaller ones *microrhyncha*, but that idea either overlooks or ignores qualitative differences of which Steadman (2006) was clearly aware (Pratt 2020).

MORPHOLOGY AND COLORATION. The genus *Gygis* exhibits two strikingly different bill shapes, one resembling that of other small terns (Sterninae) and the other quite distinctive. Those of *alba* and *microrhyncha* are of the former type, with the loreal feathering extending forward toward the nostrils and the malar feathering also extending forward onto the mandible. The bill of *alba* is somewhat thicker at the base and the gonydeal angle somewhat more anterior, but otherwise the two are similar in shape and both are black throughout. The bill of *alba* is significantly larger than that of aptly named *microrhyncha*. The bill of the more familiar *candida* is intermediate in size and dagger-like or long triangular, with a basal insertion that forms a nearly straight line in profile. The anterior half is black but from the nostrils and gonydeal angle back, it is deep cobalt

blue. These different bill shapes produce somewhat different head profiles. A picture being worth 10K words, here is Pratt's (2020) illustration:



The three forms of *Gygis* also differ in tail shape, with *candida* showing a more deeply forked tail than *microrhyncha* and *alba* intermediate, although closer to *candida*. Olson's files included these unlabeled drawings presumably of *candida* (left) and *microrhyncha* (right).



The photos below (© Pete Morris) from the Marquesas also show this feature in *candida* (a) and *microrhyncha* (b) (from Pratt 2020).



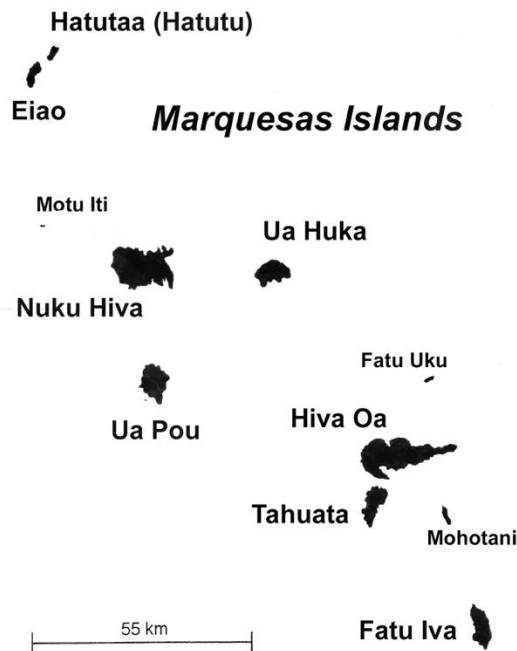
This feature figured prominently in Olson's (ms) discovery of putative hybrids in the central Pacific (see below).

The three forms also differ in the amount of pigmentation in the shafts of the outer primaries, with distinctly black shafts in *candida* but *alba* and *microrhyncha* showing less pigmentation that ranges from white to golden brown and occasionally to black (Wilds, in litt., pers. obs.). Primary shaft color is thus not as important a field mark as is sometimes believed (i. e., White et al. 2014).

VOCALIZATIONS. Pratt (2020) made the first detailed study of vocalizations, archived in Macaulay Library (ML; www.macaulaylibrary.org) and xeno-canto (XC; www.xeno-canto.org), in *Gygis*. The voice of *candida* is well documented, but recordings of *microrhyncha* and *alba* are scarce and therefore must be used with caution in making comparisons. Nevertheless, Pratt (2020:204) concluded that each taxon in the genus has "a unique vocal repertoire easily distinguishable from the other two". Calls of *microrhyncha* are higher pitched than those of *candida* (XC75212) and one recording (ML203895301) includes a two-note raspy call apparently unique to *microrhyncha*. Holyoak and Thibault (1984) described a distinctive begging call of *microrhyncha* chicks that apparently has never been recorded. The vocalizations of *alba* are particularly distinctive in being "strikingly lower pitched" than those of *candida* or *microrhyncha* with fewer obvious homologies. One vocalization (XC431354) appears to have no equivalent in either

Pacific form. Although further research on vocalizations of *alba* and *microrhyncha* is needed, current knowledge suggests that these vocal differences may well serve as isolating mechanisms among three species.

POSSIBLE HYBRIDIZATION AND GENETIC SWAMPING. Despite a long prehistoric period of sympatry with *candida*, and partly coinciding with the peopling of the Pacific islands, *microrhyncha* has disappeared from most of its original range and by the Twentieth Century was believed to be restricted to the Marquesas, where it occupied all larger islands. (For orientation, here is a thumbnail map from Pratt 2020.)



However, Baker (1951) found that two islands, the northernmost island Hatutaa (Hatutu) and enigmatically the islet of Mohotani in the southern part of the archipelago, harbored populations that he regarded as intergrades, but which Olson (ms) considered pure *candida*. Holyoak and Thibault (1976), confirmed by Olson (ms), found *microrhyncha*, *candida*, and intergrades on both islands and neighboring Eiao, which had no pure *candida*.

Interestingly, among specimens collected by the POSB in the 1920s were three specimens of pure *microrhyncha* from the equatorial central Pacific (Line Is. and Phoenix Is., Kiribati, and at sea) far from the Marquesas, as well as five specimens from the same islands that have bills like *microrhyncha* but an intermediate tail fork. Olson (ms) considered those five to be intergrades. Whether *microrhyncha* persists in Kiribati is not known, but we know of no recent records.

Pratt (2020) revisited the same specimens as Holyoak and Thibault (1984) and Olson (ms), as well as photographic evidence obtained by D. Sargeant on Hatutaa in 2013 and found that, far from being parapatric in the Marquesas as previously thought, *microrhyncha* and *candida*

maintain a zone of intergradation on Hatutaa where both parental forms and many intergrades (or hybrids) persist. Olson (ms, 2005; Pratt 2020) hypothesized that *microrhyncha* had been progressively displaced in the Pacific from west to east by hybridization with *candida* and resultant genetic swamping. Pratt's (2020) new evidence suggests that the process is either ongoing, with an aggressive invading species genetically overwhelming a relictual one, or the two forms have a stable zone of overlap and hybridization. The persistence of both parental types on Hatutaa suggests a non-random pattern of hybridization (Pratt 2020), but further research is needed. A cautionary note is that if *candida* and *microrhyncha* are separate species, as all evidence indicates, the latter may require conservation measures if it is being genetically swamped by *candida* (compare similar cases such as the Hawaiian Duck *Anas wyvilliana* and the Black Stilt *Himantopus novaezelandiae*).

The question of whether *alba* is a third species was addressed by Olson (ms), who concluded that the striking difference in size warranted species status. Pratt's (2020) observations on vocalizations add further evidence that *alba* is distinct. To date, no published genetic studies have included *alba*, but unpublished preliminary data from N. Yeung (pers. comm.) suggest that *alba* is genetically "very different". Obviously, this is fertile ground for further research.

English names:

As a single iconic species, *G. alba* has long been, and continues to be, called "fairy tern" by the lay public (Wilds, in litt.). That name has now been restricted by various "official" lists, including AOS, to *Sternula nereis* of southern Australia and New Zealand, but its use persists elsewhere for *G. alba*, especially where the birds are conspicuous to large English-speaking populations. Even among those who use "White Tern", that name is often, perhaps usually, followed by some phrase such as "also known as fairy tern," most recently by Hosein (2024). In Honolulu, where the bird is an official city icon, the hybrid name "White Fairy Tern" has gained popularity as an informal way to get around the problem (see Pratt 2020 for references, especially Floyd 2019). Note that, according to NACC guidelines, if we recognize 3 species of *Gygis*, the unmodified name White Tern would be reserved for the original unsplit species.

All other larid subfamilies, Anoinae (noddies), Larinae (gulls), Rhynchopinae (skimmers), and Sterninae (terns), have single-word group-names with their own separate listings in indexes. Use of "white terns" as a group-name, even if hyphenated, in our opinion fails to distinguish the Gyginae adequately from the Sterninae and will surely obfuscate. Pratt (2020) proposed the novel single word group-name "fairyterns" for the Gyginae to emphasize that they are NOT terns in the traditional sense, leaving Fairy Tern (sometimes Austral Fairy Tern) for *Sternula nereis*. Note that "fairytern" has a subtly different pronunciation from "fairy tern". We are aware that this committee would ordinarily prefer the construct "fairy-tern" as did Pratt et al. (1987), but experience has taught us that indexers can be stubborn and idiosyncratic in such matters and may index the three species of *Gygis* among the true terns, hyphen notwithstanding. Thus "fairy-tern" is invested with the same problems as "white-tern". "Fairytern" provides no indexing option. This exception for *Gygis* is only necessary if the subfamily Gyginae is recognized (Part A). As Pratt (2020:206) observed, using "fairytern" will "allow non-professionals to maintain a beloved and widely used name without being scolded by pedants." Pratt (2020) proposed the English names Common Fairytern (*G. candida*), Little Fairytern (*G. microrhyncha*), and Atlantic Fairytern (*G. alba*) for the three species. We acknowledge that "Common" as an adjective in

English bird names has met with some recent disfavor, but we believe it is particularly appropriate in this case because it is the fairytern most people will see, being vastly more widespread and common than the other two species, and the name has a long history of use in the Pacific region (at least since Pratt et al. 1987). AOU (1998) uses "Pacific" for *candida* but that is geographically too restrictive. Howell and Zufelt (2019) suggested the epithet Indo-Pacific for *G. candida*, but, while accurate, it is something of a mouthful and unfamiliar to most potential users.

Recommendations:

(a) We recommend that the committee recognize Anoinae and Gyginae as subfamilies and place them in a basal position relative to other subfamilies of Laridae.

(b) We recommend that the committee split *Gygis alba* into three species: *G. alba* (South Atlantic islands of Ascension, St. Helena, Fernando de Noronha, and Trindade; vagrant to St. Croix, U. S. Virgin Islands, and possibly San Salvador, Bahamas); *G. candida* (tropical Indian and Pacific oceans); and *G. microrhyncha* (Marquesas Islands south of Hatutaa, with historical occurrence in Kiribati; vagrant on Oahu, Hawaii). With this split, add *G. microrhyncha* and *G. alba* to the North American Checklist; the former based on a specimen from Hawaii (Olson 2005), the latter on a bird photographed on St. Croix 11 August 2024 (Hosein 2024) just before this proposal was submitted (the published report did not attempt to identify the bird to subspecies, but based on our examination of the photos, we believe the bill shape and color clearly identify it as *G. alba*). A previous report from San Salvador, Bahamas (White et al. 2014) was tentatively identified as *alba* but our review of the published photos suggests it may have been the Pacific *candida*, which has occurred once previously in the Atlantic at Bermuda (Wingate and Watson 1974).

We further recommend that the committee adopt the English single word group-name "fairyterns" for the Gyginae, and the English names Atlantic Fairytern (*G. alba*), Common Fairytern (*G. candida*), and Little Fairytern (*G. microrhyncha*) for the subfamily's three species.

[Note from NACC chair Terry Chesser: The status of the three forms in the NACC area is somewhat confused, largely due to an apparent error in the seventh edition of the AOU Checklist (AOU 1998). The sixth edition (AOU 1983) included the record detailed in Wingate and Watson (1974) as an accidental record under the *candida* group: "on Bermuda (photograph of individual referable to this group)." However, AOU (1998) changed this to "Accidental ... [*alba* group] on Bermuda (7-9 December 1972; photograph of individual referable to this group) and Tobago." Wingate and Watson (1974) had discussed the characters separating *candida* and *alba* and concluded that the bird from Bermuda "shows clearly the bill characters and dark primary rachis pigmentation of the *candida* group rather than those of the Atlantic *alba* population, as one would have expected." This is borne out by the photograph included in the paper. I searched the AOU files for *Gygis alba* and could find no indication that the conclusion of Wingate and Watson (1974) was disputed, so it appears that the change of the identification of the Bermuda bird to *alba* was merely an error introduced into AOU (1998).

Regarding changes to the Checklist if this 3-way split is adopted, the name of the species that breeds in the Hawaiian Islands would change from *G. alba* to *G. candida*, and *G. microrhyncha*

would be added to the Checklist based on the single specimen from Hawaii detailed in Olson (2005). Whether *G. alba* should be retained on the Checklist is less clear. The bird from St. Croix (photos at <https://www.birdscaribbean.org/category/story/>) was not identified except as *G. alba sensu lato*. As noted above, these photos appear to show an individual of the *alba* group, but we generally require records like these to have gone through committee review or peer review/publication before accepting them. However, there does not appear to be a bird records committee for the US Virgin Islands, and it's not clear whether this record will be published in a traditional format, so we may need to assess the record ourselves.

Consequently, please also provide an informal vote on the following, which if informally approved will be the subject of a more formal proposal:

(c) accept the record of *G. alba (sensu lato)* from St. Croix as pertaining to the taxon *alba* (whether as a subspecies or species *sensu stricto*).

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Submitted by: Dr. H. Douglas Pratt, Research Curator Emeritus, North Carolina Museum of Natural Sciences dpratt14@nc.rr.com; Dr. Eric A. VanderWerf, Director of Science, Pacific Rim Conservation eric@pacificrimconservation.org; and Storrs L. Olson (posthumous contributor)

Date of Proposal: 5 September 2024

Two appendices appear on the following pages:

Appendix 1. Manuscript by Storrs L. Olson: "Systematics of the White Terns, genus *Gygis* (Laridae)"

Olson *Gygis* 1

Systematics of the White Terns, Genus *Gygis* (Laridae)

Storrs L. Olson

The White ^{or Fairy} Terns of the genus *Gygis* are, as their name implies, nearly immaculate, white, oceanic terns with a circumtropical distribution. They are remarkable for their habit of building no nest and laying their single egg on a ~~bare~~ branch of a tree. Most modern works, beginning with Peters (1934) and including the latest systematic revisionary study (Holyoak and Thibault, 1976), list all forms of the genus under the single species *Gygis alba* Sparrmann. This is, as I hope to show, an oversimplification, as the genus certainly contains at least two species; in the absence of knowledge of the relationships of two long-separated, allopatric forms, it is actually preferable to recognize three species.

The present study was initiated over twenty years ago when John Farrand and I planned a revision of the genus and accordingly measured all the specimens in the American Museum of Natural History and the National Museum of Natural History, Smithsonian Institution, which include large series from the Whitney South Sea Expedition and the Pacific Ocean Biological Survey (POSB), respectively. The work was postponed and much of it was made redundant by the appearance of the revision by Holyoak and Thibault (1976), for which reason it was never completed.

In nearly two decades subsequently, however, there has been little or no improvement in understanding of ^{systematics} within the genus *Gygis*. There still remains important unpublished information concerning specimens collected by the POSB and furthermore, there has been no attempt to explain the patterns of distribution of the forms of *Gygis* and their possible evolutionary development. Thus, I felt that further review and interpretation was justified.

Remarks on the Genus *Gygis*

The genus *Gygis* has been recognized as distinct from other terns by almost all authors. It is usually placed in the vicinity of the noddies of the genera *Anous* and *Procelsterna*, which are also strictly oceanic. Moynihan (1959:25), however, merged *Gygis* with *Anous*, his only justification being that *Gygis* "is similar to the dark noddies in several significant displays, as well as being connected with them by the Blue and Gray Noddies [*Procelsterna*]." He dismissed the peculiar nesting habits of *Gygis* as being "only an exaggeration of the arboreal habits of such species as the Black Noddy." On the other hand, Schnell (1970:296), in his morphological analysis of the Laridae, found that "the implied cladistic affinities of *Gygis alba* with the *Anous* terns have no support in the skeletal or external morphological characters I examined." Hoffmann (19XX) was even more emphatic in separating *Gygis*, which he kept as a distinct genus allied with the typical terns, from the noddies, which he placed in a separate family as the sister-group of the rest of the Laridae [CHECK THIS].

I fully agree that Gygis should remain as a distinct genus and that it is not particularly closely related to Anous (which should include Procelsterna). ^{particular} ^{of the many osteological differences between Gygis and Anous,} ^{particular} points of importance are the proximal end of the humerus and the tarsometatarsus. The humerus in Anous has a single, truly pneumatic opening in the tricripital area, whereas Gygis has two non-pneumatic tricripital fossae, though their configuration is quite distinct from that in typical terns. The tarsometatarsus in Gygis is relatively the shortest of all the terns, whereas in Anous it is the longest. Both characters are probably primitive in Anous.

The Major Groups Within Gygis

Populations of Gygis fall into three major groups exhibiting two very different external morphologies differing in the shape of the bill, extent of loreal feathering, pigmentation of primary rachides, and tail shape, the characters having previously been outlined by Wingate and Watson (1974) and Holyoak and Thibault (1976).

In the Atlantic populations the bill appears relatively shallow at the base, with little bluish coloration, the feathers of the lores extend forward in a point relatively near to the nostrils, there is little pigmentation in the primary rhachides, and the tail has a relatively shallow fork. The name Sterna alba Sparrmann 1786, applies to these populations. Mathews (1912) restricted the type-locality to Ascension Island on the grounds that Sparrmann's illustration indicated an Atlantic bird. Lönnberg (19xx) later confirmed that the actual type-specimen had the morphology of Atlantic birds.

The populations in the Indian Ocean and most of the Pacific have bills that appear much deeper, with an extensive bluish area at the base, the anterior margin of the loreal feathering is a sharp diagonal that does not extend in a point towards the nostrils, the primary rhachides are distinctly black, and the tail is much more deeply forked. The oldest name applicable to birds with this morphology is Sterna candida Gmelin 1789---type-locality Christmas Island in the Line Island group [CHECK].

A third major group within Gygis occurs mainly in the Marquesas and consists of birds with essentially the morphology of Atlantic G. alba, but that are much smaller, with an even more slender appearing bill and more shallowly forked tail. The name Gygis microrhyncha Saunders 1876 is used for these birds, with the type-locality restricted to the island of Tahuata by Holyoak and Thibault (1976).

Distribution and Introgression in G. microrhyncha

The small terns of most of the islands of the Marquesas are so conspicuously different from those of the surrounding island groups of the Pacific that in the years following their description as Gygis microrhyncha by Saunders (1876) they were maintained as specifically distinct. Hartert (1927), followed by Peters (1934), listed G. microrhyncha as a subspecies of G. alba. Wetmore (1939:6) dissented, stating that "I

consider microrhyncha a full species, distinct from the wide ranging alba."

Nevertheless, lumping of species was the prevailing systematic trend in ornithology for decades to come and all forms of Gygis continued to be regarded as constituting a single species. [= almost or definitely a superspecies; thank you, Ernst]

The range of Gygis microrhyncha is generally thought to include only the Marquesas [CHECK MORE MODERN REFS E.G. HARRISON], within which it occupies all of the larger islands. Baker (1951) showed that birds from the small islands of Hatutu and Motane (=Mohotani) differed from those from the larger islands and he considered them to be intergrades between microrhyncha and "alba". Holyoak and Thibault (1976) likewise noted differences among the birds from Hatutu, the neighboring northerly island of Eiao, and Mohotani. ^(Figure 1) Specimens that they identified as pure microrhyncha, pure candida, and intergrades between the two were identified from all three islands save Eiao, from which there were no specimens of pure candida. I also examined these specimens and generally agree with the conclusions of Holyoak and Thibault, although I would have called most of the specimens from Hatutu pure candida rather than intergrades. Regardless, both forms occur in the Marquesas. Hatutu and Eiao are isolated northwestern outliers, whereas Mohotani lies in the midst of the larger islands of the archipelago.

please find enclosed a Marquesas map for your use (oops, just mailed back the maps; I'll get it for you in Albany)

Specimens collected by the POSB as well as the fossil record, show that Gygis microrhyncha occurs, or occurred, outside the Marquesas. I identified one specimen from Malden Island in the Line Islands (USNM 497599), one from Gardner Island in the Phoenix group (USNM 5430070), and one taken at sea at 2° 29' S 162° 30' W (USNM 543075---this is far from the Marquesas and near the Lines(?)) as pure G. microrhyncha. Two more birds from Malden (USNM 497601, 497605) and three from Hull Island (USNM 495592-4) appear to be intergrades between G. microrhyncha and G. candida. Those from Hull I. have bills like G. microrhyncha but tails that are intermediate. Hull = Orona

as pure G. microrhyncha
= Nukumaroro
(= near Jarvis)
in Lines betw. Phoenix + Malden but to N.

Steadman (REF) has identified bones of G. microrhyncha from (WHERE?). My notes mention six specimens (USNM 493990-4, 496025) from Christmas I. in the Cooks (specifically noted that this is not Xmas I. in the Lines) that appear to be candida but small. I need to look at these again. What the hell is Christmas Island of the Cooks?

no such thing; who collected them? I'll double check when I get to Albany (next week) if one of motus on Penrhyn might be called Christmas (I doubt it).
Variation within G. candida

I apply the specific name G. candida to all populations of Gygis in the Indian and Pacific Oceans except those belonging to G. microrhyncha. Several subspecies had been proposed within this group, but Wetmore (1939:6) noted the apparent uniformity of these terns throughout the Pacific and stated that "it seems probable that too many forms of the fairy tern have been recognized."

In their revision, Holyoak and Thibault (1976) concluded that there were no consistent mensural differences in any of the populations of G. candida that would permit division into subspecies. Their paper may be consulted for a list of synonyms. John Farrand and I measured many, if not most, of the same specimens, supplemented by the large series from the POSB in the Smithsonian collections that were not included in Holyoak and Thibault's study. Whereas it would not be particularly useful to present our statistics, as they involve so much duplication, it is worth recording that we reached the identical conclusion---that no subdivision of G. candida can be made on size. The provenance and number of specimens that we analyzed to reach this conclusion are as follows: Indian Ocean (Rodriguez, Seychelles, Aldabra) (36), Carolines (27), Marianas (29), Bismarks (4), Solomons (4), Marshalls (46), Gilberts (17), Norfolk and Kermadecs (24), Fiji, Samoa, Tonga, Tokelaus (36), Society Is. (36), Cook Is. (Suvarrow) (12), Tuamotus (111), Phoenix Is. (42), Line Is. (59), Henderson, Pitcairn, Ducie, Oeno (43), Austral Is. (26), Northwestern Hawaiian Is., Johnston, and Wake (75), Clipperton and Cocos Is. (11).

if you have the data, make a table; it's so rare now to see published measurements

On other than mensural characters, Holyoak and Thibault (1976) recognized a new subspecies, G. candida leucopes [sic---a garish vox hybrida] for the birds of Henderson Island and Ducie, with those of Oeno apparently consisting of a mixture of G. c. leucopes, G. c. candida, and intermediates. The new subspecies was characterized as have the black orbital ring reduced to a spot in front and behind the eye, and in having the feet creamy white to pale blue rather than grayish-blue. ~~We had~~ overlooked these differences but on re-examining specimens they seem to be consistent.

Farrand + I, in conversation on mensural characters

Variation in G. alba of the Atlantic

True Gygis alba occurs only at four islands in the South Atlantic---Ascension (the restricted type-locality), St. Helena, Fernando de Noronha, and Trindade (South Trinidad of many authors and often misspelled Trinidad). There is considerable size variation between birds of these four islands, but with sufficient overlap that nomenclatural recognition is probably not warranted except possibly in the case of St. Helena.

The only other name available for an Atlantic population is G. a. crawfordi Nicoll (190x) of Trindade. These birds are quite the largest of the four Atlantic populations. Those of Ascension and Fernando de Noronha are intermediate and inseparable from one another, while those from St. Helena are much the smallest. Specimens from St. Helena are unfortunately few but those available are either smaller than all other or overlap only with the smallest individuals from Fernando de Noronha. There is no overlap whatever between the birds of St. Helena and Trindade. About 70% of Trindade birds are separable from those of Fernando de Noronha and Ascension. See Figure. Need to play with this a bit more etc.

an Atlantic map would be nice

*↓
or table?
need to see the data*

Evolution in Gygis---Interpretation of the Pattern and Systematic Conclusions

Systematics in the White Terns of the genus Gygis is clearly more complicated than a matter of a single geographically variable species. I interpret the available information as indicating a probable evolutionary history as follows.

The original form of Gygis would have resembled G. alba and G. microrhyncha, and may have had the approximate circumtropical distribution that the genus has today. A second form G. candida, with different feathering and coloration of the bill and more deeply forked tail, then arose either in the western Pacific, or more likely in relative isolation in the Indian Ocean. This form has spread eastward, intergrading with, and eventually swamping out, the original species. In the far south G. candida has spread as far east as Easter Island, and in the north has entered the Hawaiian archipelago and crossed as far as Cocos Island (Costa Rica) and Clipperton. Some of these islands were perhaps never inhabited by the original G. alba/microrhyncha stock.

This process of replacement is still incomplete in the central part of the eastern Pacific, as remnants of G. microrhyncha or intergrades have persisted at least until recently in the Phoenix and Line Islands and have evidently only recently relinquished the Cooks. The last real holdout of the original Gygis stock in Pacific is the Marquesas, where G. microrhyncha predominates. Nevertheless, birds with G. candida genes have essentially taken over the northwestern outliers of Hatutu and Eiao, and have managed to take hold on tiny Mohotani in the midst of G. microrhyncha, perhaps somehow being facilitated by the small size of the island.

Baker (1951:177) viewed G. microrhyncha as an incipient species that was evolving in the Marquesas and that was "tending toward complete reproductive isolation." Instead we now see it as a relict of a once much more widespread primitive stock that is in danger of being supplanted altogether. The relationship of G. candida to G. microrhyncha is clearly not that of geographical subspecies, but of a genetically more aggressive species swamping out another. A perhaps analogous case is that of the Blue-winged Warbler (Vermivora pinus) hybridizing with and swamping out the Golden-winged Warbler (V. chrysoptera) in eastern North America (Gill REF). Separate species status for each of these entities much better reflects their history and status, as well as facilitating information retrieval.

Gygis alba in the Atlantic is also evidently a relict, preserved temporarily from the G. candida onslaught by its isolation from the Indian Ocean by the African continent. Attack could come from the other direction, however, as G. candida has once reached Bermuda (Wingate and Watson 1974), presumably by crossing the Central American isthmus from the Pacific. How are we to regard G. alba in relation to

good stuff

[I haven't looked at the pre-human Gygis from 'Eua. I will, however, next time at USNM]

G. microrhyncha? If the evolutionary progression outline above has any validity, they are more closely related to each other than either is to G. candida. Yet they differ considerably in size and in the forking of the tail. Furthermore, they have presumably been isolated from each other for as long as it took G. candida to evolve and spread throughout its present range and could conceivably be more genetically incompatible than are G. microrhyncha and G. candida. This might be a case where the superspecies designation would be appropriate, though I hate to suggest it considering how variable, inconsistent, and erroneously that term has been applied in the past. I therefore recommend the following nomenclature for the taxa of the genus Gygis:

} beautiful

Gygis [alba] alba Sparrmann
Gygis [alba] microrhyncha Saunders
Gygis candida candida Gmelin
Gygis candida leucopes Holyoak and Thibault.

Acknowledgments

Farrand, AMNH, USNM, Steadman, Claudia Wilds.

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I'll send appropriate papers when I get to Albany.

Appendix 2. Letter from Claudia Wilds regarding the Olson manuscript

CLAUDIA WILDS
3331 N STREET, N.W.
WASHINGTON, DC 20007, USA
Tel: +1-202-333-5769 Fax: +1-202-342-3719

29 May 1994

Storrs L. Olson
Wolfson College
Oxford OX2 6UD, U.K.

Dear Storrs,

You can imagine how pleased I was to get your letter and the manuscript. I would have answered sooner, but I was in the Dry Tortugas when it came and then coping with a time-consuming house guest. This week was the first chance I had to review at least some of the *Gygis* skins.

There seemed no point in writing you until I had done that and reread Holyoak & Thibault and Wingate & Watson and the appropriate section of Baker), and then Murphy's entertaining account in *Oceanic Birds of South America*. I haven't looked at your other references, but I don't know of anything else that is relevant. I looked up *Gygis* on the CD-ROM *Wildlife Review* disk in the library (updated to Feb. 1994), as well as in the most recent issues and in the *Zoo Record* and found nothing since H&T on taxonomic matters. As for range, Harrison 1983 lists only the Marquesas for *microrhyncha*, as do Holyoak and Thibault 1984. Pratt, Bruner, and Berrett (1987) say, however: "Once thought to be endemic to the Marquesas Is. (Eiao to Fatuhiva), now known to occur in Kiribati (Phoenix Is, Line Is.) where supposed hybrids or intergrades with *G. alba* have also been found." Of course they cite no reference.

I had time this week to look only at the skins of *microrhyncha*, *microrhyncha x candida*, *alba*, and *monte*. I have no quibble with anything except rachis color. In each of these groups I found rachides that were either golden-brown, dirty golden-brown, golden-brown darkening to black distally, or black (color consistent on each bird). Granted I haven't looked at any Pacific *candida* yet. I am going to spend a few days at the AMNH next week and will try to broaden my sample of these groups for the benefit of my own understanding. (God knows there are enough Pacific *candida* at the USMN.)

In reading your hypothesis that *microrhyncha* is being swamped by *candida* I was immediately reminded of Black Stilt in New Zealand being swamped by what Sibley & Monroe call White-headed Stilt.

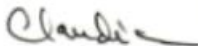
Don't forget to add Baker 1951 to your list of references.

I can see that you need to get back here to turn this paper into final form, but I'd be glad to check what I can for you.

I don't expect my book to go to press before late summer 1995 at the earliest, so I am hopeful that I will not need to cite the paper as only MS (but that's better than "in prep.!).

Would you like to explain why you put "Sic transit gloria mundi" on the tags of the St. Helena skins? I know why I might have done it, given the behavioral characters of the genus, but I don't have enough occasion to look at your skins often enough to know whether you often succumb to such commentary.

Best regards,



Treat *Myiarchus flavidior* as a separate species from Nutting's Flycatcher *M. nuttingi***Background:**

Myiarchus nuttingi flavidior was described by A. J. van Rossem, as *Myiarchus cinerascens flavidior*, in 1936. At that time, most workers on *Myiarchus* (i.e., Griscom 1934, van Rossem 1936, Dickey and van Rossem 1938) considered *cinerascens*, *inquietus*, and *nuttingi* as conspecific, based primarily on morphological evidence. However, Lanyon (1961), using morphology, vocalizations, habitat preferences, and mate preference, demonstrated that *nuttingi* and *flavidior* were not forms of *cinerascens*, and that this complex instead comprised two species, Ash-throated Flycatcher (*M. cinerascens*) and Nutting's Flycatcher (*M. nuttingi*). Lanyon (1961) considered *M. cinerascens* to have two subspecies: *M. c. cinerascens* from the western United States and the Mexican Plateau and *M. c. pertinax* in Baja California; and *M. nuttingi* to have three subspecies: *M. n. inquietus* from western Mexico, and *M. n. nuttingi* and *M. n. flavidior* from Middle America. This treatment was accepted by Traylor (1979) and has since been followed in all major world taxonomies (Clements et al. 2024, Gill et al. 2024, HBW and BirdLife International 2024). However, as Howell (2012) pointed out, Lanyon's focus was on demonstrating *M. cinerascens* to be distinct from *M. nuttingi*, not on describing vocal or morphological differences among the three subspecies of *M. nuttingi*.

Joseph et al. (2004) estimated a phylogeny for 19 of the 22 extant *Myiarchus* species and found support for two clades; they hypothesized that two of the remaining three unsampled taxa (*M. nuttingi* and *M. magnirostris*) likely belonged to Clade I and the third (*M. apicalis*) to Clade II. Sari and Parker (2012), who did sample *M. nuttingi*, used one nuclear and three mitochondrial regions to estimate the phylogeny of Clade I as presented in Joseph et al. (2004).

A 2013 proposal to split Nutting's Flycatcher into two species: *Myiarchus nuttingi* and *M. flavidior* (NACC 2013-B-2), based on vocal work presented in Howell (2012) was not accepted. Most committee members agreed that the evidence presented was suggestive of the validity of this split, but felt that more work, including a wider sampling of genetic, vocal and morphometric data, was needed. Here we summarize additional vocal and distributional data presented in Howell et al. (2024), with additional vocal analysis.

New information:

Since 2013, little has been published in peer-reviewed literature that is relevant to the taxonomy of this complex. However, hundreds of photos and many sound recordings have been archived in digital libraries like [Macaulay Library](#) and [xeno-canto](#)—creating an opportunity to study the vocalizations of these taxa, while keeping in mind that some audio recordings and photos may be misidentified, as highlighted by Howell et al. (2024).

Vocalizations

Howell et al. (2024) published an article detailing analyses of calls and songs of the complex from throughout the range, and with representatives from all three subspecies groups. All calls

and dawn songs of each subspecies group were inspected and described using phonetic English rendering (Figs. 11–12 in Howell et al. 2024). Unless otherwise stated, the following is from Howell et al. (2024).

Calls. *M. n. flavidior* has a unique long piping twitter not given by other members of the Nutting's complex (Fig. 1). Within *Myiarchus*, the Dusky-capped Flycatcher (*M. tuberculifer*) has a similar call, but in that taxon it is usually shorter and always preceded by one or more emphasized introductory notes (e.g. [ML18974](#)) not given by *M. n. flavidior*. This call is given very often; if the taxon is present, you likely will hear this call (RJ, JVD, pers. obs.). A common call, collectively described as *wheep*, is given by all subspecies in the group but is distinctly different in each, and thus it is phonetically described with slight spelling variations (Fig. 1). In *M. n. flavidior*, this call is longer and smoothly overslurred and described as *wheeéu*; it sounds like the plaintive, drawn-out whistle of *M. tuberculifer*, whereas in *M. n. nuttingi* it is acutely overslurred and described as *weep*. The short twitter, variably described as *kwidik* or *kwirri*, a presumably homologous call given by many *Myiarchus*, is unknown in *M. n. flavidior*. Additional examples of the typical calls of both taxa can be heard and compared on [Macaulay Library](#) and [xeno-canto](#): *M. n. flavidior* (e.g., [ML555210451](#) and [XC488495](#)) and *M. n. nuttingi* (e.g., [ML621331041](#) and [ML561650901](#)).

Songs. All representatives of the Nutting's complex typically sing only at dawn, and briefly at dusk. Their songs are repetitive and alternate among various notes and short phrases about every 1–3 seconds, with the pace averaging slower in *M. n. flavidior* than in *M. n. nuttingi* (Fig. 2). The songs of each taxon usually include slight variations on the taxon-specific *wheep* calls and other components that are often disyllabic, e.g., the *wh'beéeu* of *M. n. flavidior* and the clipped *wee'peu* phrase of *M. n. nuttingi* (Fig. 2). Note that both in *M. n. flavidior* and *M. n. nuttingi*, the disyllabic components appear and sound unique to each taxon as well (Fig. 2). Additional examples of the typical songs of both taxa can be heard and compared on [Macaulay Library](#) and [xeno-canto](#): *M. n. flavidior* (e.g., [ML28345211](#), [ML616428480](#), and [XC28755](#)) and *M. n. nuttingi* (e.g., [ML615537814](#) and [XC608120](#)).

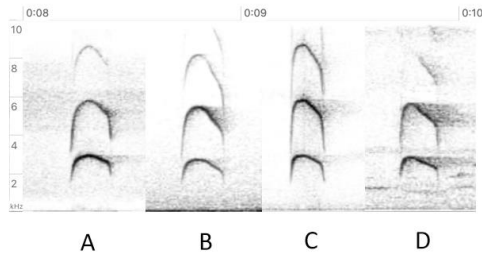
Furthermore, we analyzed the duration and the low, high, and peak frequencies of the song's disyllabic components using linear mixed models. Using recordings archived in Macaulay Library, we extracted data for 5–23 disyllabic components per individual of four individuals for each taxon. *M. n. flavidior* produces disyllabic components that are longer ($p < 0.0001$; Fig. 3A) and with higher low frequency ($p < 0.0001$; Fig. 3B) than *M. n. nuttingi*. We did not find differences in the peak frequency nor in the high frequency. The results of this analysis were presented at the II Ornithological Congress of the Americas in August 2023 in Gramado, Brazil.

In suboscines, the group to which *Myiarchus* flycatchers belong, vocalizations are innate, so are strongly indicative of evolutionary distance and reproductive isolation among taxa.

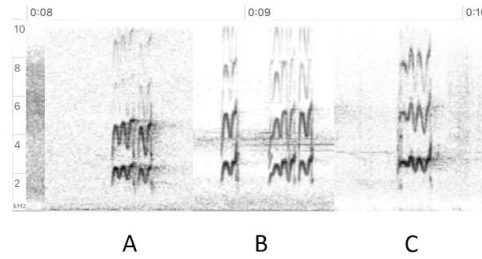
Plumage

In Honduras, where *M. n. flavidior* and *M. n. nuttingi* occur sympatrically, they are field-separable based on plumage, with care. The dark shaft stripe along the outer rectrix is typically much wider in *M. n. flavidior* compared to *M. n. nuttingi* (Figs. 4–5), although many authors, e.g.,

nuttingi

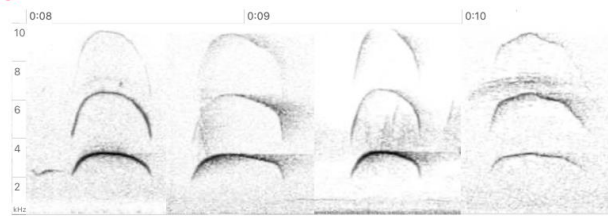


A B C D
weep acutely overslurred, clipped

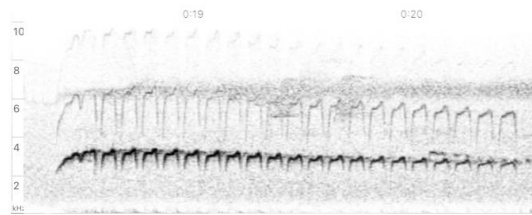


A B C
kwirri burrier, lower, less emphatic than *kwidik* of *inquietus*

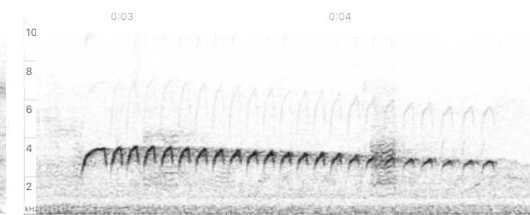
flavidior



A B C D
wheeéu smoothly overslurred, not clipped



A



B

piping twitter, no counterpart in *inquietus* or *nuttingi*

Figure 1. Sample sonograms of calls of *M. n. flavidior* and *M. n. nuttingi*. These sonograms were generated using the following recordings. For *M. n. flavidior*, in order of appearance, from left to right: [ML19736](#), [ML90243761](#), [ML7730](#), [ML67329121](#), [ML19735](#), and [ML143235461](#). For *M. n. nuttingi*, in order of appearance, from left to right: [ML19729](#), [ML169082521](#), [ML215465](#), [ML425420061](#), [ML64455591](#), [ML542230341](#), and [ML19728](#). (Figure 11 from Howell et al. 2024.)

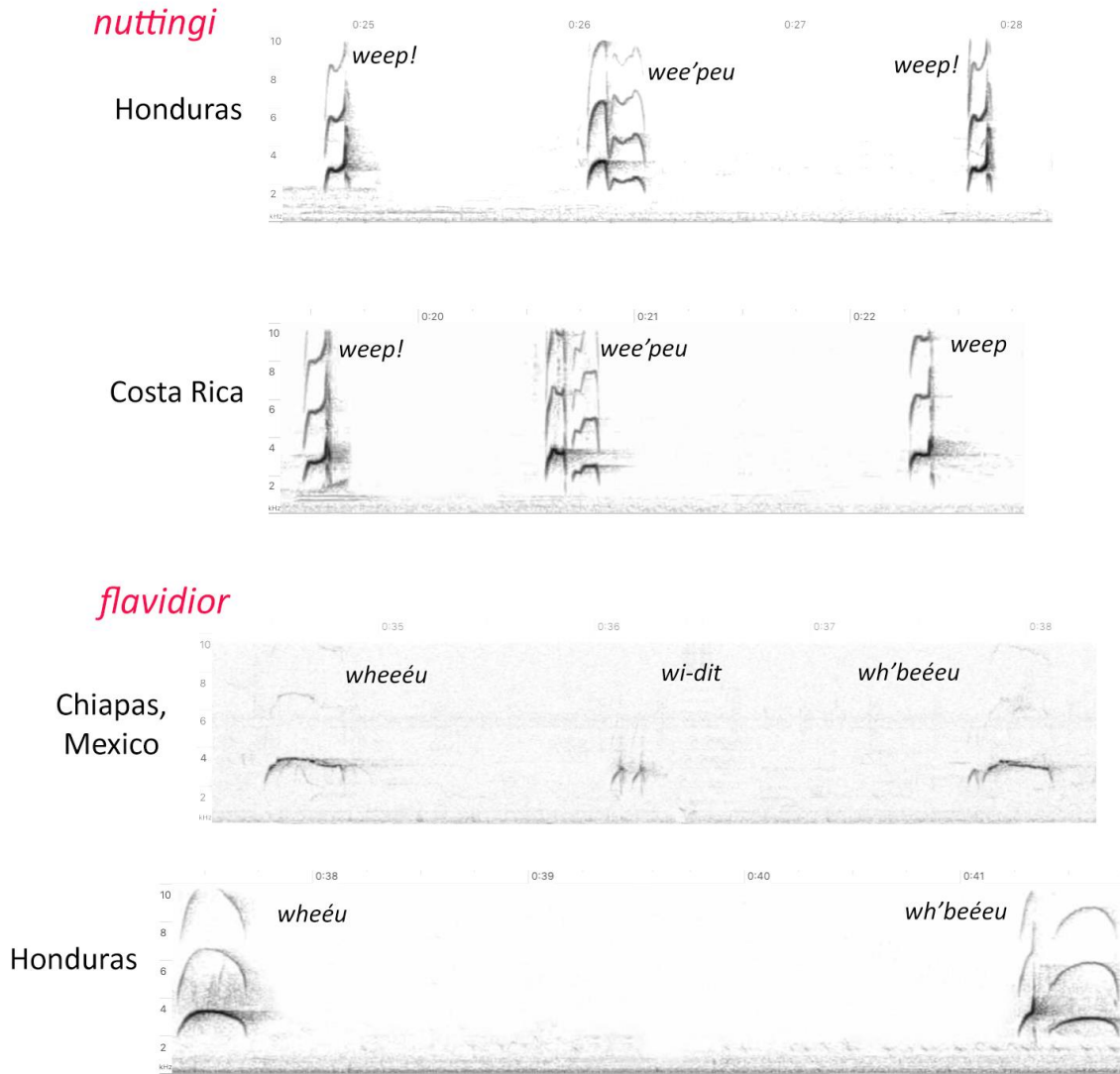


Figure 2. Sample sonograms of the dawn song of *M. n. flavidior* from Chiapas, Mexico ([ML7720](#)) and Honduras ([ML7730](#)) and of *M. n. nuttingi* from Francisco Morazan, Honduras ([ML553557801](#)) and Guanacaste, Costa Rica ([ML164028](#)). Note that no song elements are shared between taxa. (Figure 12 from Howell et al. 2024.)

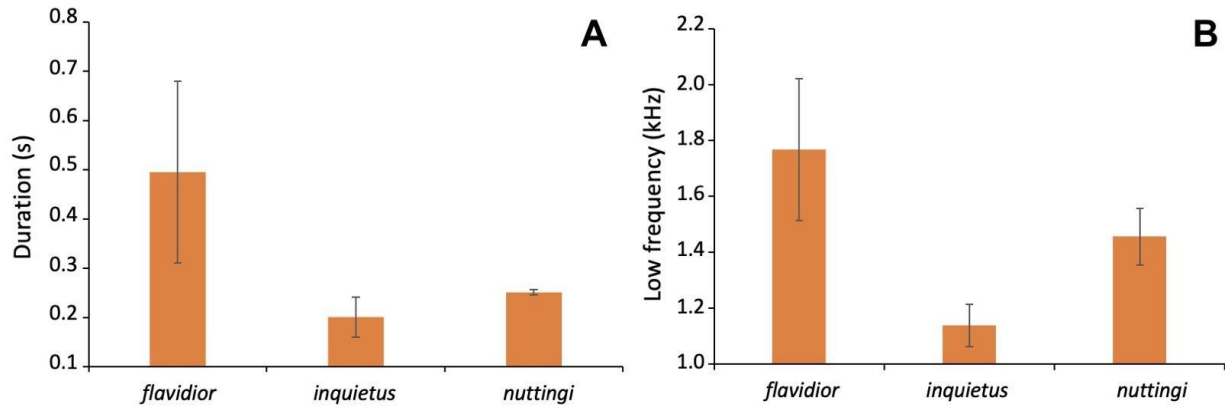


Figure 3. Comparison of the duration (A) and low frequency in the disyllabic components in the dawn songs of *M. n. flavidior* and *M. n. nuttingi*.

Lanyon (1961) and Howell et al. (2024), have noted intraspecific variation in the rectrix patterns of *Myiarchus* species. In comparable plumage, *M. n. flavidior* also has subtly brighter yellow underparts than *M. n. nuttingi* (Lanyon 1961, Dyer and Howell 2023). The definitive identification of atypical individuals within each taxon can be accomplished by voice (Howell et al. 2024); habitat type may also be a stronger identification clue (see Additional considerations).



Figure 4. Typical (left and center) and atypical (right) *M. n. flavidior*. In all cases, the identification was confirmed by voice. Atypical individuals are less extensively dark on outer rectrices, but still more so than classic *M. n. nuttingi*. (Figures 8–10 from Howell et al. 2024.)



Figure 5. Typical (left and middle) and atypical (right) *M. n. nuttingi*. In all cases, the identification was confirmed by voice. Atypical individuals are extensively dark on outer rectrices, but still less so than classic *M. n. flavidior*. (Figures 5–7 from Howell et al. 2024.)



Figure 6. Photos of the specimens collected in El Salvador and sampled for molecular material by Sari and Parker 2012 (left: KU109695; right: KU109682). Tail patterns indicate that these two specimens likely belong to *M. n. flavidior*, the only taxon of this complex known to occur in El Salvador.

Molecular data

Although Howell et al. (2024) did not carry out any additional molecular work, they did contact Eloisa Sari to clarify which subspecies of *M. nuttingi* were used for the research presented in Sari and Parker (2012). A photographic examination by Howell et al. (2024) of two of the three El Salvador specimens used by Sari and Parker (tissue 9281 is from round skin KU 109682 and tissue 9288 is also from round skin KU 109695, but tissue 9314 was obtained from a skeleton, KU 109265) shows that these belong to *M. n. flavidior*, as evidenced by a broad dark shaft stripe along the outer rectrix (Fig. 6). Furthermore, no other subspecies is known from El Salvador, either from specimens (Dickey and van Rossem 1938) or vocally (Howell et al. 2024). Their Costa Rica samples were taken from blood collected from live individuals; no specimen, photographs, or vocal recordings exist from those individuals (Sari and Parker 2012; E. Sari, personal communication). However, the only confirmed subspecies from Costa Rica is *M. n. nuttingi* (Slud 1964). This strongly suggests that Sari and Parker (2012) did indeed sample *M. n. flavidior* and *M. n. nuttingi*, and they found that the two taxa were not monophyletic (Fig. 7). Although the node support values are not terribly strong, they also show a very deep split between the taxa, strongly indicative of species status (Sari and Parker 2012). Harvey et al. (2020) sampled *nuttingi* (from Costa Rica) and *inquietus* (from Sinaloa) but did not sample *flavidior*. These two subspecies of *M. nuttingi* (*inquietus* and *nuttingi*) were sister taxa, and the two were sister to *M. cinerascens*.

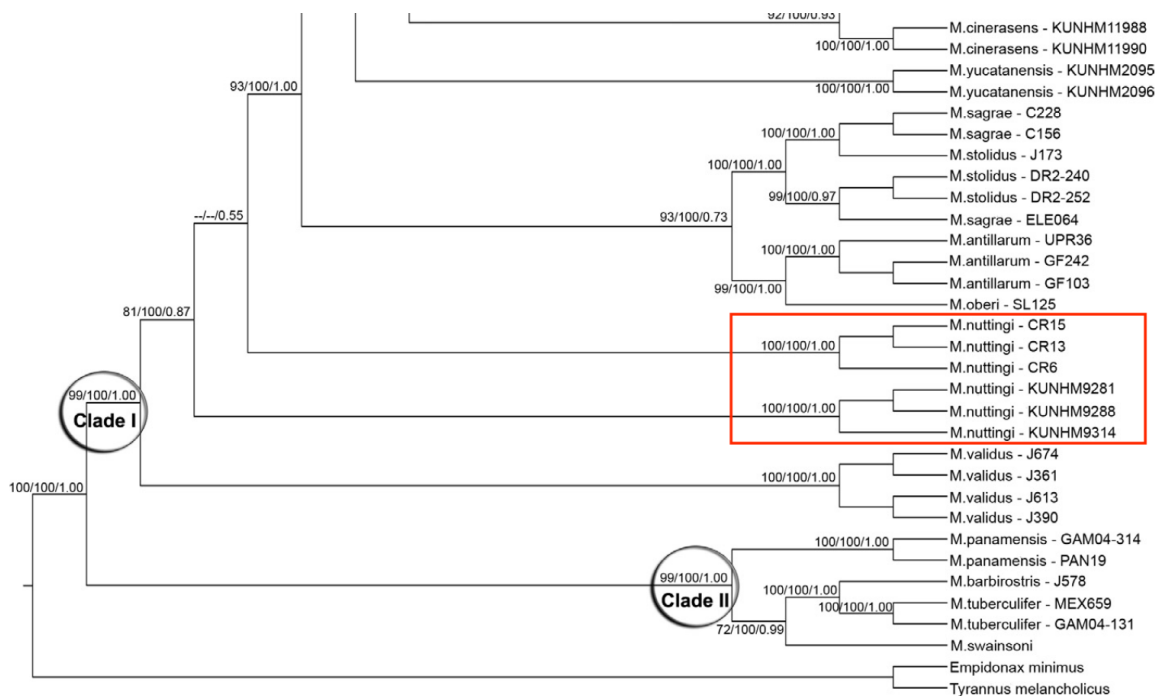


Figure 7. Phylogenetic distance between two “subspecies” groups of *M. nuttingi* (red box). (Figure 2 from Sari and Parker 2012.)

Additional considerations

As early as 2012, using field observations compiled during the previous decade, Steve Howell noted that both *M. n. inquietus* and *M. n. flavidior* were found in close proximity in Puerto Arista, Chiapas (Howell 2012). In the dense thorn forests in the foothills near Puerto Arista, he found only *M. n. inquietus*, whereas on the coastal plain, within sight of the hilly terrain, he found only *M. n. flavidior* inhabiting the open hedgerows in pasturelands. The observations of two distinct forms so close together without any evidence of interbreeding, or co-occurrence, suggests that the forms are parapatrically separated. Howell et al. (2024) indicated that in Honduras, specifically in Comayagua, Francisco Morazán, Valle, and presumably elsewhere in northern Central America, *M. n. nuttingi* occurs sympatrically with *M. n. flavidior*. In fact, Howell et al. (2024) found these two taxa less than one kilometer apart (Fig. 8). The two taxa also segregate by habitat type: whereas *M. n. nuttingi* prefers densely vegetated habitats (thorn forests, secondary shrubs, and edges) *M. n. flavidior* occupies relatively open habitats (Dickey and van Rossem 1938, Slud 1964; Fig. 9).

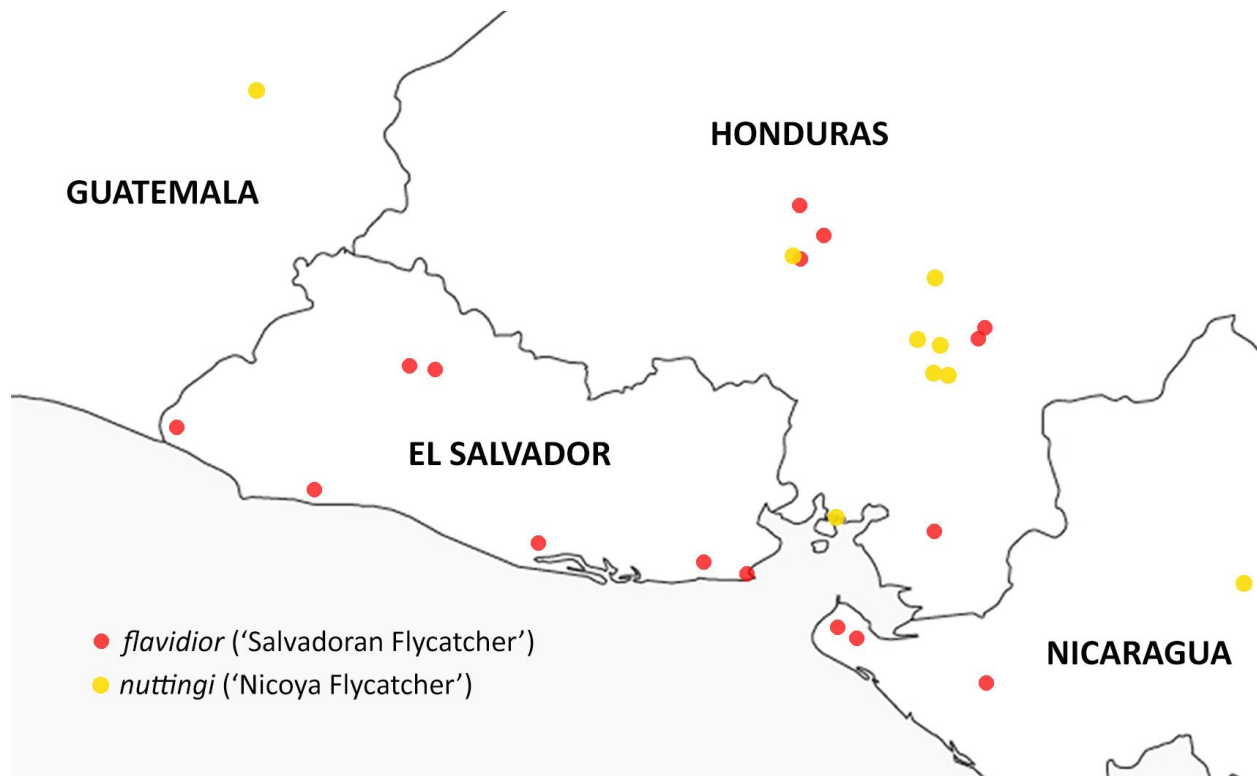


Figure 8. Map showing the spread of sample locations for the vocal analysis. Note that in Honduras, *M. n. flavidior* and *M. n. nuttingi* occur sympatrically, without interbreeding, in multiple locations. (Figure 1 from Howell et al. 2024.)



Figure 9. Photos showing habitat preferences. Top: open habitats utilized by *M. n. flavidior*; bottom: dense thorn forest utilized by *M. n. nuttingi*. All photos taken in Honduras. (Photos A and D from Howell et al. 2024.)

In El Salvador and Honduras, RJ and JVD, assigning individuals to subspecies using vocal and plumage characters, have not found any evidence of mixed pairs in any of the 95 locations where they found either of the subspecies to be present. Some of those locations have been surveyed 12–23 times and, based on audiovisual evidence, pairs are formed by *M. n. flavidior* or *M. n. nuttingi* only (e.g., *flavidior* in [Finca Ecoturística La Chaparrosa](#) and [El Jicarito Reserve](#) in Choluteca, Honduras, and *nuttingi* in [Sendero El Tinamú](#) and [Sendero a Poza La Sirena](#) in Francisco Morazán, Honduras). Furthermore, *M. n. flavidior*, *M. n. nuttingi*, and *M. n. inquietus*, show different behavior when confronted with vocalizations of each other or of their own songs and calls (Howell et al. 2024). In Honduras, although the behavioral responses have not been quantified, it is evident that all respond more strongly (i.e., approach more quickly, come closer, and produce more vocalizations) to their 'own' songs and calls compared to playback from the other subspecies group ($n = \sim 20$ pairs of *M. n. flavidior* and *M. n. nuttingi* combined). Finally, in places of sympatry, the vocalizations of *M. n. flavidior* and *M. n. nuttingi* are fixed, i.e., there is no evidence of hybridization (see [>80 recordings from Francisco Morazán, Honduras](#)). In conclusion, two functionally independent characters, vocalizations and habitat, are functioning as isolating mechanisms in these taxa, despite minimal differences in plumage.

Recommendation:

We strongly recommend the elevation of *flavidior* to species status. The two taxa are sympatric in multiple locations with no sign of interbreeding, have diagnostic songs that are as different as those between other species of *Myiarchus*, and occupy different habitats across a broad swath of Central America. The available genetic data also indicate that these may not be sister taxa. Morphological differences between these two taxa are relatively modest, as is true for many New World flycatchers, yet are appreciable in the field and thus offer additional taxonomic support.

English names

As suggested by Howell et al. (2024), we recommend the English common name Salvadoran Flycatcher for *M. flavidior*. This name reflects the core range of the taxon, is already used in Dyer and Howell (2023), and is in line with Clements et al. (2024), which lists it as “Nutting’s Flycatcher (Salvadoran)”. Furthermore, Salvadoran Flycatcher was described from an adult male collected from San Miguel, El Salvador, and highlights the range that is centered on the country of El Salvador. We believe the taxonomy of the remaining taxa in the Nutting’s Flycatcher (i.e., *M. n. nuttingi* and *M. n. inquietus*) requires further study, and thus we recommend keeping the English common name Nutting’s Flycatcher for that group. Because the molecular data indicate that *flavidior* may not be sister to the rest of the Nutting’s complex, a change to the English common name is not required for *nuttingi*.

Please vote on the following:

- A) Treat *flavidior* as a species separate from *M. nuttingi*
- B) Adopt the English common name Salvadoran Flycatcher for *flavidior*

Acknowledgments:

Many thanks to Mark Robbins for providing the photos of the specimens illustrated in Figure 6 and to Eloisa Sari for additional information on samples used in her phylogenetic analyses.

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Submitted by: Roselvy Juárez, John van Dort, and Oscar Johnson

Date of Proposal: 11 September 2024

Revise the linear sequence of *Dumetella* and *Melanoptila* (Mimidae)

Effect on the Checklist:

Approval of this proposal would change the current linear sequence of two monotypic genera in Mimidae to *Dumetella* followed by *Melanoptila*, in accordance with the most recent phylogeny.

Phylogenetic information:

The current linear sequence within the family Mimidae, adopted in 2013 (Chesser et al. 2013), follows a phylogenetic study that included complete representation of species in the family (Lovette et al. 2012). The phylogeny was based on sequences of mitochondrial DNA (ATP 6 and 8, ND2, CO1, CO2) and four nuclear introns (FGB-5, FGB-7, TGFB-2, RHO-1). The concatenated Bayesian phylogeny suggested that *Melanoptila* should be listed before *Dumetella*, since the *Melanoptila* split was recovered as more basal than the *Dumetella* split.

A more recent study examined the biogeographic and evolutionary history of the tremblers and thrashers of the Antilles (DaCosta et al. 2019). Although the Antillean tremblers and thrashers were the focus of this study, the authors included representatives of *Dumetella carolinensis* and *Melanoptila glabirostris* given that the two species are closely related to Antillean tremblers and thrashers. Based on 2223 loci generated through ddRAD sequencing, concatenated maximum likelihood and quartet-based species tree analyses recovered *D. carolinensis* and *M. glabirostris* as sister taxa with 100% support (Fig. 1).

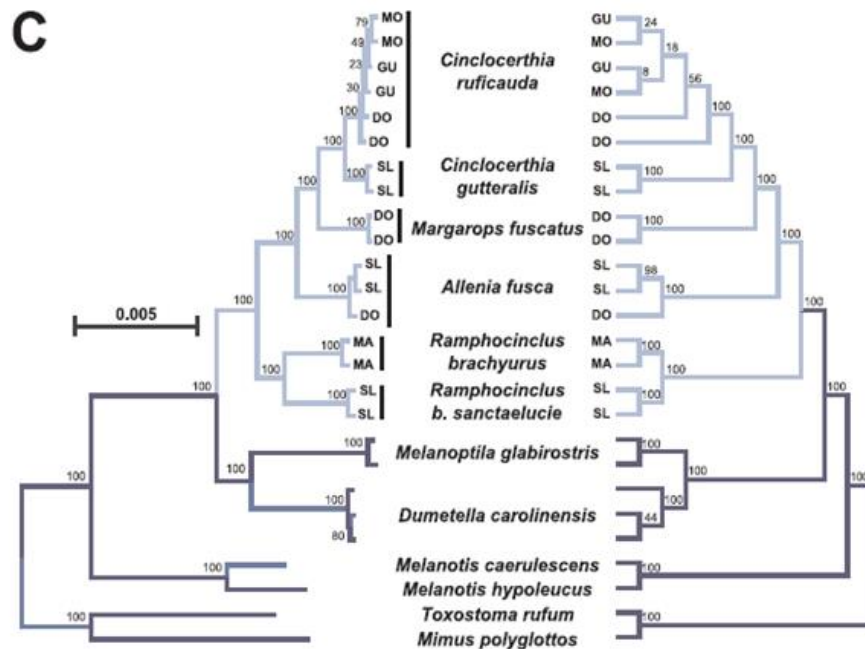


Figure 1. Phylogenetic hypotheses based on a concatenated matrix of 2223 ddRAD loci. Left: concatenated maximum likelihood. Right: quartet-based species tree. Numbers at nodes represent bootstrap percentages. MO: Montserrat; GU: Guadeloupe; DO: Dominica; MA: Martinique; SL: Saint Lucia. From Figure 2 of DaCosta et al. (2019).

New linear sequence:

Following the most recent phylogeny (DaCosta et al. 2019), a slight change in the current linear sequence of the taxa in Mimidae is recommended. The monotypic genus *Dumetella* should be listed before *Melanoptila* because they are sister taxa and *Dumetella* has the most northwesterly geographic range. The linear sequence of the Antillean tremblers and thrashers does not require any change.

Current linear sequence:

Melanoptila glabirostris
Dumetella carolinensis

New linear sequence:

Dumetella carolinensis
Melanoptila glabirostris

Recommendation:

I recommend acceptance of the new linear sequence; it is strongly supported by phylogenetic analysis of genomic data.

References:

- Chesser R.T., Banks R.C., Barker F.K., Cicero C., Dunn J.L., Kratter A.W., Lovette I.J., Rasmussen P.C., Remsen Jr. J.V., Rising J.D., Stotz D.F., and Winker K. (2013). Fifty-fourth supplement to the American Ornithologists' Union Check-list of North American birds. *The Auk*, 130(3), 558–571.
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Submitted by: Rosa Alicia Jiménez, Universidad de San Carlos de Guatemala

Date of proposal: 16 September 2024

Transfer Slaty-winged Foliage-gleaner *Philydor fuscipenne* to new genus *Neophilydor*

Note: This is a slightly modified version of SACC proposal 991, which passed unanimously. Note that the only species in our area currently placed in *Philydor* is *P. fuscipenne*.

Molecular phylogenies have revealed that the traditional genus *Philydor* is highly polyphyletic (Derryberry *et al.* 2011). Some issues have been solved in the past with the transfer of *P. ruficaudatum* and *P. lichtensteini* to *Anabacerthia*, and the transfer of *P. erythropterum* and *P. rufum* to *Dendroma*. However, the current genus *Philydor* is still not monophyletic because *P. erythrocercum* and *P. fuscipenne* are not closely related to *Philydor atricapillus*, the type species of the genus. The latter is more closely related to the genera *Heliobletus* and *Cichlocolaptes* than to the former. This has been shown with datasets of few loci (Derryberry *et al.* 2011) and next-generation datasets of UCE data (Harvey *et al.* 2020), in both cases with Bayesian posterior probabilities of 1.0 and bootstrap support of 100% (Figure 1).

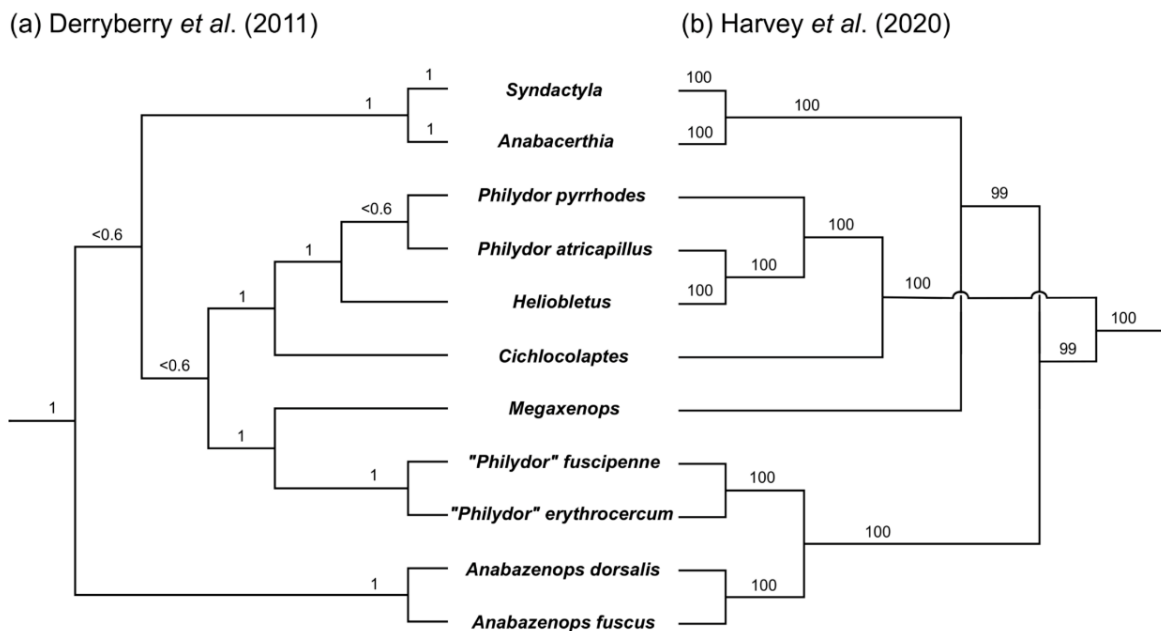


FIGURE 1. Phylogenetic trees (cladograms) of *Philydor* and select representatives from related genera based on (a) Derryberry *et al.* (2011) and (b) Harvey *et al.* (2020). Numbers above branches refer to (a) posterior probability values and (b) bootstrap values. Nomenclature follows Gill *et al.* (2023).

Figure 1. Phylogenetic relationships of *P. erythrocercum* and *P. fuscipenne* in trees of Derryberry *et al.* (2011) and Harvey *et al.* (2020). Figure from Sangster *et al.* (2023).

The exact affinities of the clade formed by *P. erythrocercum* and *P. fuscipenne* are not fully determined; at least there is a conflict between the Derryberry *et al.* (2011) tree, which shows them as sister to *Megaxenops*, and the Harvey *et al.* (2020) tree, which shows them as sister to

Anabazenops. In any case, they are estimated to be very divergent from either (10 and 6 million years, respectively), and phenotypically they don't resemble species from either genus: *P. erythrocerum* and *P. fuscipenne* have smaller bills, more elongated wings, more squared tails, and shorter tarsi compared to *Megaxenops* and *Anabazenops*.

Therefore, the most obvious solution is to separate this clade into its own genus. Given that there are no generic names available for this clade, Sangster et al. (2023) described the new genus *Neophilydor* for this pair of foliage gleaners. The new genus is neuter so the specific epithets remain the same: *Neophilydor erythrocerum* and *Neophilydor fuscipenne*.

Recommendation:

Without any sensible alternative available, I recommend the adoption of the new generic name *Neophilydor* for *erythrocerum* and *fuscipenne*.

References:

- Derryberry, E. P., S. Claramunt, R. T. Chesser, J. V. Remsen Jr., J. Cracraft, A. Aleixo, & R. T. Brumfield. 2011. Lineage diversification and morphological evolution in a large-scale continental radiation: the Neotropical ovenbirds and woodcreepers (Aves: Furnariidae). *Evolution* 65(10):2973-2986.
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Submitted by: Santiago Claramunt

Date of Proposal: January 2024, modified by Terry Chesser for NACC on 17 September 2024

Comments from SACC on Proposal 991:

Comments from Remsen: "YES. I've been aware of this one for quite some time, and a new genus name is required to maintain monophyletic genera (or to avoid merging a bunch of very distinctive, long-standing genera.)"

Comments from Robbins: "YES. This seems like a straightforward proposal given our current understanding. So, I vote yes for placing both taxa in the new genus."

Comments from Bonaccorso: "YES. Given their phylogenetic affinities and their lack of close relationship with "real" *Philydor* species, it makes sense to give them a new genus name."

Comments from Stiles: “YES for reasons clearly stated in the proposal and supported by various comments from other SACC members (and others).”

Comments from Lane: “YES. The phylogenetic reconstruction seems to necessitate the recognition of this new genus.”

Comments from Areta: “YES [for reasons given in the proposal].”

Comments from Jaramillo: “YES [for reasons given in the proposal].”

Comments from Zimmer: “YES, for reasons stated in the Proposal. We already knew that traditional *Philydor* was polyphyletic, and therefore, untenable. In this case, the recognition of a new genus for this clade is far preferable to merging the two species involved into either *Megaxenops* or *Anabaxenops*, not only because the exact affinities of the clade are unresolved due to conflicting data sets, but also because the clade has been shown to be highly divergent from either of the two putative closest genera. To merge *erythrocerum* and *fuscipenne* into either of these long-recognized genera, would, in my opinion, be the epitome of trying to force a square peg into a round hole, diluting the cohesiveness and informative value of either *Megaxenops* or *Anabaxenops*.”

Transfer Little Ringed Plover *Charadrius dubius* to *Thinornis*

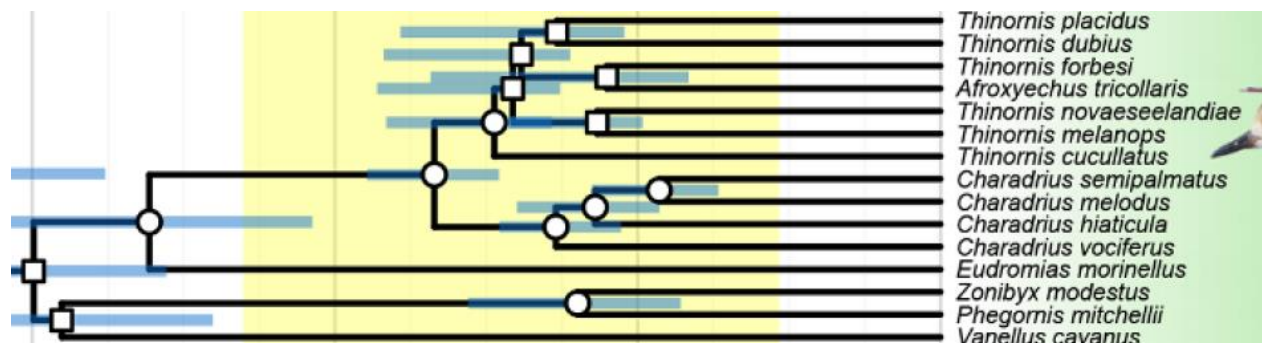
Background:

The transfer of Little Ringed Plover *Charadrius dubius* to *Thinornis* was previously considered as part of proposal 2024-A-3. In that proposal, Oscar, despite reservations based on the deep genetic divergence between two clades within the newly restricted genus *Charadrius*, tentatively recommended that we follow WGAC and not recognize *Thinornis*. The only species in our area that would have been placed in *Thinornis* is *C. dubius*; accordingly, we voted to keep *C. dubius* in *Charadrius* rather than transferring it to *Thinornis*.

In a later vote, however, WGAC agreed to adopt *Thinornis* for the species of *Charadrius* occurring mainly in the Old World. Dick Schodde argued for this additional change as follows:

I recommend we go a step further, and that is to split *Charadrius* into 2 genera: *Charadrius s.str.*, with 4 species centred in the New World except for *hiaticula*, and *Thinornis* with 7-8 species centred in the Old World. I give three reasons. First, the split between the two is relatively deep, dated between the mid Miocene and mid Oligocene (Barth et al. 2013; Černý & Natale 2022). Secondly, they represent separate zoogeographic radiations. Thirdly, while relationships are settled in New World *Charadrius*, they are very much unsettled in Old World *Thinornis*, with mini-radiations in Africa, Indo-Asia and Australasia, and weak support values for sister species that vary across phylogenies. Even within Australasia, the species *melanops* (*Elseyornis*) and *cucullatus* (*Thinornis*) are very different in appearance and ecology. The first is small with round-tipped wings and is freshwater-adapted, and the second is large, pointed winged and confined to sea shores and salt lakes. Christidis & Boles (2008, *Systematics and Taxonomy of Australian Birds*) placed them in separate genera! So subgeneric categories are likely to be needed for the different continental groups of *Thinornis s. lat.*, and these won't be available if *Charadrius s.str.* and *Thinornis s. lat.* are placed together in one genus *Charadrius*. That is because the subgeneric categories will be needed instead to distinguish between the deeper New World/Old World split.

Below is the part of the Černý and Natale (2022) tree showing the placement of *melanops* and the division of *Thinornis* and *Charadrius* (the yellow section is the Miocene; as noted by Dick, Barth et al. (2013) had estimated the division to date to the Oligocene):



Recommendation:

I recommend that we follow the revised WGAC decision to further split *Charadrius* and that we transfer *Charadrius dubius* to *Thinornis*.

References:

- Barth, J. M. I., Matschiner, M. & Robertson, B. C. (2013). Phylogenetic position and subspecies divergence of the endangered New Zealand Dotterel (*Charadrius obscurus*). *PLOS One*, 8(10), e78068. <https://doi.org/10.1371/journal.pone.0078068>
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Submitted by: Terry Chesser

Date of Proposal: 18 September 2024

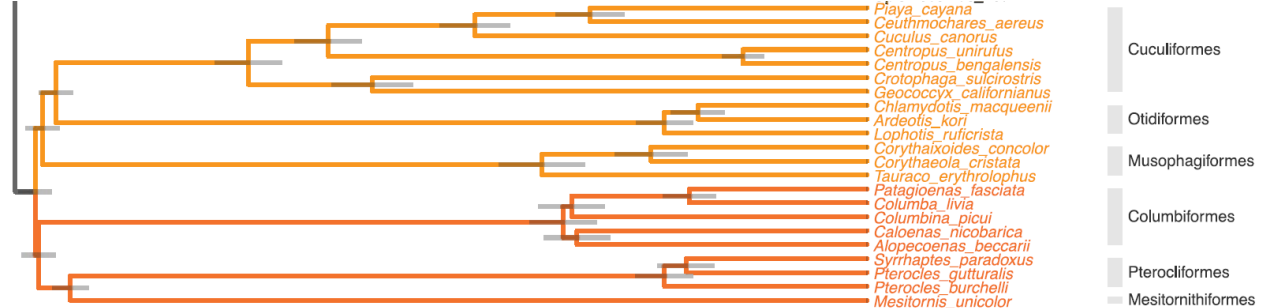
Make changes to our linear sequence of families and orders

Background and New Information:

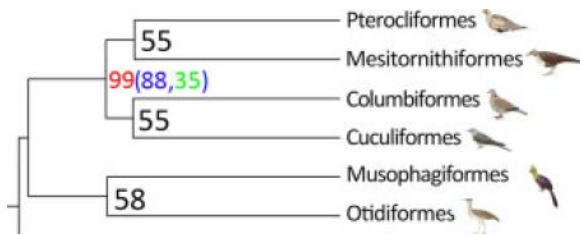
Stiller et al. (2024) recently published a family-level phylogeny based on whole genome sequencing. We compared the current NACC linear classification with the linear sequence that would be derived from the main Stiller et al. tree, which was based on coalescent-based analysis of 63,430 intergenic loci, and noted seven minor discrepancies in the linear sequencing of families or orders. Note that the proposed changes involving families are generally better supported (i.e., internally consistent or consistent with other phylogenetic studies) than those involving orders, which are typically characterized by poor internal support or inconsistent relationships among studies. Relationships among these orders are long-standing problems in avian phylogenetics.

(a) Pterocliiformes-Columbiformes precedes Cuculiformes in our current linear sequence, and the groups that include these orders, Pterocliiformes-Columbiformes-Mesitornithiformes and Cuculiformes-Otidiformes-Musophagiformes, are sister groups in Stiller et al. tree. Although this was identified as a node with high discordance by Stiller et al., this result is also present in the Prum et al. (2015) tree based on 394 “anchor loci”, although also with low support. This node is not present in the Kuhl et al. (2021) tree based on 3'-UTRs, in which Cuculiformes are sister to Columbiformes, with Pterocliiformes- Mesitornithiformes sister to this group, and Otidiformes-Musophagiformes the next successive sister group. Pterocliiformes-Columbiformes-Mesitornithiformes contains more species than Cuculiformes-Otidiformes-Musophagiformes, so applying standard linear sequencing criteria to the tree, Cuculiformes-Otidiformes-Musophagiformes should precede Pterocliiformes-Columbiformes-Mesitornithiformes. For NACC, if following the main Stiller et al. and Prum et al. trees, this means that Cuculiformes should precede Pterocliiformes-Columbiformes in the linear sequence.

From Stiller et al. (2024):



From Kuhl et al. (2021):



(b) Rallidae-Heliornithidae precedes Aramidae-Gruidae in our current linear sequence, and the groups that include these families, Rallidae-Heliornithidae-Sarothruridae and Aramidae-Gruidae-Psophiidae, are sister groups in Stiller et al. tree, as well as in the Prum et al. and Kuhl et al. trees. Rallidae-Heliornithidae-Sarothruridae contains more species than Aramidae-Gruidae-Psophiidae, so Aramidae-Gruidae-Psophiidae should be first in the linear sequence. Moreover, Rallidae contains more species than Heliornithidae and therefore should follow Heliornithidae. Applying standard linear sequencing criteria to the tree, the linear sequence should be Psophiidae-Aramidae-Gruidae-Heliornithidae-Sarothruridae-Rallidae. For NACC, this means that our linear sequence, if following the Stiller, Prum, and Kuhl trees, should change to Aramidae-Gruidae-Heliornithidae-Rallidae.

From Stiller et al. (2024):



(c) Orders from our area that form part of the Strisores (Caprimulgiformes-Steatornithiformes-Nyctibiiformes-Apodiformes) precede Gruiformes-Charadriiformes in our current linear sequence. Strisores and the clade dubbed Phaethoquornithes (Phaethontiformes-Eurypygiiformes-Gaviiformes-Sphenisciformes-Procellariiformes-Pelecaniformes) are sister groups in the Stiller et al. tree, and Phaethoquornithes-Strisores is sister to Gruiformes-Charadriiformes-Opisthocomiformes. Phaethoquornithes-Strisores contain more species than Gruiformes-Charadriiformes-Opisthocomiformes so, according to the Stiller et al. tree, Gruiformes-Charadriiformes-Opisthocomiformes should precede Phaethoquornithes-Strisores. For the NACC area, this would mean that Gruiformes-Charadriiformes should precede Strisores in the linear sequence. However, as with the Columbiformes result discussed above, there was high discordance at the node uniting Strisores and Phaethoquornithes. Furthermore, no previous studies reported this result, instead placing Strisores as sister to the Otidimorphae (Jarvis et al. 2014), Cursorimorphae (Wu et al. 2024), Opisthocomiformes (Kuhl et al. 2021), or all other Neoaves (Prum et al. 2015).

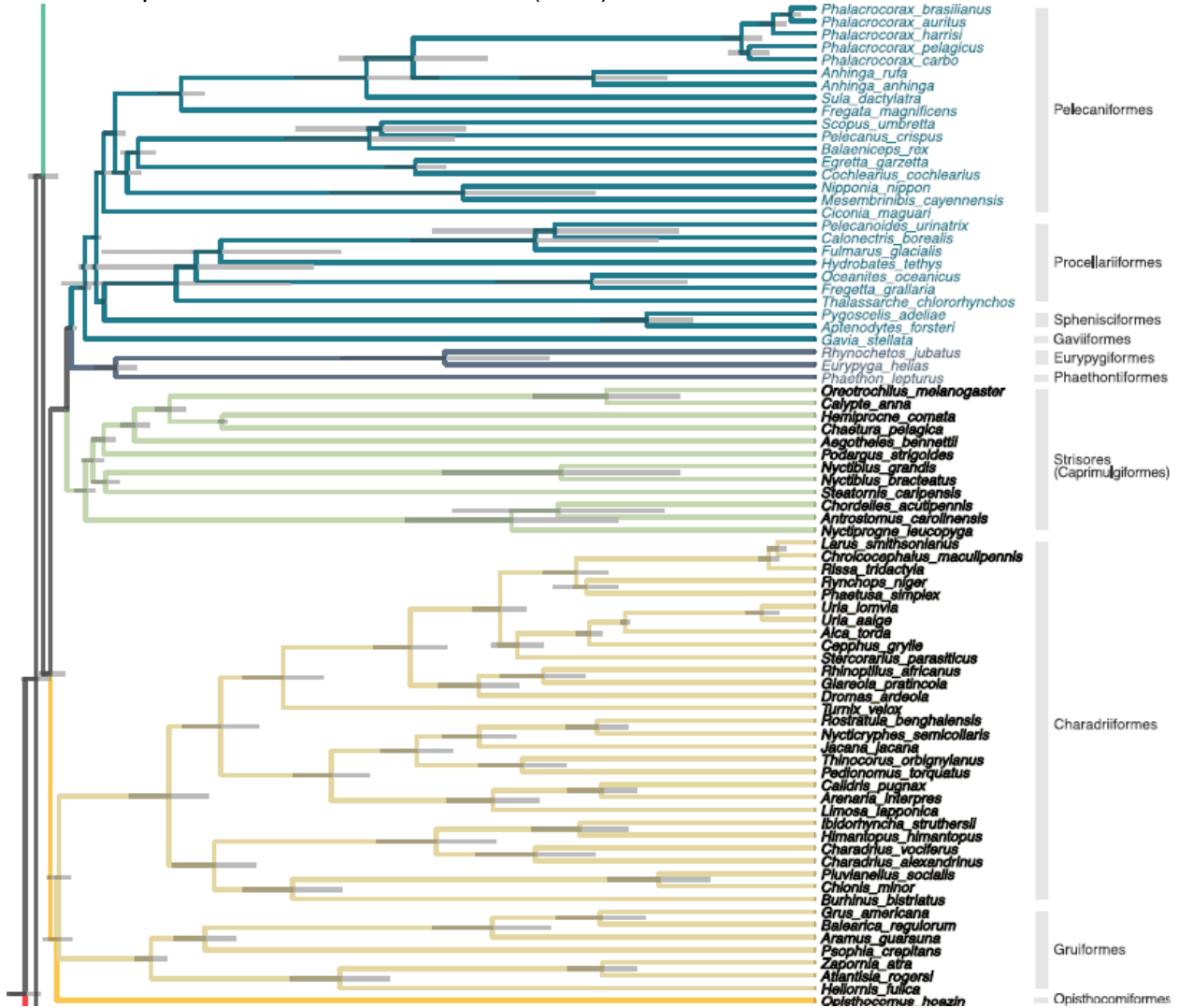
(See this part of the Stiller et al. (2024) tree on the next page.)

(d) Pelecanidae-Ardeidae precedes Threskiornithidae in our current linear sequence, and Balaenicipitidae-Scopidae-Pelecanidae-Ardeidae is the sister group to Threskiornithidae in the Stiller et al. tree, as well as in the Prum et al. and Kuhl et al. trees. Balaenicipitidae-Scopidae-Pelecanidae-Ardeidae contains many more species than Threskiornithidae, so Threskiornithidae should precede Balaenicipitidae-Scopidae-Pelecanidae-Ardeidae in the linear sequence, if following the Stiller, Prum, and Kuhl trees. For the NACC-area families, this would mean a linear sequence of Threskiornithidae-Pelecanidae-Ardeidae.

From Stiller et al. (2024):



Relationships of Strisores from Stiller et al. (2024):



(e) Cathartiformes-Accipitriformes precedes Strigiformes in our current linear sequence. These are sister groups in the Stiller et al. tree, although the branch leading to this node is very short and shows high discordance. Moreover, although this result was also present in the Jarvis et al. coalescent tree, this result is not present in the Stiller et al. or Jarvis et al. concatenated trees, nor in trees based on other types of data, such as those of Prum et al. (2015) and Kuhl et al. (2021). Cathartiformes-Accipitriformes contains more species than Strigiformes and should follow Strigiformes in our linear sequence, if following the Stiller et al. and Jarvis et al. coalescent trees.

From Stiller et al. (2024):

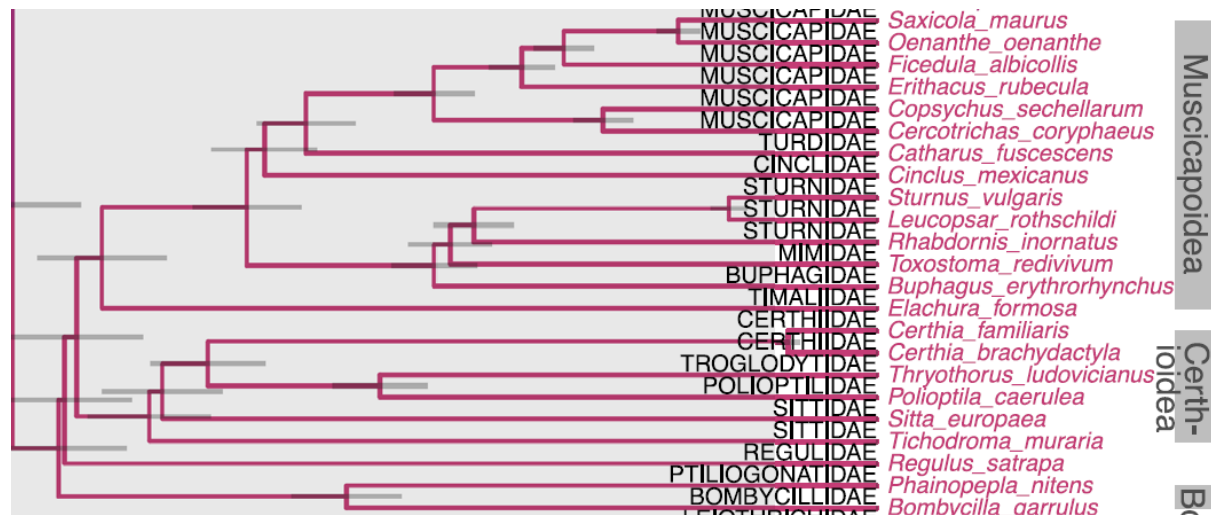


(f) *Bucconidae* precedes *Galbulidae* in our current linear sequence. These families are sister groups in the Stiller et al. tree, as well as in the Prum et al. and Kuhl et al. trees. *Bucconidae* contains more species than *Galbulidae*, so it should follow *Galbulidae* in our linear sequence.

From Stiller et al. (2024):



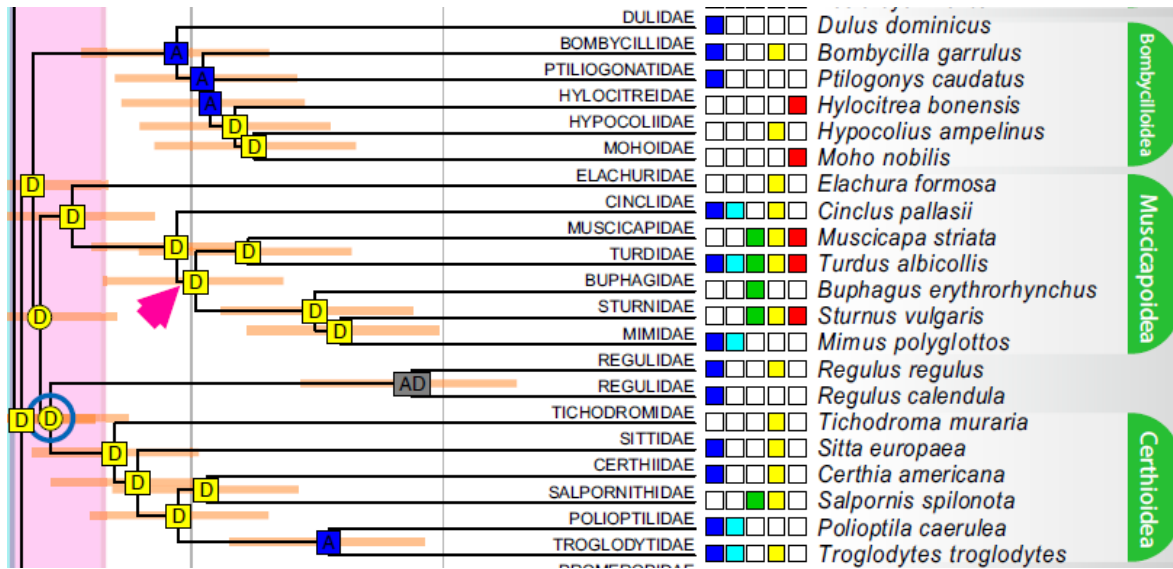
(g) *Regulidae* precedes *Dulidae*-*Bombycillidae*-*Ptiliogonatidae*-*Mohoidae* in our current linear sequence. In the Stiller et al. (2024) tree, *Regulidae* is sister to a clade consisting of the *Certhioidea* and *Muscicapoidea*, and *Bombycillidae* and *Ptiliogonatidae* form a clade sister to the *Regulidae*-*Certhioidea*-*Muscicapoidea* clade (*Dulidae*, *Mohoidae* and extralimital families *Hypocoliidae* and *Hylocitridae* were not sampled):



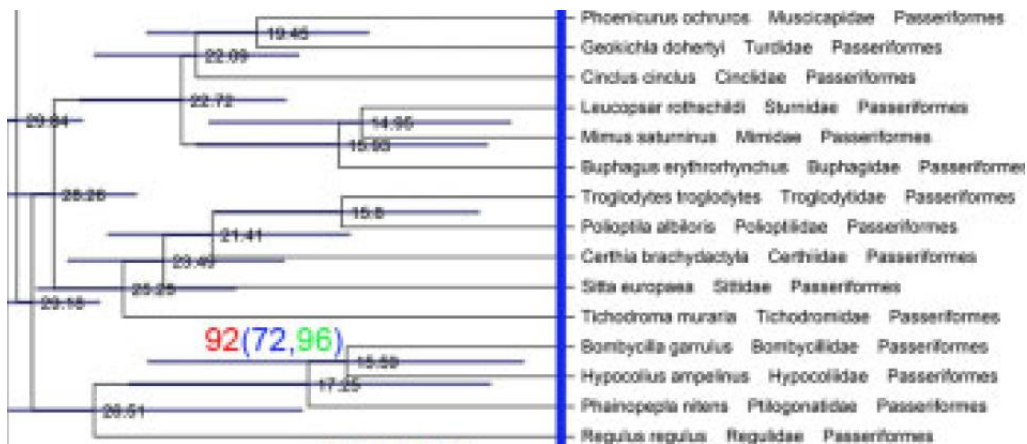
In the UCE-based passerine tree of Oliveros et al. (2019; see below), *Dulidae*, *Bombycillidae*, *Ptiliogonatidae*, *Mohoidae*, *Hypocoliidae*, and *Hylocitridae* were all sampled. These families form a clade sister to a clade consisting of *Regulidae*, *Certhioidea*, and *Muscicapoidea*, although in their tree *Regulidae* is sister to *Certhioidea* rather than to *Certhioidea*-*Muscicapoidea*.

Regardless of the details of the affinities of *Regulidae*, these two studies indicate that *Dulidae*-*Bombycillidae*-*Ptiliogonatidae*-*Mohoidae*-*Hypocoliidae*-*Hylocitridae* (or parts thereof) is sister to a clade consisting of *Regulidae*, *Certhioidea*, and *Muscicapoidea*, and that in our linear sequence *Regulidae* should follow *Dulidae*-*Bombycillidae*-*Ptiliogonatidae*-*Mohoidae* and precede *Certhioidea*.

From Oliveros et al. (2019):



However, in the Kuhl et al. (2021) tree, Regulidae was sister to Bombycillidae-Ptilionatidae-Hypocoliidae, and this group was sister to Certhioidea-Muscicapoidae. According to this phylogeny, Regulidae should precede Dulidae-Bombycillidae-Ptilionatide-Mohoidae, and our current linear sequence does not need to be changed.



Recommendations:

We recommend the following:

(a) Flip Pterocliiformes-Columbiformes and Cuculiformes so that Cuculiformes precedes Pterocliiformes-Columbiformes in the linear sequence: YES/NO (split decision). In our view, this is the most difficult of the seven subproposals. RTC is very slightly in favor of adopting this change to the linear sequence, based on the presence of the underlying relationships in the

Stiller et al. and Prum et al. trees, albeit with weak support in both. SMB would prefer to keep the linear sequence as it is now until we have a better handle on these relationships.

(b) Change our current linear sequence of Rallidae-Heliornithidae-Aramidae-Gruidae to Aramidae-Gruidae-Heliornithidae-Rallidae: YES. Given the consistent placement in multiple studies of the Aramidae-Gruidae clade as sister to the Rallidae-Heliornithidae clade, we strongly recommend voting to adopt this linear sequence change.

(c) Flip Strisores (Caprimulgiformes-Steatornithiformes-Nyctibiiformes-Apodiformes) and Gruiformes-Charadriiformes so that Gruiformes-Charadriiformes precedes Strisores in the linear sequence: NO. Strisores has been so inconsistently placed that we prefer to wait for more strongly or consistently supported information on the relationships of this group.

(d) Flip Pelecanidae-Ardeidae and Threskiornithidae so that Threskiornithidae precedes Pelecanidae-Ardeidae in the linear sequence: YES. As with the linear sequence change in Gruiformes, we strongly recommend a YES vote to move Threskiornithidae to precede the Pelecanidae-Ardeidae clade in the linear sequence, following the results of Stiller et al., Kuhl et al., and Prum et al.

(e) Flip Cathartiformes-Accipitriformes and Strigiformes so that Strigiformes precedes Cathartiformes-Accipitriformes in the linear sequence: NO. This was a somewhat novel (and poorly supported) finding in the Stiller et al. phylogeny (although recovered in one analysis from Jarvis et al.), with both Prum et al. and Kuhl et al. instead finding that the Cathartiformes-Accipitriformes clade was sister to the Strigiformes plus many of the other “higher” landbird orders, including Coraciiformes, Piciformes, and Passeriformes.

(f) Flip Bucconidae and Galbulidae so that Galbulidae precedes Bucconidae in the linear sequence: YES. These two families have long been considered sister groups, but the corresponding change to the linear sequence has not yet been made.

(g) Flip Regulidae and Dulidae-Bombycillidae-Ptilogonatidae-Mohoidae so that Dulidae-Bombycillidae-Ptilogonatidae-Mohoidae precedes Regulidae in the linear sequence: YES. This is another difficult subproposal: our current linear sequence has support from the Kuhl et al. tree, but the Stiller et al. and Oliveros et al. trees indicate that a change is warranted. We recommend making the change, albeit with reservations.

References:

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- Kuhl, H., C. Frankl-Vilches, A. Bakker, et al. 2021. An unbiased molecular approach using 3'-UTRs resolves the avian family level tree of life. *Mol. Biol. Evol.* 38: 108–127.
- Oliveros, C. H., D. J. Field, D. T. Ksepka, et al. 2019. Earth history and the passerine superradiation. *Proceedings of the National Academy of Sciences* 116: 7916–7925.
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Stiller, J., S. Feng, A.-A. Chowdhury, et al. 2024. Complexity of avian evolution revealed by family-level genomes. *Nature* 629: 851–860.

Wu, S., et al. 2024. Genomes, fossils, and the concurrent rise of modern birds and flowering plants in the Late Cretaceous. *Proceedings of the National Academy of Sciences* 121: e2319696121.

Submitted by: Terry Chesser and Shawn Billerman

Date of Proposal: 30 September 2024

Transfer Spotted Dove *Streptopelia chinensis* to *Spilopelia*

Background:

The Spotted Dove *Streptopelia chinensis*, an introduced species in the NACC area, was placed in *Spilopelia* when it first appeared on the Checklist in 1931 (4th edition) but was transferred to *Streptopelia* in the 19th supplement to the Checklist (AOU 1944, citing Peters 1937). However, IOC and BirdLife now use *Spilopelia* for *S. chinensis* and *S. senegalensis*, which is extralimital to our area, and WGAC recently voted to recognize *Spilopelia* for these two species, as well as *Nesoenas* for two other extralimital species formerly placed in *Streptopelia* (*mayeri* and *picturata*).

Note that although *Spilopelia* (type species *chinensis*) and *Stigmatopelia* (type species *senegalensis*) were introduced in the same work (Sundevall 1873), the first reviser action of Schodde and Mason (1997) established the priority of *Spilopelia* when these two species are placed in the same genus.

New Information:

Two phylogenetic studies focused on the relationships of the Passenger Pigeon included extensive sampling of species of *Streptopelia* and close relatives. In a tree based on sequences of nuclear (beta-fibrinogen intron 7) and mitochondrial DNA (cytochrome b, ATPase 8), Johnson et al. (2010) found three well-supported clades (97-100% bootstrap, 1.0 posterior probabilities) within *Streptopelia* corresponding to *Streptopelia sensu stricto*, *Spilopelia*, and *Nesoenas* (Fig. 1). However, support for the monophyly of *Streptopelia sensu lato* was poor (<50% bootstrap, 0.95 pp).

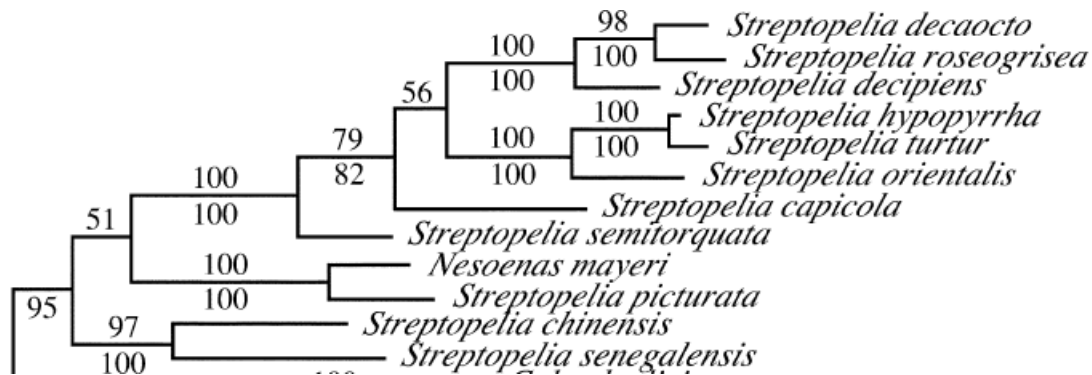


Figure 1. Relevant part of the phylogenetic tree from Johnson et al. 2010, based on parsimony analysis of nuclear and mitochondrial DNA (bootstrap support values above branches, posterior probabilities below).

Fulton et al. (2012) sequenced the same genes (cytochrome b, ATP8, and FGB intron 7) but added 12S rRNA. Unsurprisingly, their results (Fig. 2) were very similar to those of Johnson et

al. (2010): three strongly supported clades representing *Streptopelia sensu stricto*, *Spilopelia*, and *Nesoenas*, and middling support for the monophyly of *Streptopelia sensu lato* (65% bootstrap, 0.97 pp):

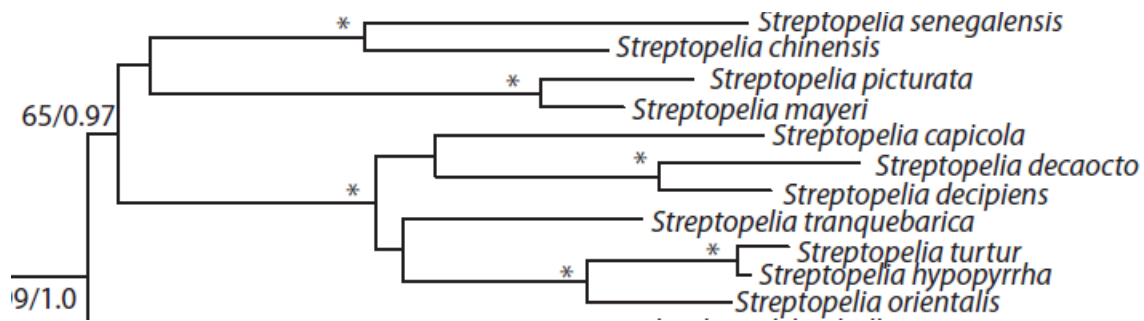


Figure 2. Relevant part of the phylogenetic tree from Fulton et al. 2012, based on maximum likelihood analysis of nuclear and mitochondrial DNA (bootstrap support values above branches, posterior probabilities below).

Analysis of the nuclear data by itself (Fig. 3) resulted in a 4-way polytomy with Old World pigeons (*Columba* spp.):

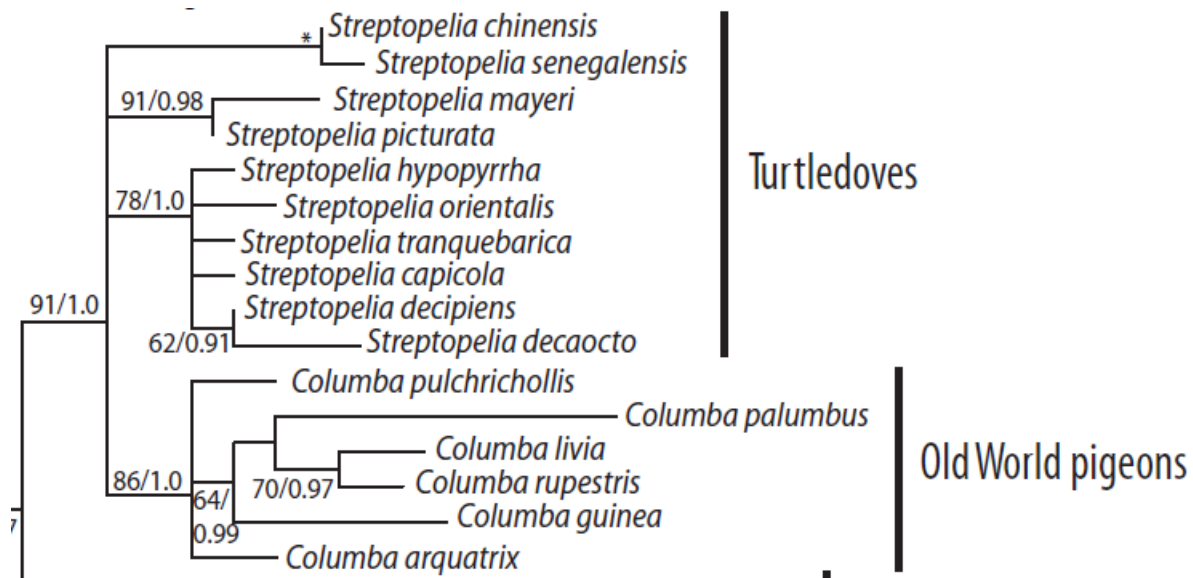


Figure 3. Relevant part of the phylogenetic tree from Fulton et al. 2012, based on maximum likelihood analysis of sequences of beta-fibrinogen intron 7 (bootstrap support values above branches, posterior probabilities below).

More recently, Bruxaux (2018) sequenced complete mitochondrial genomes for a sample of Columbidae (she also sampled UCEs but apparently did not include any species of *Spilopelia* or

Nesoenas). Analyses of these data also produced a 4-way polytomy with *Columba* species, although it differed from the 4-way polytomy in Fulton et al. (2012) in some details (Fig. 4).

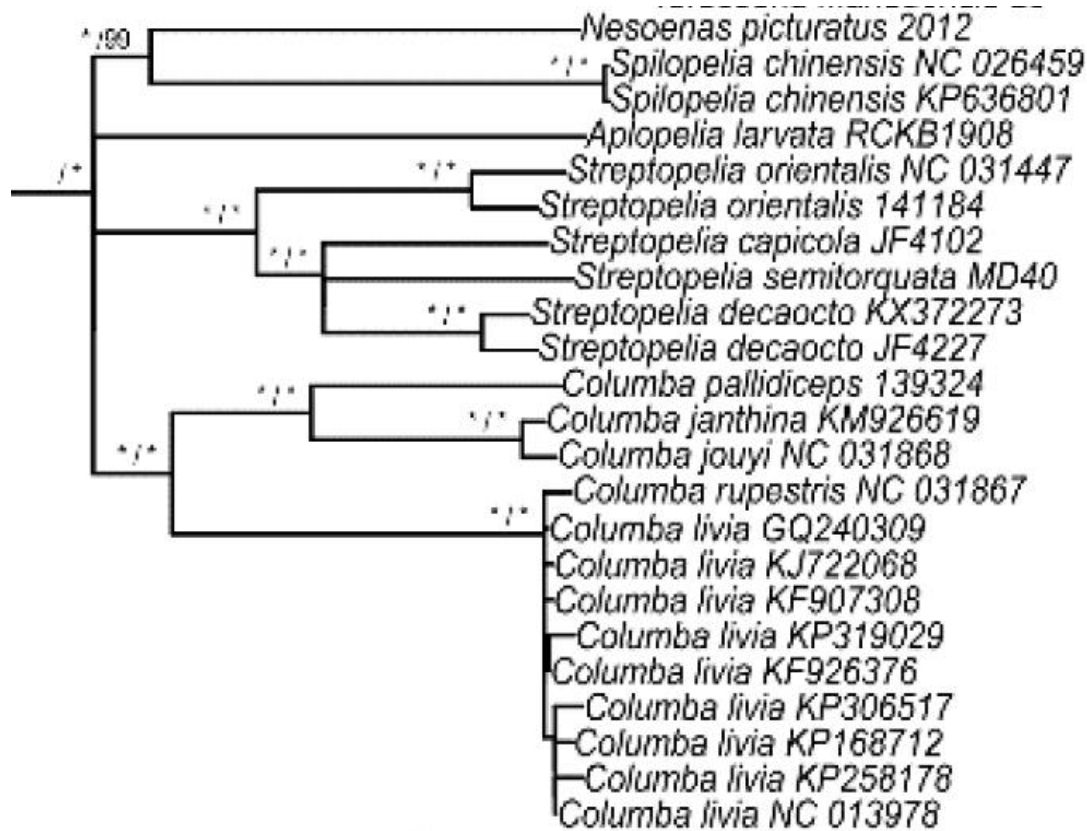


Figure 4. Relevant part of a tree from Bruxaux (2018) based on phylogenetic analysis of mitochondrial genomes. Numbers above branches to the left are posterior probabilities, with ML bootstrap values to the right (* = 1.0 pp or 100% bootstrap).

Bruxaux (2018) also conducted a BEAST analysis of the mtDNA data on a reduced number of individuals, which included *Streptopelia capicola*, *S. [Spilopelia] chinensis*, and *S. [Nesoenas] picturatus*. In this analysis, the polytomy was resolved such that *Streptopelia sensu lato* is not monophyletic: *S. chinensis* and *S. picturatus* were sister species, but *S. capicola* was sister to *Columba pallidiceps* rather than to *S. chinensis* and *S. picturatus* (Fig. 5):

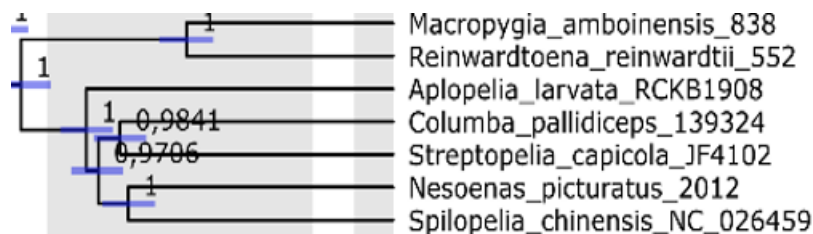


Figure 5. Relevant part of the BEAST tree from Bruxaux (2018).

Recommendation:

I recommend that we once again treat *Spilopelia* as a separate genus from *Streptopelia*, transferring introduced species *S. chinensis* to *Spilopelia*. Molecular support for a monophyletic *Streptopelia sensu lato* is weak, whereas support for the monophyly of *Streptopelia sensu stricto*, *Spilopelia*, and *Nesoenas* is very strong. Furthermore, the depth of the nodes supporting each of these three genera is similar to the depth of nodes supporting other closely related genera of Columbidae, and this change has already been made by most Old World and global sources.

References:

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Submitted by: Terry Chesser

Date of Proposal: 3 October 2024

Treat Plain *Xenops* *Xenops minutus* as three species

Note: This is a modified version of three proposals recently considered by SACC: Proposal 996 (<https://www.museum.lsu.edu/~Remsen/SACCprop1022.htm>) to treat *Xenops minutus* as three species, and Proposals 1022 (<https://www.museum.lsu.edu/~Remsen/SACCprop1022.htm>) and 1022x (<https://www.museum.lsu.edu/~Remsen/SACCprop1022x.htm>) to establish English names for the three species.

Background:

That *Xenops minutus* may include multiple biological species has long been suspected (Remsen 2003). It is the objective of the present proposal to suggest that currently available evidence is sufficient to split *X. minutus* into three biological species.

New information:

Vocalizations.—*Xenops minutus* includes three populations that differ markedly in vocalizations. An analysis of geographic acoustic trait variation documented three distinct vocal groups (Fig. 1) in *Xenops minutus*: (1) the nominate taxon *X. m. minutus* in the Atlantic rainforest south of the São Francisco River, (2) the *genibarbis* group, comprising all taxa in lowland Amazonia plus *X. m. alagoanus* of the Atlantic rainforest north of the São Francisco River, and (3) the *mexicanus* group, comprising trans-Andean birds from Central America to northwestern South America (Boesman 2016). Vocal differences between *minutus* and the *genibarbis* group sound as great or greater than those among the three species currently recognized in the genus *Xenops*.

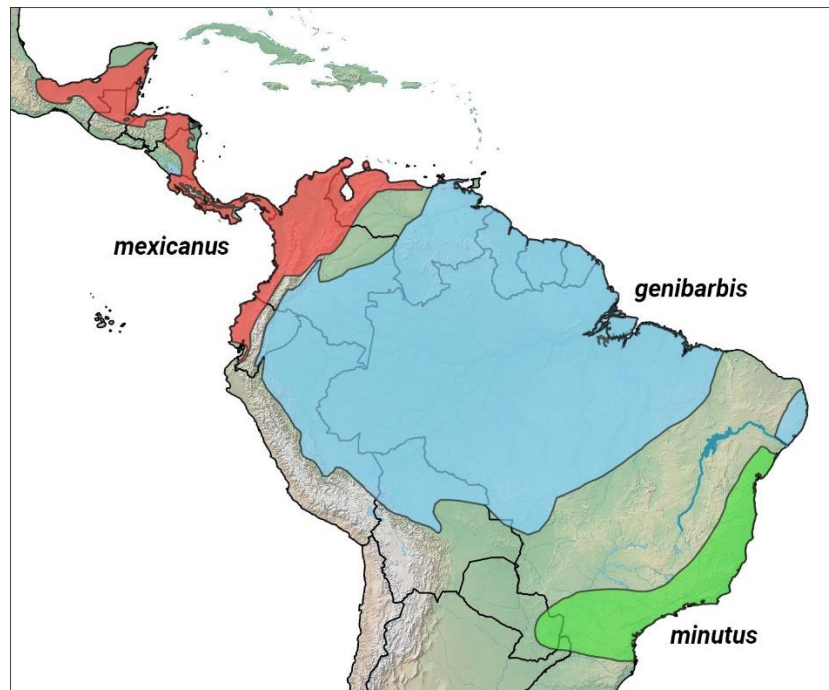


Figure 1. Distribution of the three vocal groups present within *Xenops minutus* (from Harvey and Brumfield 2015).

Vocal differences among *X. minutus* populations generate behavioral discrimination. Field playback experiments between *X. m. obsoletus* (of the *genibarbis* group) and *X. m. littoralis* (of the *mexicanus* vocal group) revealed strong behavioral discrimination between these two vocal groups (Freeman & Montgomery 2017). Given that the vocal differences between these two vocal groups translate into behavioral discrimination (and presumably into premating isolation), the relatively greater vocal differences between the nominate subspecies and these two vocal groups should also be expected to act as effective premating barriers if they were to come into contact.

Genetics.—The three vocally distinct groups show high levels of genome-wide differentiation. A phylogenomic analysis of SNPs from genotype-by-sequencing data found three deeply divergent clades within *X. minutus* (Figs. 2a and 2b) congruent with the three groups delineated by vocal variation, although the northern Atlantic forest subspecies *alagoanus*, which groups with the *genibarbis* group based on vocalizations, was not sampled (Harvey & Brumfield 2015). In these trees, the *mexicanus* and *genibarbis* groups were sister taxa, and *minutus* was sister to *mexicanus/genibarbis*.

In contrast, an analysis of sequences of the mitochondrial gene cytochrome-b (Fig. 2c, evidently based on Burney 2009 and Smith et al. 2014) resulted in a 3-way polytomy among *minutus* and two parts of the *genibarbis* group (the Guianan samples vs. all other samples of this group). The *mexicanus* group was sister to the clade united by this polytomy. The mitochondrial tree, which is based on far fewer base pairs of sequence data than the nuclear SNP tree, contrasts not only with the vocal and nuclear sequence data, but also with the plumage data, which also show that nominate *minutus* is the most distinctive group within *X. minutus* (Fig. 3).

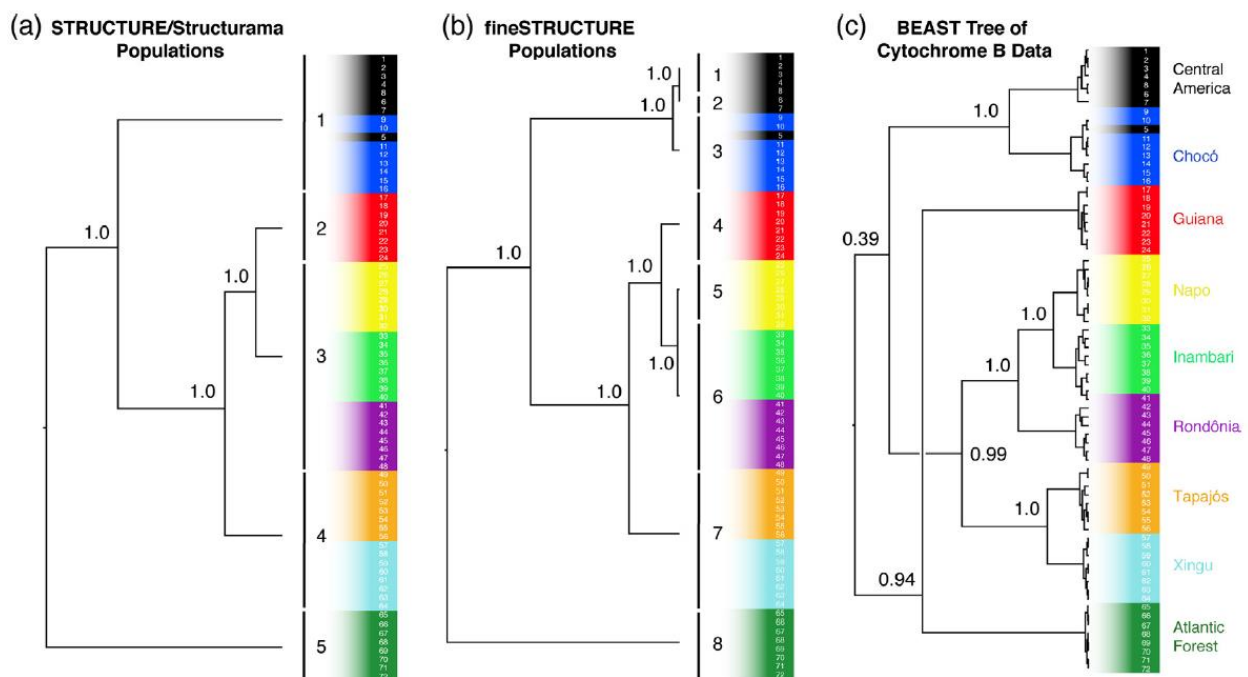


Figure 2. Contrasting phylogenetic trees based on the genome-wide SNP data (a and b) and cytochrome-b data (c). Figure from Harvey and Brumfield (2015).



Figure 3. Specimens of representatives of the three groups of *X. minutus* from the LSMZ. From top to bottom: *X. m. minutus*, two from the mostly Amazonian *genibarbis* group (*X. m. remoratus* and *X. m. ruficaudus*), and *X. m. mexicanus*. (Photo by Van Remsen.)

Based on phenotypic differences between the *genibarbis* group and *minutus*, BirdLife International/IBW split them into separate species based on the following rationale, but treated the *mexicanus* group as part of the newly elevated *X. genibarbis*:

[*X. minutus*] hitherto treated as conspecific with *X. genibarbis*, but differs in its bold plain white chin and throat connecting to white submoustachial streak with relatively little brown on malar below it (prominent and completely separating chin from-submoustachial streak in *X. genibarbis*, all races of which have brown-streaked whitish throat) (2); less pale streaking-extending onto breast (1); loudsong a series of 4–5 upslurred notes, the first slightly lower-pitched and subdued, vs much-faster-delivered (2), more numerous and overslurred (3) notes (1). Claimed smaller size (in IBW) not apparent vs (at least)-nominate *X. genibarbis*, but further study needed; molecular evidence supports the split (2). Monotypic.-Distribution-E & SE Brazil (Bahia S to Santa Catarina), E Paraguay (E from Canindeyú, Caaguazú) and NE Argentina (Misiones).

Nevertheless, currently available evidence suggests that *Xenops minutus* is best treated as three biological species:

Xenops minutus — monotypic, in the Atlantic rainforest south of the São Francisco River
Xenops genibarbis — polytypic, including *obsoletus*, *ruficaudus*, *remoratus*, and *alagoanus*
Xenops mexicanus — polytypic, including *ridgwayi*, *littoralis*, *olivaceus*, and *neglectus*

English names:

After a preliminary discussion of English names based on Proposal 1022, SACC unanimously adopted the English names recommended in Proposal 1022x:

Xenops minutus - Atlantic Plain-Xenops
Xenops genibarbis - Amazonian Plain-Xenops
Xenops mexicanus - Northern Plain-Xenops

For more information, see the SACC proposals and discussion at the links posted above.

Recommendation:

I recommend that we follow SACC and vote YES to treat *Xenops minutus* as three species and adopt the English names listed above. The effect of this on the NACC area would be to remove Plain Xenops *X. minutus* from the Checklist and replace it with Northern Plain-Xenops *X. mexicanus*.

References:

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- Smith, B. T., et al. (2014). The drivers of tropical speciation. *Nature*, 515(7527), 406–409. <https://doi.org/10.1038/nature13687>

Submitted by: Rafael D. Lima, modified for NACC by Terry Chesser

Date of Proposal: April 2024, modified for NACC on 4 October 2024

Appendix: Comments from the SACC on Proposal 996 (see the links provided above for comments on the subsequent English name proposals, SACC 1022 and 1022x):

Comments on Proposal 996:

Comments from Robbins: “YES. Based on vocal and genetic data this seems to be a straightforward split. Additionally, the clear white throat of nominate appears to be distinct from the other two taxa (based on the photo included in this proposal and Marshall's assessment in BirdLife/HBW. Thus, I vote to treat the current *Xenops minutus* as three species.”

Comments from Mike Harvey (voting for Bonaccorso): “YES. I believe this proposal is well justified and the recommendation is eminently reasonable. Although our 2015 genetic study was one of the first to use RAD-Seq for phylogeography/phylogeny, recent years have established the utility of the approach for this purpose. I think this fact, combined with the subsequent vocal and playback analyses, provides more-than-sufficient support for the existence of these three species.”

Comments from Del-Rio: “YES. Based on nuclear genome structure and phenotypic differentiation. Vocalizations are also pretty distinctive.”

Comments from Lane: “YES to the split into three species. The voices of these three groups are quite distinctive (more so than between several of the other species of *Xenops*, to my ear), and combined with plumage features, I think it makes sense to separate these three groups into species-level taxa.”

Comments from Stiles: “YES to the 3-way split of *Xenops minutus*, which is justified by multiple lines of evidence. Again, a proposal on E-names should be pending.”

Comments from Claramunt: “YES. I think the combination of plumage, voice, and genetic differences make a compelling case for treating this complex as three species. The mitochondrial information is somewhat muddling but it can be explained as vagaries of the coalescent process in large populations. The assignment of subspecies to each species looks correct. Note that Arbeláez-Cortés (2020) confirmed with mtDNA data that the sis-Andean *neglectus*, described as very similar to *littoralis* but with cinnamon rather than rufous wings and tail (Cory & Hellmayr 1923), is closer to the trans-Andean and Central American forms. It would be super interesting to see what happens in a potential contact zone in Colombia, but with the information at hand, the three-way split is the most reasonable classification.”

Arbeláez-Cortés, E. (2020). Defining the phylogeographic relationship between cis- and trans-Andean populations of *Dendrocincla fuliginosa* and *Xenops minutus* in Colombia. *Revista Mexicana de Biodiversidad*, 91: e912984

Comments from Areta: “YES. The Boesman note indicates the existence of 3 vocal types, each of which corresponds to the main deep breaks in phylogenetic structure shown by Harvey & Brumfield. However, no proper analysis has been published and we do not know where the samples that Boesman analysed came from. In a rapid survey of sounds, I found that this recording (<https://xeno-canto.org/245253>) in the eastern slope of the eastern Andes sounds like *mexicanus* on the other side of the Andes, and it therefore seems that the simple cis/trans Andean pattern is an illusion. Incidentally, this would seem to provide more support for the split of *mexicanus* from *genibarbis*. Overall, a look at available sounds recordings is consistent with Boesman’s analysis. The Atlantic Forest *minutus* is clearly distinct in plumage and vocalizations and it is difficult to argue in favour of its merger with the other two groups. In this case, it seems that vocalizations trump mtDNA in terms of taxonomic weight. I would much prefer to see a convincing integrative work discussing the details of vocalizations, genetics and plumage, but I think that there is enough data to move forward and accept the 3-way split.”

Comments from Remsen: “YES. Vocal differences carry the most weight with me. We even have the Freeman-Montgomery playback trial for one of the combos that is consistent with these vocalizations being important to species recognition, and we can use that to extrapolate (“if, then”) for the other combination. I think the proposal makes it clear that burden-of-proof clearly falls on treating these taxa as a single species.

Comments from Curtis Marantz: “Looking at the spectrograms, I am not sure I would find the vocal differences between the Amazonian and Trans-Andean taxa to be overly compelling, at least if *Xenops* vary vocally in the way that most woodcreepers do. The spectrograms presented in Boesman's additional notes demonstrate what I would consider to be compelling differences between the Atlantic Forest and other taxa, but not the other two, which are more reflective of variations on a theme as opposed to the different themes that I like to see for splitting taxa on the basis of vocal differences.”

Comments from Zimmer: “YES. Make that a strong YES for recognizing nominate *minuta* as a distinct species from the others, based upon diagnostic vocal differences, genetic data, and consistent plumage differences. The vocal differences between Atlantic Forest birds and all other populations currently treated in *minuta*, are much greater, at least to my ears, than say, the differences between the songs of *X. tenuirostris* and most subspecies of *X. rutilans*. I’ve advocated for this split for a long time, and I already had a separate species account planned for the Atlantic Forest nominate subspecies in my forthcoming Brazil field guide. As for the separation of Central American + trans-Andean populations from Amazonian populations, I’m a bit more hesitant here. I think that both the plumage distinctions and vocal distinctions, although real, are less clear-cut – at least, I can’t personally vouch for the vocal distinctions of some Central American populations including all Trans-Andean taxa, so the break, as Nacho suggests, may not be the Andes. However, the genetic work suggests otherwise, so I’m inclined to treat these two groups as distinct from one another as well.”