AOS Classification Committee – North and Middle America

Proposal Set 2023-C

27 February 2023

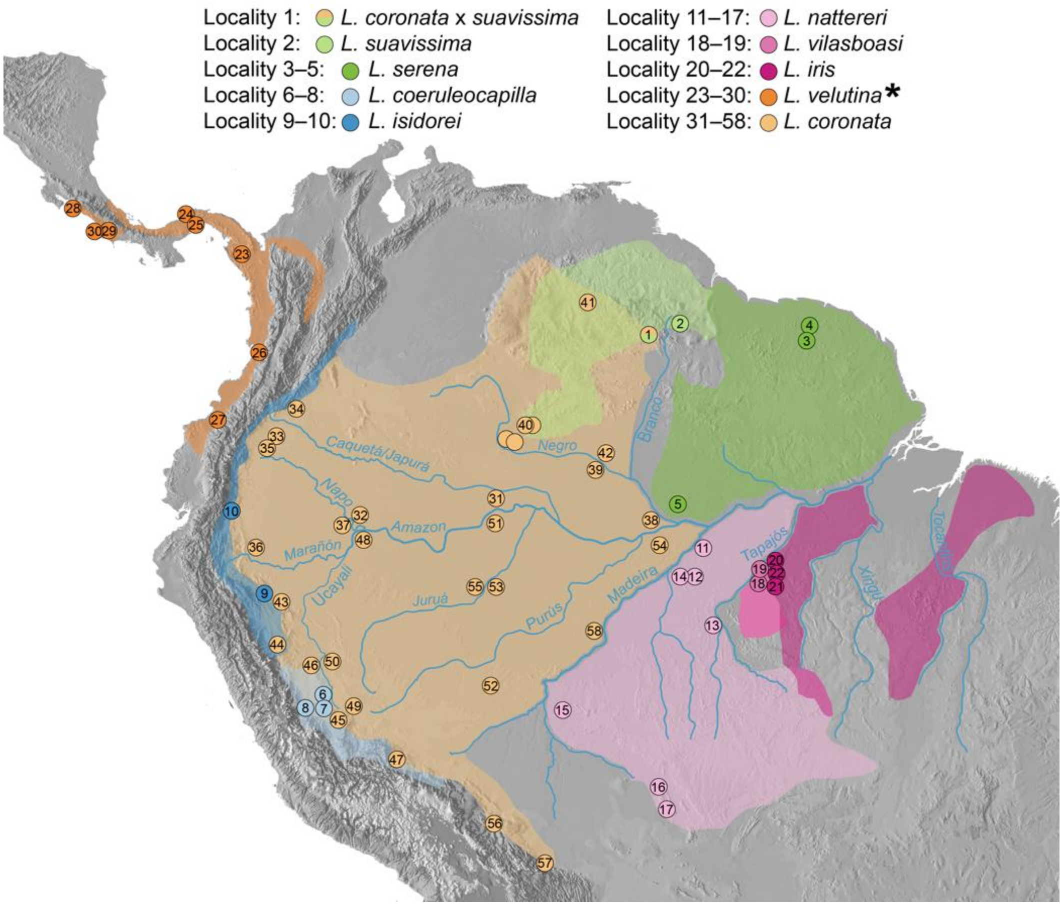
Treat *Lepidothrix velutina* as a separate species from Blue-crowned Manakin *L. coronata*

Note: This is a slightly modified version of SACC proposal 943, which passed unanimously.

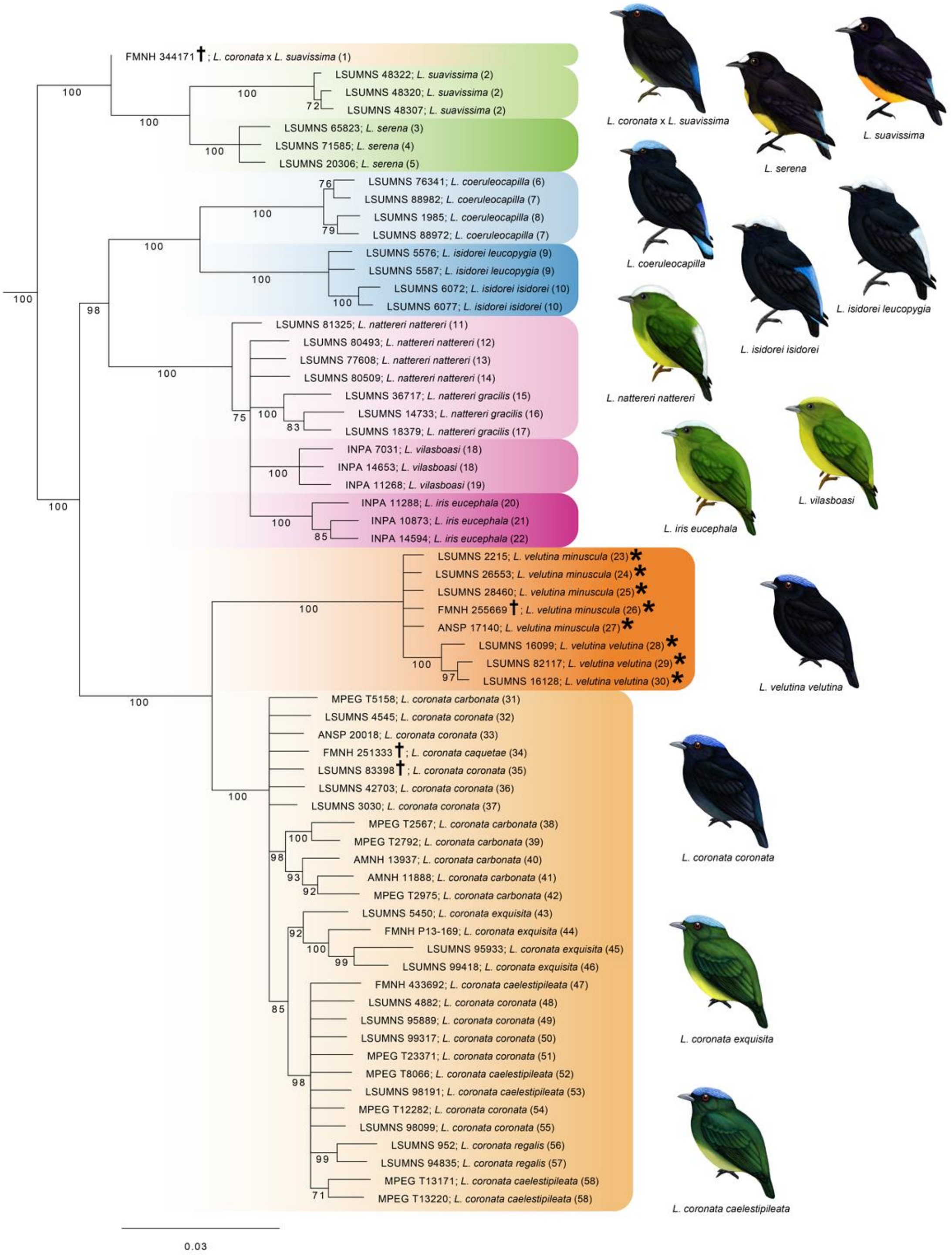
Background:

Many authors have suggested that west-of-Andes populations of *Lepidothrix coronata* (*L. c. velutina* and *L. c. minuscula*) may deserve species-level recognition apart from east-of-Andes populations found in Amazonia and the adjacent Andean foothills (*L. c. coronata*, *L. c. caquetae*, *L. c. carbonata*, *L. c. exquisita*, *L. c. caelestipileata*, and *L. c. regalis*; Hilty, 2021; Kirwan and Green, 2011; Ridgely and Tudor, 1994; Snow, 2004). However, factors including the lack of extensive genomic data from across the large geographic range of *L. coronata* and the complex plumage variation within Amazonian populations of *L. coronata* have posed a challenge to clarifying the classification of this species group.

Moncrieff et al. (2022) published a phylogenetic hypothesis of the genus *Lepidothrix* with widespread sampling within the *L. coronata* species group, including all currently recognized subspecies (Dickinson and Christidis, 2014). Below is a sampling map, which includes the proposed *L. velutina* marked with an asterisk.

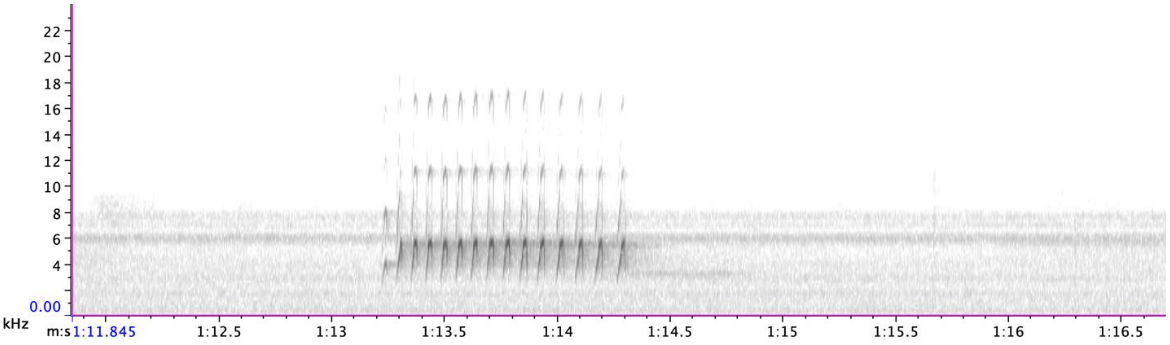


Moncrieff et al. (2022) used both coalescent and concatenation methods to estimate phylogenies, which consistently identified a deep divergence within *L. coronata* corresponding to west-of-Andes and east-of-Andes clades. Below is a concatenated tree (estimated with IQ-TREE2 and based on 5,025 SNPs) that is representative of the results found using other methods and data filtering schemes. Numbers at the end of the tip labels refer to locality numbers shown on the sampling map above.

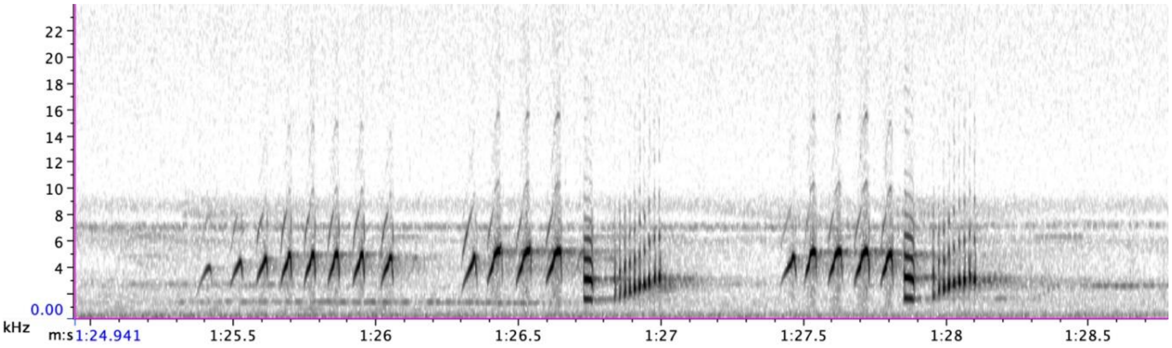


Moncrieff et al. (2022) also pointed out that populations west of the Andes differ markedly in plumage (males have a much deeper black and more extensive black on forehead) and in voice from populations east of the Andes. Below we highlight the main vocal differences with sonograms.

A single trilled primary call from *Lepidothrix coronata velutina.* By contrast, east-of-Andes populations of *L. coronata* have a sweet, rising whistle as their primary call. Recording by Jay McGowan from Sendero Ibe Igar, Kuna Yala, Panama (ML202732201).

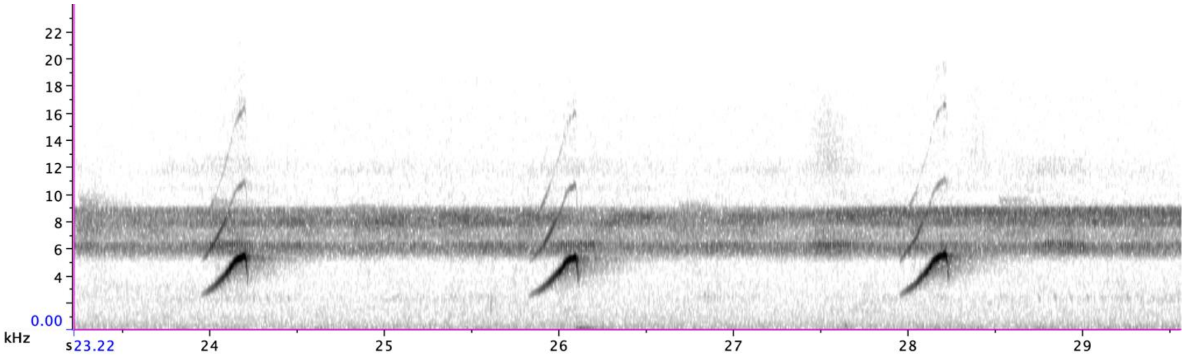


An abbreviated “ti’ti’t’t’t’t’t’t’t’t” call followed by two “ti’t’t’t’t’t, chu’WAK” advertisement songs from *Lepidothrix coronata velutina*. The trilled calls and trilled introductions to the advertisement song are unique to west-of-Andes populations of *L. coronata*. Recording by David L. Ross, Jr. from Parque Nacional Corcovado, Puntarenas, Costa Rica (ML55245).

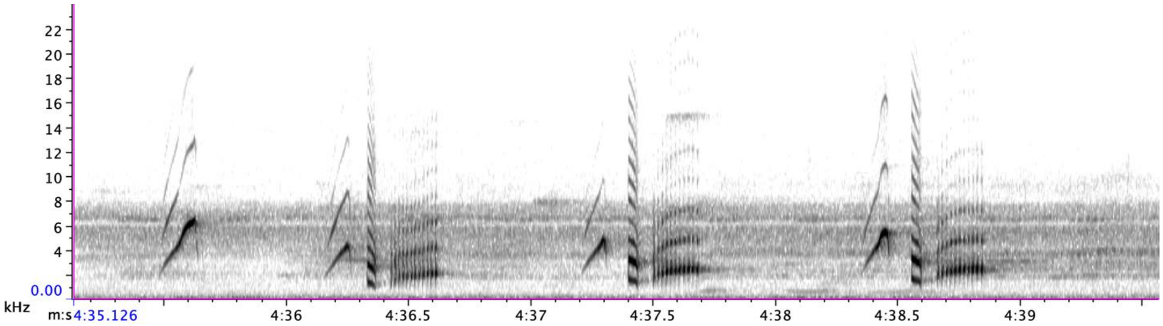


Populations of *L. coronata* east of the Andes have males with either a paler black plumage or variations of green with a yellow belly; they also have a whistled primary call and whistled introductory note to the advertisement song that is highly distinctive and consistent.

A series of three “swee” primary calls from *Lepidothrix coronata*. This “swee” call given by east-of-Andes populations contrasts with the trilled call of west-of-Andes populations. Recording by Curtis Marantz from Parque Nacional do Jaú, Amazonas, Brazil (ML117006).



A single “swee” primary call followed by a series of three “swee chí-wrr” advertisement songs from *Lepidothrix coronata*. The sweet, whistled calls and whistled beginning to the advertisement song is unique to east-of-Andes populations of *L. coronata*. Recording by Gregory Budney from Bushmaster Trail, Yanamono Camp, Iquitos, Loreto, Peru (ML34194).



Using locally sympatric species of *Lepidothrix* (*L. coronata* and *L. coeruleocapilla*) as a benchmark, Moncrieff et al. (2022) also pointed out that vocalizations of west-of-Andes and east-of-Andes *L. coronata* differ more than apparently necessary for maintenance of reproductive barriers within the genus.

Finally, to provide additional context for the level of genetic divergences involved, the mean sequence divergence between west-of-Andes and east-of-Andes *L. coronata* populations at mitochondrial gene ND2 is 4.25%, which is greater than that observed between species in the *L. nattereri* + *L. vilasboasi* + *L. iris* clade (1.4–3.1%) and between *L. suavissima* and *L. serena* (3.7%).

Discussion:

Based on my ongoing genetic work within the east-of-Andes populations of *L. coronata*, further splits within the species group do not seem warranted. Although *L. c. exquisita* of the Andean foothills of central Peru is highly distinctive in its plumage around the type locality, it appears to intergrade with *L. c. coronata* near the Marañón River in the San Martín and Amazonas Regions. More sampling in that area is highly desirable. Also, the voice of Amazonian and east-slope Andean foothill populations is remarkably consistent. If any further splits are considered in the future, these would only involve east-of-Andes populations and should therefore not hold up a split of west- vs. east-of-Andes populations, which are monophyletic and differ in the various ways pointed out above.

Recommendation:

This vote consists of three parts, one for the split of *L. velutina* from *L. coronata* and two concerning English names for the newly split species. I recommend voting YES on all parts.

A. Recognize *Lepidothrix velutina* (Berlepsch, 1883) as a separate species from *Lepidothrix coronata. Lepidothrix velutina* would include *L. velutina minuscula* (Todd, 1919).

B. Use the English name Velvety Manakin for west-of-Andes populations, following use by various authorities (e.g., Hilty, 2021; Snow, 2004).

C. Use the English name Blue-capped Manakin for east-of-Andes populations, following the use of this common name by Hellmayr (1929). This would avoid ambiguity in usage of "Blue-crowned Manakin".

References:

Berlepsch, H. von, 1883. Descriptions of six new species of birds from Southern and Central America. Ibis 5, 487–494.

Dickinson, E.C., Christidis, L. (Eds.), 2014. The Howard and Moore complete checklist of birds of the world, fourth. ed. Aves Press, Eastbourne, U.K.

Hellmayr, C.E., 1929. Catalogue of birds of the Americas. Part 6. Oxyruncidae-Pipridae-Cotingidae-Rupicolidae-Phytotomidae. Publications of the Field Museum of Natural History No. 266.

Hilty, S.L., 2021. Birds of Colombia. Lynx and Birdlife International field guides, Lynx Edicions, Barcelona.

Kirwan, G.M., Green, G., 2011. Cotingas and manakins. Princeton University Press, Princeton.

Moncrieff, A.E., B. C. Faircloth, and R. T. Brumfield. 2022. Systematics of *Lepidothrix* manakins (Aves: Passeriformes: Pipridae) using RADcap markers. *Molecular Phylogenetics and Evolution* 173. https://doi.org/10.1016/j.ympev.2022.107525

Ridgely, R.S., Tudor, G., 1994. The suboscine passerines. Volume II. The birds of South America. University of Texas Press, Austin.

Snow, D.W., 2004. Family Pipridae (Manakins), in: Del Hoyo, J., Elliott, A., Christie, D. (Eds.), Handbook of the Birds of the World. Vol. 9. Cotingas to Pipits and Wagtails. Lynx Editions, Barcelona, pp. 110–169.

Todd, W.E.C., 1919. Descriptions of apparently new Colombian birds. Proc. Biol. Soc. Washington 32, 113–118.

Submitted by: Andre E. Moncrieff

Date of Proposal: June 2022 (SACC proposal), slightly modified for NACC on 12 January 2023

SACC comments:

Comments from Remsen:
A.YES. The differences in vocalizations alone are sufficient evidence for me, regardless of degree of genetic differentiation.
B. YES. Not only does Velvety have a long track record, but it also is an apt description that is also memorable. The word "velutinus" means "velvety" in Latin, so that's nice.

C. YES. Good idea. This maintains the connection with “Blue-crowned” and has the bonus advantage of already being used historically. Retaining Blue-crowned for either daughter species would be contrary to our guidelines because this is a classic parent-daughter split with both daughters having large ranges; therefore, retaining “Blue-crowned” for one of the daughters would lead to perpetual confusion. This is a case in which “stability” (retaining Blue-crowned) is disadvantageous because the species classification itself has been destabilized --- time to learn new names to go along with a new taxonomic concept.

Comments from Areta: “A. YES. The deep split, different calls/introduction to song, and distinct plumages argue in favor of the recognition of *L. velutina*. Regarding the common names, I am fine with Velvety. Changing the name Blue-crowned by Blue-capped seems to create unnecessary instability, for a bird that encompasses more than 90% of the range and for which no species-level name change has been made. Whether these are sister or not is immaterial to me.”

Comments from Lane: “A. YES. Phylogenetic and vocal datasets warrant this split.
”B and C: YES.”

Comments from Donsker:
“B. YES. Velvety Manakin is an excellent English name for the west-of-Andes populations with roots extending at least back to Hellmayr.

“C. YES. Use Blue-capped Manakin for the east-of-Andes populations by restoring a very appropriate Hellmayr name. “Blue-crowned” Manakin would best be retired, and reserved for the broader species concept, as it was by Meyer de Schauensee, if the split is accepted.”

Comments from Steve Hilty:
“A. Aside from firm genetic evidence (see Moncrieff 2022, gene tree) the vocal differences between west-of-the Andes, and east of the Andes populations is striking. Displaying western birds give a soft rattling trill, this often (but not always) followed by a couple harsh notes. Displaying eastern birds commonly give a slightly rising two-noted "cha-vick" repeatedly (which I have always assumed to be advertising, but could be given in other context); and a simple, rather soft rising "pweeet!" repeated a few times (also advertising, or given in other context?). In any case, the differences between the vocalizations of these western and eastern populations are hard to miss. In fact, to my ears, the two-note call of the eastern birds (*carbonata)* sounds most like that of Dwarf Tyrant-Manakin, *Tyranneutes stolzmanni*, although the latter's call is harsher, and will always come from mid-levels or higher in forest (not understory as in case of Blue-crowned (Blue-capped) Manakin.

Moncrieff (2022) also points out plumage differences between western and eastern birds. Although these differences can be discerned in the hand in direct comparison, they are (in my opinion) of minimal value at best for a field observer—especially in the typically low light conditions of tropical forest understory, where individuals of both populations occur. It is likely that these relatively subtle plumage differences (if they are important) are better appreciated in life by the birds themselves, who undoubtedly have sharper color resolution, than we (humans) do. However, because these two populations do not overlap, the importance of these differences, in life, may be minimal.
(voting for Areta)
“B & C: YES”

Comments from Josh Beck (voting for Claramunt):
"B & C: YES. I am in favor of the proposed names (Velvety and Blue-capped). Velvety has precedence, is unique, is apt, and is memorable. For *coronata* (sensu stricto), although the range is, as pointed out, at least an order of magnitude larger than for *velutina*, a 10 minute dig into eBird shows that about 65% of observations are trans-Andean, and about 35% are cis-Andean. This is obviously tilted by bias in where birders go, where there are greater numbers of domestic birders, and where eBird is used more, but still clearly shows that there is observation bias towards *velutina***,** which to me is a strong argument against retaining Blue-crowned, despite the instability that will result."

Comments from Bonaccorso: "YES. The combination of genetic differentiation, voice differentiation, and very modest plumage differences (which, I agree with Steve, seem very difficult to discern in the field), make the case for giving species status to *Lepidothrix velutina*. Fortunately, the species do not overlap geographically! Nice proposal, by the way. Proposals are much easier to evaluate when all the available graphic information (maps, trees, songs) are included directly in the proposal."

Comments from Claramunt: "YES. Genetic, plumage, and vocal evidence point to the species status of *velutina*. MtDNA shows instead *velutina* sister to the N Amazonian forms of coronata (Smith et al., 2014), but maybe just a case of incomplete lineage sorting."

Comments from Robbins: "YES for recognizing *Lepidothrix velutina* as a species given the dramatic differences in vocalizations and genetics between it and east of the Andes populations as thoroughly documented in the Moncrieff et al. (2022) paper."

Comments from Stiles: "YES on A,B, and C. The genetic and vocal evidence, as well as geography strongly support splitting *velutina* from the cis-Andean *coronata* group. I find the claim that retaining Blue-crowned for *velutina* would go against SACC policy: the only way this could be possible would be to use Eastern and Western Blue-crowned for the cis- and tran-Andean species, which would go over like a lead balloon for SACC, and I very much doubt that the name Blue-capped for *coronata* S.S. would cause irremediable confusion for northern birders in Brazil!"

Comments from Schulenberg: YES on B and C. I am totally onboard with Velvety (*velutina*) and Blue-capped (*coronata*) manakins."

Comments from Pacheco: "YES. Genetic and vocal repertoire data sets provide satisfactory support for this division."

Transfer Thicket Antpitta *Hylopezus dives* to *Myrmothera*

Note: This is a modified version of SACC proposal 832, the relevant part of which (832B) passed unanimously.

Background:

The current taxonomic organization of the genera *Hylopezus*, *Myrmothera*, and *Grallaricula* is not congruent with the phylogenetic history of the group. Consequently, it is necessary to redefine their generic boundaries while avoiding the erection of highly heterogeneous non-diagnosable taxa and minimizing the number of required taxonomic changes. Our assessments of phenotypic variation in combination with their phylogenetic reconstruction (Carneiro et al. 2018, 2019) suggest that four monophyletic groups are suitable units to be treated as separate genera. Of relevance to NACC, this means that some *species of Hylopezus* should be transferred to *Myrmothera*

Ridgway (1909) erected the genus *Hylopezus* with *H. perspicillatus* as its type species, and a couple of years later *H. dives* and *H. macularius* were allocated therein (Carriker 1910; Ridgway 1911). However, Cory and Hellmayr (1924) and Peters (1951) rejected this genus and maintained species of these genera in *Grallaria*. In the most recent and currently accepted genus-level taxonomic revision of the Grallariinae (now treated as the family Grallariidae), Lowery and O'Neill (1969) resurrected and redefined the genus *Hylopezus*, to which they allocated five species: *H. perspicillatus*, *H. macularius*, *H. fulviventris* (including *dives*), *H. berlepschi*, and *H. ochroleucus*, including *nattereri* from the Atlantic Forest.

In its original description, Pinto (1937) diagnosed *Grallaria nattereri* as a species distinct from *Grallaria ochroleuca* on the basis of longer tarsi and overall plumage differences. However, in the brief text of the description of the holotype, he acknowledged that "in the future it might prove to be subspecifically related to *G. ochroleuca*." In fact, only 2 years later, Naumburg (1939) treated *nattereri* as a subspecies of *G. ochroleuca* and its status as subspecies was maintained throughout most of the 20th century (Meyer de Schauensee 1970; Peters 1951; Pinto 1978), when it was elevated to species status on the basis of vocal, plumage, habitat, and distributional differences (Krabbe & Schulenberg 2003; Whitney et al. 1995).

New Information:

A comprehensive molecular phylogeny of lowland antpittas in the genera *Hylopezus* and *Myrmothera* (Carneiro et al. 2018) indicated that *Hylopezus*, as currently defined, is paraphyletic with respect to *Myrmothera* and *Grallaricula* (Fig. 1). Specifically, both species now placed in *Myrmothera* (*M. simplex* and *M. campanisona*), *H. dives*, *H. fulviventris*, and *H. berlepschi* form a strongly supported clade that is sister to a clade comprised by *H. perspicillatus*, *H. auricularis*, *H. ochroleucus*, *H. whittakeri*, *H. paraensis*, *H. macularius*, and *H. dilutus*. Our approach to assess diagnosability and define generic boundaries among these taxa integrates phylogenetic relationships with morphological and acoustic traits. Given the phenotypic and molecular differences, we proposed that generic limits in *Myrmothera* and *Hylopezus* (as well as in the extralimital *Grallaricula* and *H. nattereri*) be redefined to produce a taxonomic classification concordant with their phylogenetic relationships.

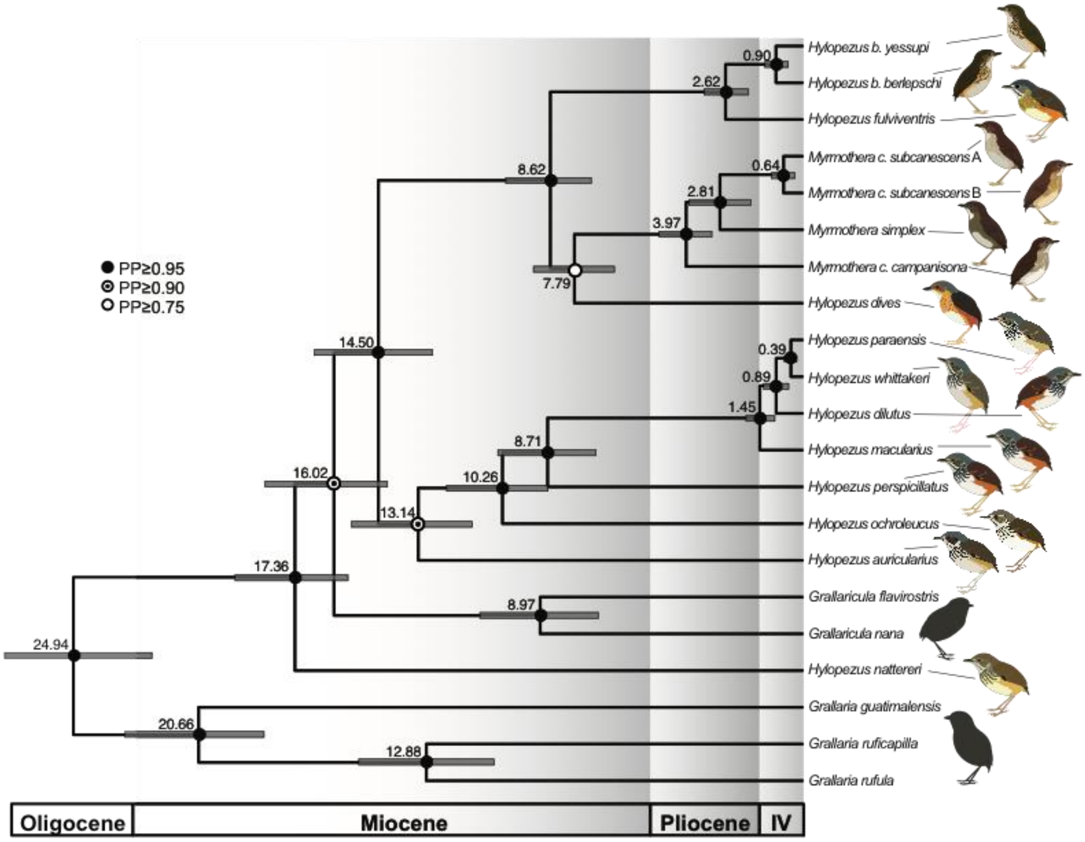


Figure 1. Reconstruction for antpittas estimated from multilocus dataset (species tree) using *BEAST. Bars indicate 95% highest posterior densities of divergence dates. The mean estimated dates are shown above nodes. Bayesian posterior probability (PP) support for nodes is indicated by coded circles according to the figure legend. IV = Quaternary. Images of antpittas species are adapted from Krabbe and Schulenberg (2003) and the Handbook of Birds of the World Alive. (Retrieved from Carneiro et al. 2019.)

Recommendation:

Given the obtained topology, Carneiro et al. (2019) suggested transferring *H. berlepschi*, *H. fulviventris*, and *H. dives* into *Myrmothera*, to keep *H. perspicillatus*, *H. auricularis, H. ochroleucus, H. macularius, H. dilutus, H. whittakeri*, and *H. paraensis* in *Hylopezus* (as well as maintaining the extralimital *Grallaricula* and placing the extralmital *H. nattereri* in the new genus *Cryptopezus*). This arrangement not only reflects more accurately the phylogenetic relationships in the group, but also produces diagnosable taxa while minimizing the number of required taxonomic changes. Any further splitting would lead to taxonomically inflated classifications, which would be undesirable from the point of view of the stability of the International Code of Zoological Nomenclature (ICZN, 1999). Therefore, it is recommended that the committee vote YES to transferring *H. dives* to *Myrmothera*.

Literature Cited:

Carneiro, L., Bravo, G. A, Aristizbal, N., Aleixo, A. (2018) Molecular systematics and biogeography of lowland antpittas (Aves, Grallariidae): The role of vicariance and dispersal in thye diversification of a widespread Neotropical lineage. Molecular Phylogenetics and Evolution 120:375-389.

Carneiro, L., Bravo, G. A, Aleixo, A. (2019). Phenotypic similarity leads to taxonomic inconsistency: A revision of the lowland's antpittas. Zool Scr. 48:46–56. https://doi.org/10.1111/zsc.12324

Carriker, M. A. Jr (1910). An annotated list of the birds of Costa Rica including Coco Island. Annals of the Carnegie Museum 6:314–915.

Cory, C. B., & Hellmayr, C. E. (1924). Catalogue of birds of the Americas and adjacent islands in Field Museum of Natural History. Pt. III. Pteroptochidae — Conopophagidae — Formicariidae. Field Museum of Natural History, Zoological Series 13(3):1–369.

ICZN [International Commission on Zoological Nomenclature] (1999). International code of zoological nomenclature, 4th ed. London, UK: International Trust for Zoological Nomenclature.

Krabbe, N. K., & Schulenberg, T. S. (2003). Family Formicariidae (Ground-Antbirds). In J. del Hoyo, A. Elliott, & D. Christie (Eds.), Handbook of the birds of the world (Lynx Edicions) Vol. 8 (pp. 682– 731). Barcelona, Spain: Lynx Edicions.

Lowery, G. H., & O'Neill, P. O. (1969). A new species of antpitta a from Peru and a revision of the subfamily Grallariinae. The Auk 86:1–12.

Peters, J. L. (1951). Check-list of birds of the world (7th Volume). Cambridge, MA: Museum of Comparative Zoology.

Ridgway, R. (1909). New genera, species and subspecies of Formicariidae, Furnariidae, and Dendrocolaptidae. Proceedings of the Biological Society of Washington 22:69–74.

Ridgway, R. (1911). The birds of North and Middle America. Bulletin of the United States National Museum 50(5):1–859.

Submitted by: Lincoln Carneiro

Date of Proposal: May 2019 (SACC proposal), modified for NACC on 21 January 2023

SACC comments:

Note from Remsen on voting procedure: Vitor Piacentini informed me that there may be a problem with the name *Cryptopezus* as an available name (comments to follow), so let's structure the voting as Part A. *Cryptopezus*, and Part B. Transferring species to *Myrmothera*.

Comments from Stiles: "YES to transferring the mentioned species to *Myrmothera* and to naming a new genus for *nattereri.* However, because *Cryptopezus* is preoccupied, I think it's up to Carneiro to propose a replacement name.. for now, call it "genus to be renamed" (much as we did for *Elliotia* for the same reason)."

Comments from Robbins: "This should be divided into two proposals given that *Cryptopezus* is apparently not available. That should be sorted out and a new proposal created. Thus, "No" to that element. "YES" to the transfer of *berlepschi*, *fulviventris*, and *dives* to the genus *Myrmothera* based on the genetic data."

Comments from Zimmer: (A) "YES" to erecting a new genus for *H. nattereri*, based upon the phylogeny presented by Carneiro et al 2019, which establishes *nattereri* as sister to a clade which contains all of the other species currently recognized in *Hylopezus*, as well as all of *Myrmothera* and *Grallaricula*. However, given the raised possibility that "*Cryptopezus*" may not be available, I think that Gary's suggestion ("genus to be renamed") is a good one until Carneiro proposes another name. (B) "YES" to the third option presented in the Proposal, which is to maintain the cohesive *Grallaricula* as it is currently constituted, and to transfer *berlepschi, fulviventris* and *dives* into *Myrmothera*, while maintaining the other species in *Hylopezus.* Some of these moves make sense to me on the basis of vocal characters, natural history, morphology, etc., whereas others are not particularly intuitive, but such a rearrangement does at least conform to the relationships revealed in the phylogeny, and does so in the least objectionable and destabilizing way in my opinion. I would be opposed to any restructuring that diluted the cohesion and distinctiveness of *Grallaricula*, and the heterogeneity that would result from lumping everything else into an expanded *Myrmothera* would result in a less informative, overly heterogeneous grouping."

Comments from Areta: "A. YES to the idea of placing *nattereri* in its own genus (a surprising but solid result), pending on the resolution of whether *Cryptopezus* is available or not. This being said, and until this is solved, we would need to put *nattereri* somewhere.
"B. YES to moving *dives*, *berlepschi* and *fulviventris* to *Myrmothera*."

Comments from Claramunt: "A NO. Need to wait until there is a name available for *nattereri*. Indeed, the name *Cryptopezus* was proposed in an on-line appendix, thus not properly published under ICZN rules, thus not available. Also, I would like to see how well supported is the position of *nattereri* as a basal lineage. It is definitely supported by the mitochondrial dataset but nuclear trees are not shown.
"B. YES. I think the proposed solution is reasonable."

Comments from Stotz: "A. YES and NO. I think that *H. nattereri* needs to be moved out of *Hylopezus*, but we need to make certain there is an available name. I think in other cases when we were certain a species was misplaced in its current genus, but didn't have an alternative genus to place it in, we've used double quotes around the generic name, so, while we wait for a clear generic name, would could call it "*Hylo[ezus*" *nattereri*.
"B. YES. This treatment seems the clear best choice given the phylogenetic tree and the degree of morphological distinctiveness in the group."

Comments from Pacheco: "A. NO. The treatment of *nattereri* in genus apart although evidenced needs to wait for a validly proposed name.
"B. YES. To relocate *dives*, *berlepschi* and *fulviventris* to *Myrmothera*.

Comments from Bonaccorso: "A. YES, move *nattereri* to its own genus whenever a name is available; but I do not agree with using the double quotes on "*Hylopezus*" since most non-taxonomists will be confused. I think we should urge Carneiro et al. to do a proper description (as Santiago says, according to ICNZ rules) so the issue is solved as soon as possible, without further confusion.
"B. YES to transfer *H. berlepschi*, *H. fulviventris*, and *H. dives* to *Myrmothera*."

Comments from Remsen (5 Apr. 2020): "Gustavo Bravo informed me today that *Cryptopezus* now registered in ZooBank: http://zoobank.org/References/533674EE-6734-4B37-A7D1-30523E62016A

Comments from Jaramillo: "A YES – As I understand it *Cryptopezus* is now available, or did I get this wrong? If so, then yes move *nattereri* to *Cryptopezus*.

"B YES – Specifically to transferring *berlepschi*, *fulviventris* and *dives* into *Myrmothera."*

Additional comments from Robbins: “A. YES. Given that *Cryptopezus* has been verified as an available name, I support placing the genetically distinct (very long branch) *nattereri* in that genus.”

Additional comments from Stiles: “A. YES. With Vitor's approval, I will vote YES to accept *Cryptopezus*.”

Additional comments from Claramunt: “With the name registered in Zoobank and reported in the publication, the name has been made available, I change my vote to YES.”

Treat American Three-toed Woodpecker *Picoides dorsalis* as a subspecies group of *P. tridactylus*

Effect on NACC:

This would change our treatment of *Picoides dorsalis* (American Three-toed Woodpecker) to be a subspecies group (of three subspecies) of *Picoides tridactylus* (what is presently Eurasian Three-toed Woodpecker but which would thus be best rendered as Three-toed Woodpecker). If this sounds familiar, this is how we treated it in the last four editions of the *Check-list* (1931-1998), only changing the English name after the 5th ed. (deleting "Northern" from Three-toed Woodpecker), then later splitting *P. dorsalis* out as a full species in Banks et al. (2003). There are three North American subspecies: *dorsalis*, *fasciatus*, and *bacatus*; all three would revert to being subspecies of *tridactylus* sensu lato (e.g., AOU 1931-1998, Peters 1948, Short 1982, Winkler et al. 1995, del Hoyo et al. 2002).

Background:

I am going to skip a deep dive into the taxonomic history of the treatment of *dorsalis*. In brief, prior to adoption of the biological species concept (BSC) *dorsalis* was often considered a full species, then it was generally lumped as a subspecies of *tridactylus* during the era of adoption of the BSC. After AOU (1931) we treated it this way until Banks et al. (2003), who wrote:

> New World and Old World populations of Three-toed Woodpeckers are split on the basis of differences in mitochondrial DNA (Zink et al. 1995, 2002) and voice (Winkler and Short 1978, Short 1982). Ridgway (1914) considered New World and Old World populations to be separate species, and the merger of New World *dorsalis* into Old World *tridactylus* (e.g., AOU 1931, Peters 1948) was never explained.

I want to break this down beginning with the last sentence first. The editorial style constraints of AOU (1931) and the "Peters" et al. volumes generally (if not completely) precluded the authors from explaining their treatments. Retrospectively finding fault with knowledgeable people for not doing something they couldn't actually do in that forum seems to me a weak argument. Thankfully, we have left that unfortunate style behind and make our decisions more transparent today, but I tend to have some respect for historic treatments by our predecessors. The absent explanation, of course, though unwritten at the time in order to meet to the style of these publications, was their recognition that phenotypic differences were, relatively speaking, more in line with subspecies-level treatment under the BSC. Concordance in this treatment was broad, and, basically, it is this phenotypic similarity, now quantified (del Hoyo and Collar 2014; see below), that brings us back to this issue today.

Next let's consider the differences in voice cited by Banks et al. (2003). While Winkler & Short (1978) and Short (1982) noted vocal differences between North American and Eurasian birds, they did not consider them sufficient to suggest that these groups should be split as biological species. Nor would we be likely today to consider their evidence to be sufficient for such a split. As they wrote:

> The Call Note of Central European birds (Germany, Austria) is shaped like a broad arrowpoint, with the fundamental tone emphasized and possesses significant

> introductory and ending elements (fig. 3L, M, table 2; see Ruge, 1975). Swedish birds have essentially the same calls. North American birds (New York) are different in all their measurable characters. Unfortunately, our recordings are insufficient for comparison of these geographical groups. This species, the only Holarctic woodpecker, would be an ideal subject for the study of geographical variation ... (Winkler & Short 1978:16).

Overall, authors who really know their woodpeckers and did not have the editorial constraints of the earlier AOU *Check-lists* or the "Peters" volumes in either this (Winkler & Short 1978) or later works considered the evidence to treat these taxa as one biological species sufficiently strong that they didn't even mention the possibility of a species-level split, despite repeated opportunities to do so (e.g., Winkler & Short 1978, Short 1982, Winkler et al. 1995).

Enter mtDNA. Three mtDNA datasets for these taxa have been published upon, and all three groups of authors recommended a species-level split. The first study (Zink et al. 1995) was a small sampling (n = 9) using RFLPs to compare Eurasian and North American populations and found ~5.5% divergence. The second study (Zink et al. 2002) used more birds (n = 29), broader geographic sampling, and 1234 bp (from ND2, ND3, and cyt-*b*) and found 3.8% divergence. The third mtDNA dataset published upon is that of Johnsen et al. (2010), who used COI barcode data (sampling details not given in paper) to report a 3.7% COI divergence. (In addition, I have access to a small as-yet unpublished mtDNA data indicating that between continents the birds are ~2.5% divergent in ND2 using Jukes-Cantor corrected *p*-distance.)

The mtDNA data are intriguing, and they played a prominent role in splitting these taxa. (With genetic data available, Winkler & Christie (*in* del Hoyo et al. 2002) also split the two groups into separate species.) But that was a time when we were still in thrall to the powers of mtDNA to diagnose species limits ─ which we know today to often be a mirage.

Plumage variation of the entire complex is rather pronounced (Figure), showing that there is quite a bit of variation occurring without much mtDNA variation to correspond with it; the continental clades show little if any structure (see Zink et al. 2022).

Finally, something to keep in mind, as Winkler & Short (1978) noted, when *P. tridactylus* is treated as a single species, it is the only Holarctic woodpecker.

New information:

Currently, the world lists treat *P. dorsalis* either as a species (Dickinson & Remsen 2013, Clements et al. 2022), or as a subspecies group of *P. tridactylus* (del Hoyo & Collar 2014, Gill et al. 2022).

Between del Hoyo et al. (2002) and del Hoyo and Collar (2014) the Tobias et al. (2010) method was applied to this taxonomic question and the two groups scored so low on that scale (~2) that they were lumped into one species. Here is the reasoning given for the lumping in the HBW-Birdlife checklist (http://datazone.birdlife.org/species/taxonomy).

> In recent decades North American subspecies commonly treated as forming a separate species (*P. dorsalis*) on basis of genetic evidence (Johnsen et al. 2010), but morphological differences involve merely narrower postocular stripe (1) and smaller size (according to published measurements, no more than 1); all-white outer tail feathers shared by East Asian subspecies *albidior* and

> *crissoleucus*, and notion of less white in forecrown not supported by specimen evidence. [I include more here as relevant for species limits in the group…] Distinctive form *funebris*, however, here allowed species status (see related note/s). Currently accepted subspecies designated according to coloration, but variation is clinal, birds becoming darker and larger from N to S; comprehensive revision based on genetic and biogeographical grounds required.

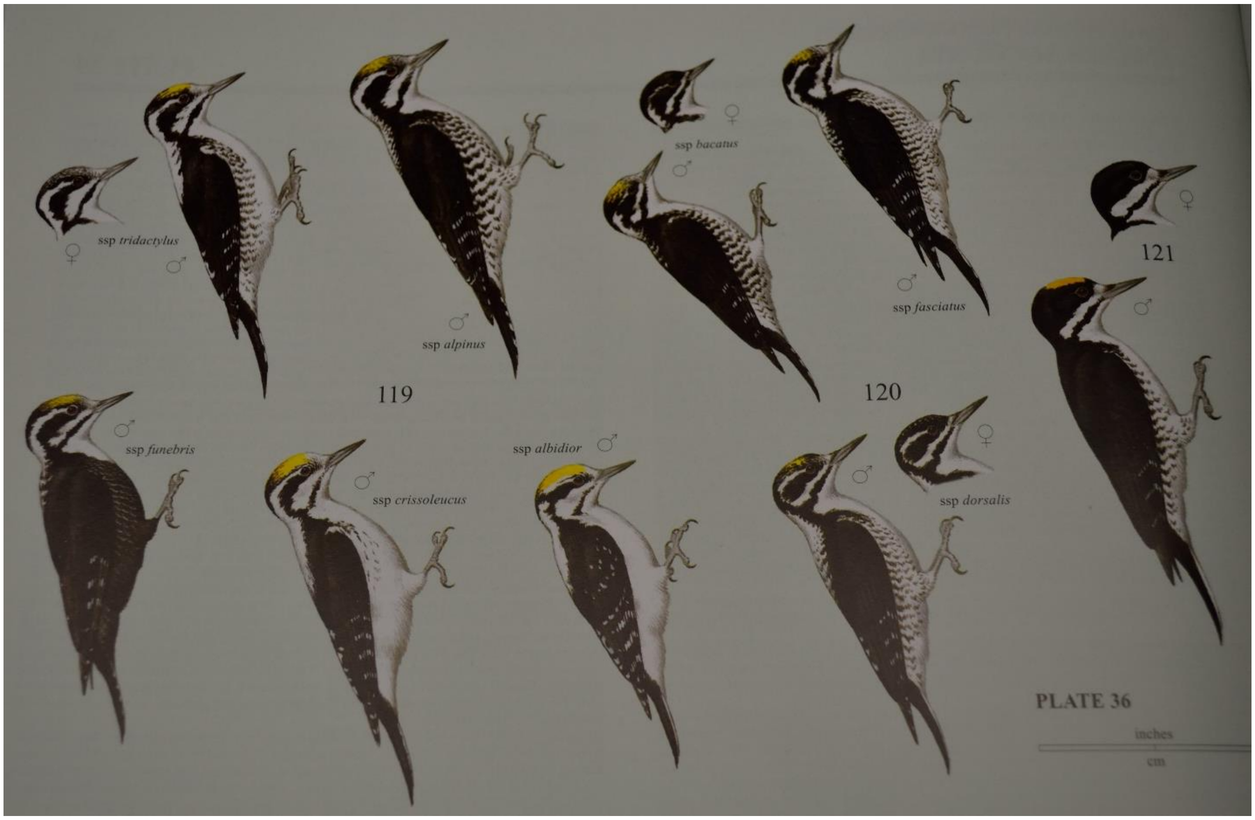


Figure. *Picoides tridactylus* (no. 119), *P. dorsalis* (no. 120), and *P. arcticus* (no. 121), from del Hoyo et al. (2002).

Note, however, that the HBW-BirdLife (2014) treatment effectively ignores genetic differences: genetic data are not part of the Tobias et al. (2010) scoring methodology. While the mtDNA data are in my mind equivocal, they are intriguing. Study of the nuclear genome is warranted (and likely forthcoming).

Taxonomy and Nomenclature:

If both parts of this proposal are approved (taxonomic and English names changed), we would consider *Picoides dorsalis* (American Three-toed Woodpecker) to be a subspecies group (of three subspecies) of *Picoides tridactylus* (Three-toed Woodpecker).

Recommendation:

While I think that a proposal to split these taxa today based on current information would fail, and that single-species status is probably warranted, I recommend voting “No” on this proposal to re-lump them at this time. The phenotypic evidence alone suggests single-species treatment, but the mtDNA data indicate that something interesting is going on. Until we have a better handle on that through nuclear data, I think it would be premature to make another change based essentially on different opinions about a body of evidence that has not really changed much. In other words, let’s eventually do one change if clearly needed and not risk having to make two because the future nuclear data (and perhaps that much-needed comparative work on voice across the range) do end up supporting our current treatment.

Please vote on the following:

a) Treat *P. dorsalis* (and its three subspecies) as a subspecific group of *P. tridactylus*.
b) If (a) passes, change our English name of Eurasian Three-toed Woodpecker back to Three-toed Woodpecker.

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Submitted by: Kevin Winker

Date of Proposal: 31 January 2023

Treat *Colaptes aeruginosus* as a separate species from Golden-olive Woodpecker *C. rubiginosus*

Background:

Colaptes rubiginosus was described by Swainson in 1820 as *Picus rubiginosus*, and it is currently treated by NACC-SACC as a highly polytypic species ranging from northeastern Mexico south to northwestern Argentina. Under this classification, *aeruginosus*, described by Malherbe in 1862, is the northernmost subspecies, distributed from Nuevo León and Tamaulipas south to central Veracruz. The main plumage differences between *aeruginosus* and the nearest subspecies of *rubiginosus* (*yucatanensis*, which is found from southern Mexico to Panama) are the extent of the male's red supercilium, which extends only from the nape to behind or above the eye in *aeruginosus* but from the nape to the bill in *rubiginosus*; the rear ear-coverts, which are plain in *aeruginosus* but barred in *rubiginosus*; the shape of the barring on the underparts, which is wavy or scale-shaped in *aeruginosus* but straight in *rubiginosus*; and the proportionately longer tail of *aeruginosus*.

Standard taxonomic references from the first half of the 20th century, e.g., Ridgway (1914), Cory (1919), and Peters (1948), considered the current NACC species *C. rubiginosus* to consist of more than one species but had different views of species limits. Ridgway (1914) considered *C. rubiginosus sensu lato* to consist of four species: *C. aeruginosus*, *C. rubiginosus*, *C. chrysogaster* of Peru, and *C. gularis* of Colombia. Cory (1919) merged *gularis* into *C. rubiginosus* and thus recognized only three species: *C. aeruginosus*, *C. rubiginosus*, and *C. chrysogaster*. Peters (1948) further merged *chrysogaster* into *C. rubiginosus* and thus recognized only two species: *C. aeruginosus* and *C. rubiginosus*. The latter two species were apparently first lumped by Short 1982 (at least I cannot find an earlier reference), who considered the differences between the two to fall within the scope of variation shown by the other 17 subspecies of *C. rubiginosus*. Short specifically mentioned subspecies *tucumanus*, as follows: *aeruginosus* "is judged to be no more distinct than other ones such as *tucumanus*, and it shares the sexual dimorphic pattern of other races of *rubiginosus*" (the latter statement is a reference to the closely related *C. auricularis*, which is not sexually dimorphic).

Indeed, the plumage differences shown by *aeruginosus* represent only a small part of the variation within *C. rubiginosus*, and some of the characters that purportedly distinguish *aeruginosus* from *C. rubiginosus* are highly variable within *C. rubiginosus*. For example, the extent of the red on the head varies from a rather short supercilium in *paraquensis* and *guianae*, in addition to *aeruginosus*, to covering most or all of the head in subspecies such as *gularis*; the rear ear-coverts are also variable. Other characters that differ among subspecies of *C. rubiginosus* include ventral coloration and the extent and coloration of the ventral barring. The shape of the barring, however, does appear to distinguish *aeruginosus* from other subspecies of *C. rubiginosus*, and is the only qualitative plumage feature mentioned by Ridgway (1914) in his key to this complex. He distinguished *C. aeruginosus* by "Chest and breast irregularly barred or squamated; larger (wing averaging more than 130; tail more than 85)" whereas *C. rubiginosus* was characterized as "Chest and breast regularly barred; smaller (wing averaging less than 130; tail less than 80)."

The following photos show males of eight subspecies of *C. rubiginosus*. From left to right in the photos are specimens of the following subspecies (with the general collecting locality in parentheses): *aeruginosus* (northeastern Mexico), *yucatanensis* (southern Mexico), *guianae*

(Guyana), *gularis* = “*pacificus*” (western Colombia), *buenavistae* (eastern Colombia), *chrysogaster* (central Peru), *canipileus* (Bolivia), and *tucumanus* (northwestern Argentina).

Unfortunately, the USNM lacks several distinctive subspecies, such as *paraquensis* and *viridissimus*.

AOU (1983) and AOU (1998) treated *aeruginosus* as conspecific with *C. rubiginosus*, presumably following Short, but the two taxa were tentatively split by Howell and Webb (1995) based on differences in plumage and voice, the latter characterized as:

> *rubiginosus* – "A sharp, slightly explosive *kee'ah* or *k'yaah*, recalling a flicker, and a rapid, shrill, churring rattle"
>
> *aeruginosus* – "A sharp, nasal, squirrel-like *kyow'n* or *chey-ey*, at times repeated in short series, and a steady series of sharp *weeyk!* or *wheeir* notes, 10/4-6 s, suggesting Squirrel Cuckoo song; also a low, short, guttural chatter, audible at close range. Voice thus quite different from Golden-olive Woodpecker [*rubiginosus*]."

Howell and Webb's taxonomic note on a potential split was as follows: "Distinct vocalizations and plumage differences suggest specific status for Bronze-winged [*aeruginosus*] and Golden-olive [*rubiginosus*] woodpeckers. Field studies are needed to investigate the extent of intergradation (if any?) in cen Ver." Accordingly, their text and distribution maps indicated that the range of *aeruginosus* extends south to central Veracruz and that the range of *rubiginosus* extends north to central Veracruz.

New information:

As part of a study of the genera *Piculus* and *Colaptes*, Moore et al. (2011) sequenced four individuals of *rubiginosus s.l.*, two from Mexico and two from Peru, for three mitochondrial genes (cyt b, COI, 12S rRNA), and found that the Mexican and Peruvian individuals were not sisters: the two from Peru were sister to *C. atricollis* whereas the two from Mexico were sister to *C. auricularis*:

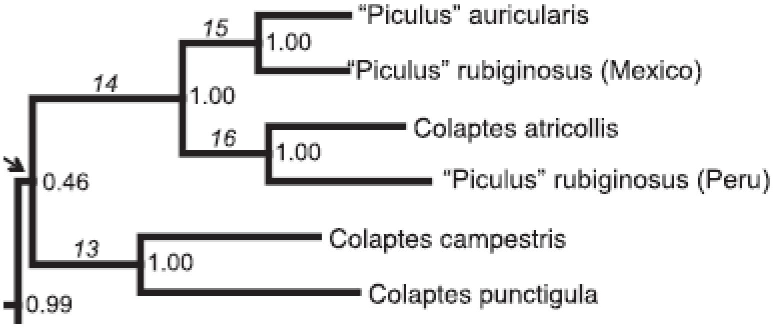


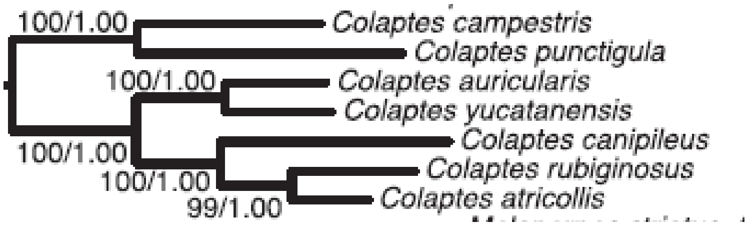
Fig. 1. Excerpt from the Bayesian phylogenetic tree in Moore et al. (2011) showing the paraphyly of *C. rubiginosus*. Numbers to the right of the nodes are posterior probabilities; numbers above the branches are simply reference numbers.

Moore et al. did not identify their samples to subspecies and described their samples from Mexico simply as belonging "to a Mexican subspecies of *rubiginosus*". However, based on collecting localities, their Mexican samples (from the Sierra de Santa Martha in southern Veracruz) would be subspecies *yucatanensis* and their Peruvian samples (from Lambayeque) would be subspecies *rubripileus*. They concluded their paper by stating the following: "Genetic analyses based on extensive taxon sampling of *rubiginosus*, *auricularis* and *atricollis* that includes the many subspecies of *rubiginosus* and the two disjunct subspecies of *atricollis* are required to clarify these relationships."

Gill evidently assumed that Moore's Mexican samples were referable to *aeruginosus* and consequently split *aeruginosus* from *rubiginosus* in the IOC list (e.g., Gill et al. 2021), retaining all other subspecies, including *yucatanensis*, in *rubiginosus*. The note on the IOC list is as follows: "*C. aeruginosus*, previously treated as a ssp. of *rubiginosus*, is sister to *auricularis*; *rubiginosus* is sister to *C. atricollis* (Moore et al. 2010)."

Although both Mexican tissues used by Moore are Field Museum tissues, only one of them is vouchered there (FMNH 343228); the other (FMNH 395799) is vouchered at UNAM (as UNAM 7788). Ben Marks and Blanca kindly provided photos of the vouchers and the IDs have now been confirmed as *yucatanensis* rather than *aeruginosus*, meaning that the IOC's recognition of *C. aeruginosus* as a separate species is based on mitochondrial differences between *C. r. yucatanensis* and *C. r. rubripileus*, and that data from *aeruginosus* are lacking.

Dufort (2016) published a woodpecker supertree, using sequences from GenBank, that apparently (I couldn't find a list of samples used in this paper) included Moore's samples and identified them as *C. yucatanensis*, because there is a terminal taxon labeled with this name in the same position as in the Moore tree (as sister to *C. auricularis*). Two other terminal taxa in the Dufort tree are also part of *C. rubiginosus*, i.e., "*Colaptes canipileus*" and "*Colaptes rubiginosus.*" These two taxa are not sister to *yucatanensis*, nor do they form a monophyletic group themselves; instead, they are successive sisters to *C. atricollis*:



I searched GenBank for sequences of *C. rubiginosus* and found that the only records for this species, other than the Moore sequences from Mexico and Peru, are from Guyana, suggesting that the taxon labeled "*Colaptes canipileus*" in the Dufort tree actually represents Moore's samples of subspecies *rubripileus* (*canipileus* is found in southern Peru and Bolivia rather than northwestern Peru) and that the taxon labeled "*Colaptes rubiginosus*" represents samples from Guyana, which would be either subspecies *guianae* or *nigriceps*.

Of note is the fact that none of the subspecies that form separate lineages in the Moore et al. (2011) or Dufort (2016) studies (*yucatanensis*, *rubripileus*, and *guianae/nigriceps*) correspond to the subspecies formerly considered species by Ridgway, Cory, or Peters, which were *aeruginosus*, *chrysogaster*, and *gularis*. Instead, all taxa sampled for mtDNA were considered conspecific with *C. rubiginosus* by these references, and their distinctive mtDNA lineages provide an indication of the complexity of variation in this species.

(More recently, Shakya et al. (2017) published a phylogeny of most species of woodpeckers based on both mtDNA and nuclear introns. Unfortunately, they only included a single tissue of *C. rubiginosus*, a sample from Guyana.)

Birdlife has also split *aeruginosus* from *rubiginosus*, using the same division as Gill, but basing their split on plumage and the vocal descriptions in Howell and Webb:

> *aeruginosus* "Until recently treated as subspecies of *C. rubiginosus*, but differs in male's red supercilium extending from nape to above eye vs extending from nape to bill (2); rear ear-coverts clear vs barred (1); bars on underparts more scale-shaped (1); wings and tail longer (effect size for tail vs *C. r. yucatanensis* 3.63; score 2); wholly different song (deliberate slow-paced series of c. 6 typical picoid high-pitched calls, "kwi, kwi, kwi, kwi, kwi, kwi" vs protracted rising rattling trill), extensive playback experiments yielding frenzied response from own taxon, no response from other taxon (Howell & Webb 1995, Howell 2013b) (4)."

As noted above, the extent of the red supercilium and the barring on the ear-coverts are variable within *C. rubiginosus* and should not be considered diagnostic differences with *aeruginosus*. Also note that "Howell 2013b", which appears to be the sole basis for the playback statement and is cited in the manner of a publication, is actually Howell "in litt." rather than a publication.

The vocal data to me are much more convincing than the genetics or morphology, at least based on current sampling. The difference in what some call "songs' and others call "long calls" seems clear, although the sample size for *aeruginosus* isn't huge (I found 8 independent recordings on xeno-canto and Macaulay). There are no recordings of some subspecies of *C. rubiginosus*, but variations of the "rattle" call can be heard in many parts of its range (based on spot-checking samples on xeno-canto and Macaulay), including in *yucatanensis*, and none of the recordings of *aeruginosus* includes the rattle. Although several vocal samples of *aeruginosus* are from Veracruz (mostly from the vicinity of Xalapa), there is only one recording of *yucatanensis* from the southern half of the state, where *yucatanensis* occurs. This recording is of an individual not seen when recorded but later identified as *C. rubiginosus* (xeno-canto doesn't list it under *yucatanensis*, perhaps because the ID was made after the recording was submitted). The call of this individual, from Orizaba, ca. 80 km south of Xalapa, did include the rattle (see https://xeno-canto.org/305868). Nevertheless, it's difficult to draw conclusions from a sample size of one, and the degree of intergradation where the two forms meet remains to be investigated, as noted previously by Howell and Webb (1995). The fact that Moore's samples from southern Veracruz might contain mtDNA from *aeruginosus* (mitochondrial introgression being one possible explanation of their genetic results) suggests that the degree of intergradation may be a significant question.

Summary and Recommendation:

When I first looked into this potential species split, I expected to recommend that the split be adopted due to the aggregate weight of the vocal and genetic differences, added to the earlier recognition of *C. aeruginosus* by Ridgway, Cory, and Peters. This was in spite of drawbacks to each individual dataset: the relative lack of vocal sampling in the northern part of the range of *yucatanensis*, the lack of nuclear genetic data and the limited sampling of *C. rubiginosus*, and the morphological variation within *C. rubiginosus*.

Now that we know that there are no genetic data for *aeruginosus*, that the three subspecies of *C. rubiginosus* sampled to date form different mitochondrial lineages, and that none of the other species recognized by Ridgway or Cory have been sampled so far, the situation is much more complex than it at first appeared. It is extremely likely that *C. rubiginosus* consists of more than one species, but how many and how the various subspecies should be apportioned is unclear. However, it does appear that a simple separation of *C. aeruginosus* from all other subspecies of *C. rubiginosus* would still leave us with a paraphyletic *C. rubiginosus*.

I recommend that we vote NO on the recognition of *C. aeruginosus* as a separate species from *C. rubiginosus* pending a more complete study of genetic and phenotypic variation within *C. rubiginosus* and its close relatives (at a bare minimum, I would like to see some genetic data for *aeruginosus*). In my view, this would be a very interesting grad student project.

English names: if this proposal were to pass, then I suggest that we adopt the English name Bronze-winged Woodpecker for *C. aeruginosus*. This name was used in AOU (1983) and AOU (1998) for the *aeruginosus* group and is also in use for *C. aeruginosus* (e.g., IOC list). Golden-olive Woodpecker would be retained for the much more widespread *C. rubiginosus s.s*.

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Submitted by: Terry Chesser

Date of Proposal: 3 February 2023

Treat *Melanerpes santacruzi* as a separate species from Golden-fronted Woodpecker *M. aurifrons*

Melanerpes aurifrons (Golden-fronted Woodpecker) is a sedentary, polytypic species of the temperate and tropical regions of Middle America, from Texas to Central America. This species has pronounced geographic variation, with strong clinal variation in body size, barring of the plumage, and coloration of the nasal tufts, nape, and belly (from black to barred with white). Nape color of males, typically yellow to orange in Texas and the Mexican Plateau, is red on the Yucatán Peninsula, and orange in Guatemala and Chiapas, El Salvador, and Honduras. The breast color is lighter in northern populations to olive in Central America. The black-and-white dorsal bars are wider in the northern populations and less wide to the south (Husak and Maxwell 2020). See the specimen photos on the following pages for an indication of the variation in this species.

Ridgway (1914) and Cory (1919) recognized four species within what we currently treat as the single species *M. aurifrons*: *Centurus aurifrons*, *C. dubius*, *C. polygrammus*, and *C. santacruzi*. Interestingly, *C. dubius* was well separated from the rest in both publications, suggesting that it was not considered a close relative. Four species intervened: *C. rubriventris*, *C. subelegans*, *C. seductus* (these three now considered conspecific as *M. rubricapillus*), and *C. hoffmannii*. Peters (1948) placed these species in *Melanerpes* and lumped *aurifrons*, *dubius*, *polygrammus*, and *santacruzi*, as well as *hoffmannii*, under the species *M. aurifrons*, while recognizing *M. rubricapillus* as a separate species. Selander and Giller (1963) treated the forms lumped by Peter as *M. aurifrons* as two species: *M. aurifrons* (including *dubius*, *polygrammus*, and *santacruzi*) and *M. hoffmannii*. This taxonomy was followed by Short (1982) and AOU (1983, 1998).

In Birds of the World online, Husak and Maxwell (2020) treated the four species of Ridgway as groups within *M. aurifrons*:

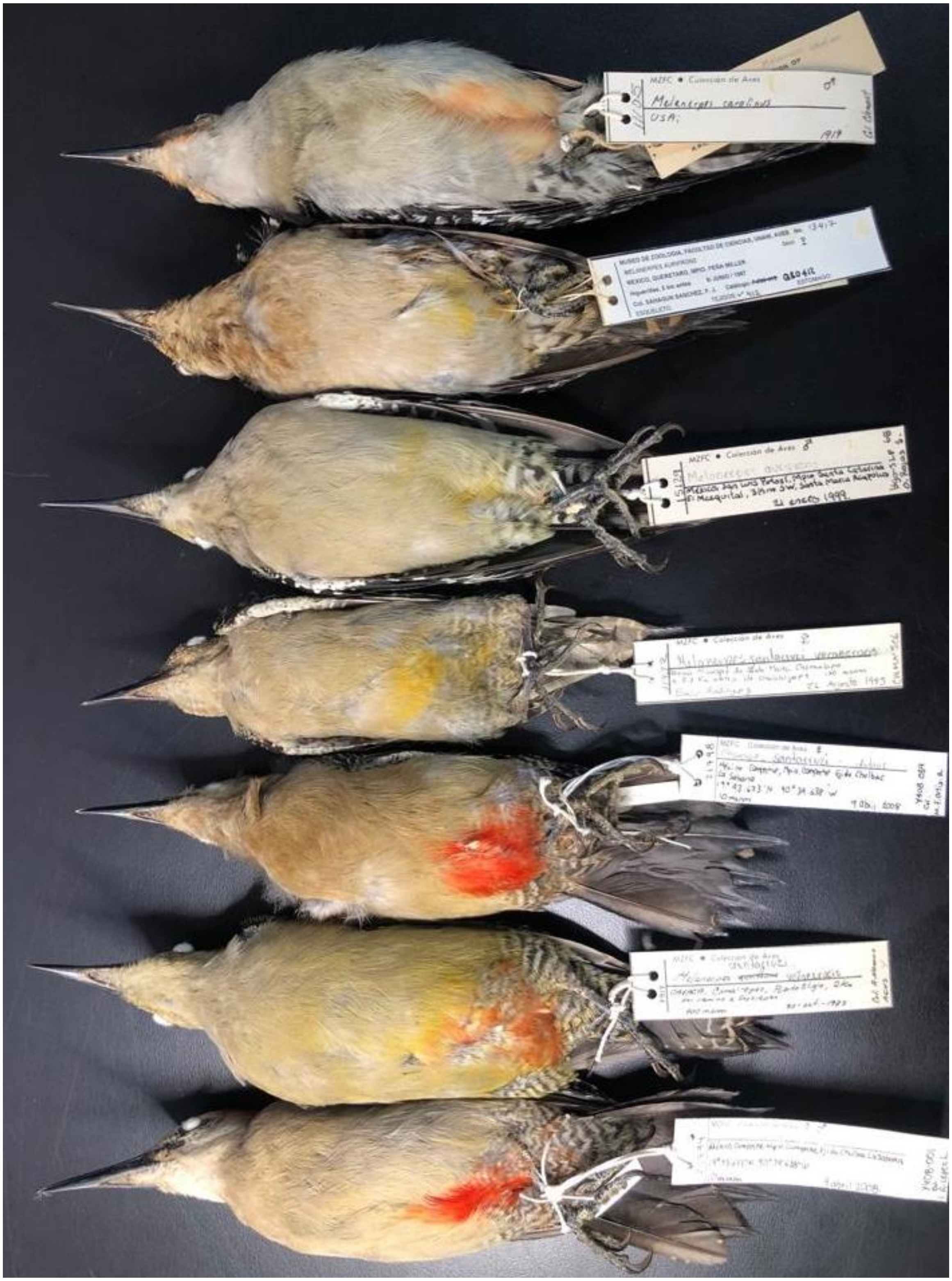
(1) *aurifrons* group (monotypic), distributed from Oklahoma and Texas across the Mexican Plateau to Jalisco, Michoacán, Hidalgo, and nw San Luis Potosí (México), with paler gray below and yellow on head and wider white barring.

(2) *dubius* group, including five subspecies (*M. a. veraecrucis*, *M. a. dubius*, *M. a. leei*, *M. a. turneffensis* and *M. a. canescens*) distributed from Veracruz to Central America, with red nape, nasal tufts, and belly, narrow white bars dorsally.

(3) *polygrammus* group (monotypic), distributed on the Pacific slope of Oaxaca and Chiapas, like *aurifrons*, but with white barring on central rectrices, yellow nape merging with red crown-patch, and with barring slightly narrower.

(4) *santacruzi* group, including five subspecies (*M. a. grateloupensis*, *M. a. santacruzi*, *M. a. hughlandi*, *M. a. pauper* and *M. a. insulanus*), distributed from east-central Mexico to Nicaragua, with orange nape continuous with red crown-patch, belly yellow to yellow orange, nasal tufts yellow to orange, white bars relatively narrow, central rectrices sometimes with white at base, white wing-patch reduced or absent.

Selander and Giller's (1963) classification of the *M. aurifrons* complex was based on a detailed analysis of phenotypic variation in plumage and morphometric characters. Regarding the key



Ventral views of specimens from Museo de Zoología, UNAM. From top to bottom: *M. carolinus* (male), two *M. aurifrons* (female and male), and four *Melanerpes santacruzi* (females and males).

Dorsal views of specimens from Museo de Zoología, UNAM. From top to bottom: *M. carolinus* (male), two *M. aurifrons* (female and male), and four *Melanerpes santacruzi* (females and males).

subspecies *grateloupensis*, the northernmost subspecies of the proposed *M. santacruzi* and the subspecies in direct contact with *aurifrons*, they concluded that *grateloupensis* is characterized by clines that join *aurifrons* with the southern subspecies *dubius*:

> As indicated above in our discussion of patterns of variation, the characters of the strikingly marked races *C. a. aurifrons* and *C. a. dubius* (as herein defined) intergrade completely in clinal fashion over an extensive area from central San Luis Potosi south to southern Veracruz. Largely because it is convenient to have a name by which to refer to these intergradient populations, we follow general practice in recognizing *C. a. grateloupensis* (Lesson, 1839, p. 41), with type locality "Mexico," but, contrary to general practice, we would apply this name to all populations from central San Luis Potosi south to southern Veracruz. Wetmore (1943) and others recognize a second race, *C. a. veraecrucis* (Nelson, 1900, p. 259), with type locality at Coatzacoalcos, Veracruz, but we prefer to follow Griscom (1932) in considering it a synonym of *C. a. grateloupensis*. (p. 235)

Regarding the *M. aurifrons* complex as a whole, they stated:

> Our studies fully support the view that all populations of the *aurifrons* complex belong to a single species, since even the most highly differentiated forms have been shown to intergrade in zones of contact. We have already discussed in detail the complete and gradual transition from *C. a. aurifrons* of the Mexican plateau to *C. a. dubius* of the Yucatán Peninsula through populations assigned to *C. a. grateloupensis*. (p. 237)

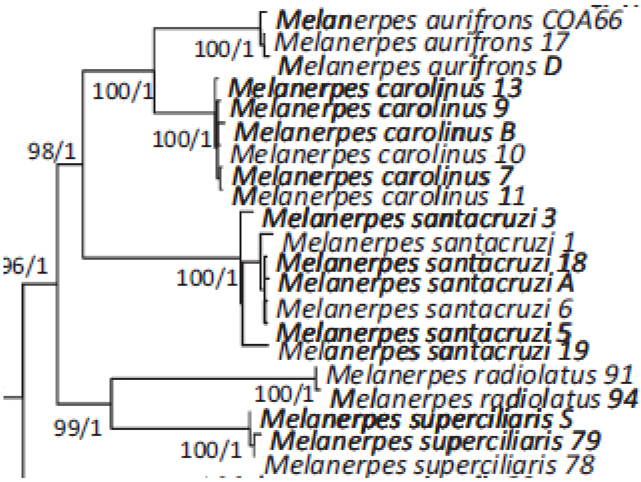
García-Trejo et al. (2009) sequenced 872 bp of mitochondrial DNA for 11 species of *Melanerpes*, including broad sampling within *M. aurifrons*. Their results showed that “northern *M. aurifrons*” is sister to *M. carolinus*, whereas “tropical *M. aurifrons*” is sister to these two taxa (thus indicating that an *M. aurifrons* that includes *M. santacruzi* is paraphyletic in mtDNA). They concluded that *M. santacruzi* (“tropical *M. aurifrons*”) should be recognized as a separate species from *M. aurifrons* (“northern *M. aurifrons*”), a conclusion later adopted by the IOC list (e.g., Gill et al. 2021). Under this species concept, *M. aurifrons* is monotypic whereas *M. santacruzi* contains all other subspecies and is distributed from east-central Mexico to northern Nicaragua. *Melanerpes santacruzi* shows ample intraspecific phenotypic variation, and some of its populations are morphologically similar to other species of the genus.

Our committee considered a proposal to separate *M. santacruzi* from *M. aurifrons* in 2013 (Proposal 2013-A-2, written by Nathan Pieplow) based on the mitochondrial results and evidence from online vocal recordings (see below for vocal details). The proposal is here: https://americanornithology.org/wp-content/uploads/2020/02/2013-A.pdf
and the comments are here: https://americanornithology.org/about/committees/nacc/current-prior-proposals/2013-proposals/comments-2013-a/#2013-A-12.
The vote on this proposal was 5-5 and the change was therefore not adopted, largely due to the lack of nuclear sequence data and the lack of information from contact areas, especially between subspecies *grateloupensis* and *M. aurifrons*.

New information:

Navarro-Sigüenza et al. (2017) sequenced 2 mitochondrial genes and 4 nuclear introns in a broad-scale study of the genus *Melanerpes*. Their results indicated, in agreement with those of

García-Trejo et al. (2009), that *M. aurifrons* and *M. carolinus* are sister species, and that *M. santacruzi* is sister to them (Fig. 1 below).



However, this result was based entirely on the mitochondrial signal – trees based on the nuclear genes alone did not support the monophyly of the three species, instead indicating a polytomy in which samples of the three taxa were mixed (Llanes-Quevedo et al. 2022).

Benites et al. (2020) subsequently analyzed geographic variation in phenotype in *M. santacruzi*. Across its range, distinct plumage morphs (both color and pattern) were associated with locality, whereas size did not show a clear geographic pattern. These patterns did not correspond to subspecies (Fig. 2); rather, they found correlations of phenotypic characters with environmental variables, with a tendency towards more barred and redder plumage patterns in habitats with more stable and less seasonal year-round precipitation. Plumage characters were also partially correlated, with redder coloration associated with a more densely barred back pattern. They suggested that local phenotypic adaptation in response to environmental variation could drive the high geographic variation present in this species.

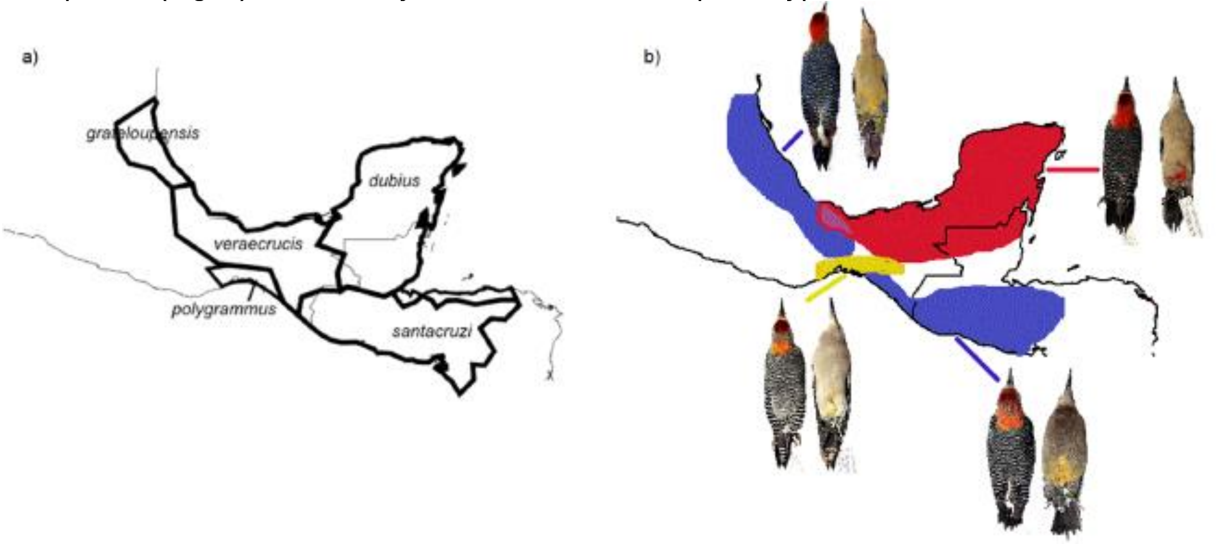


Fig. 2. Distribution of (a) mainland subspecies recognized by Benites et al. (2020) and three plumage types: red nape/red belly in red, red nape/yellow belly in yellow, and yellow nape/yellow belly in blue (from Llanes-Quevedo et al. 2022, modified from Benites et al. 2020).

Following up on García-Trejo et al. (2009) and Navarro-Sigüenza et al. (2017), Llanes-Quevedo et al. (2022) used NextRAD genotypes (SNPs) and Ecological Niche Modelling to analyze the distinctiveness of *M. santacruzi* using genomic data, and to analyze the correspondence of genetic structure and ecological differentiation with phenotypic variation and geographic distribution. According to their Table S1, their sampling of *M. santacruzi* included 4 samples of subspecies *santacruzi*, 5 of *grateloupensis*, 12 of *veraecrucis*, 5 of *polygrammus*, and 7 of *dubius* (although their trees showed no samples of *veraecrucis* or *polygrammus* and many more than 5 samples of *grateloupensis*, suggesting that *veraecrucis* and *polygrammus* were lumped with *grateloupensis* in most of the analyses). They also sequenced 6 samples of *M. carolinus* and 5 samples of *M. aurifrons*. Their genomic data were analyzed extensively, including analyses of phylogenetics, population genetics, and gene flow, with interesting and varied results.

A phylogenetic tree estimated using ML methods in IQ-Tree (Fig. 3) indicated, in contrast to the mitochondrial results, that *M. aurifrons* is sister to *M. santacruzi* and that *M. carolinus* is sister to the clade formed by these two taxa, although bootstrap support for this result was <85% (exact figures were not provided for bootstrap results below 85%). Furthermore, although *M. aurifrons* and *M. carolinus* received strong support as monophyletic (100% and 99%, respectively), support for monophyly of *M. santacruzi* was less than 85% and the branch leading to *M. santacruzi* was very short. In contrast, a tree estimated using SVDQuartets (Fig. 4) indicated that *M. carolinus* is monophyletic and sister to most samples of *M. aurifrons* (with 86% bootstrap), but that one of the five samples of *aurifrons* was sister to *M. santacruzi*. Thus, *M. aurifrons* was not monophyletic and although *M. santacruzi* was monophyletic, support for this was again less than 85%.

Llanes-Quevedo et al. (2022) also used their data to construct a phylogenetic network using SplitsTree based on the unlinked SNPs (Fig. 5). The resulting network showed that *M. aurifrons* and *M. carolinus* are reciprocally monophyletic sister taxa, and that the relationships among samples of *M. santacruzi* are complex, with some samples of the latter seemingly closer to the outgroups *M. chrysogenys* and *M. pucherani* than to other *santacruzi* (especially so among samples labeled *grateloupensis*).

Llanes-Quevedo et al. also conducted population genetics analyses, including DAPC (Discriminate Analysis of Principal Components) and population structure analyses. Their DAPC results indicated that their samples of *M. aurifrons*, *M. carolinus*, and *M. santacruzi* divided into two genetic groups, one consisting of samples of *carolinus* and the other consisting of samples of *aurifrons* and *santacruzi*. Following removal of *M. carolinus*, the samples of *M. aurifrons* and *M. santacruzi* again formed two clusters. In this case, one cluster consisted of samples of *M. s. santacruzi* and the other of samples of *M. aurifrons* + *M. s. polygrammus-veraecrucis-grateloupensis-dubius*. The structure-like results (Fig. 6 and 7) indicated that the number of populations within *carolinus-aurifrons-santacruzi* was most likely either two or five (i.e., K=2 or

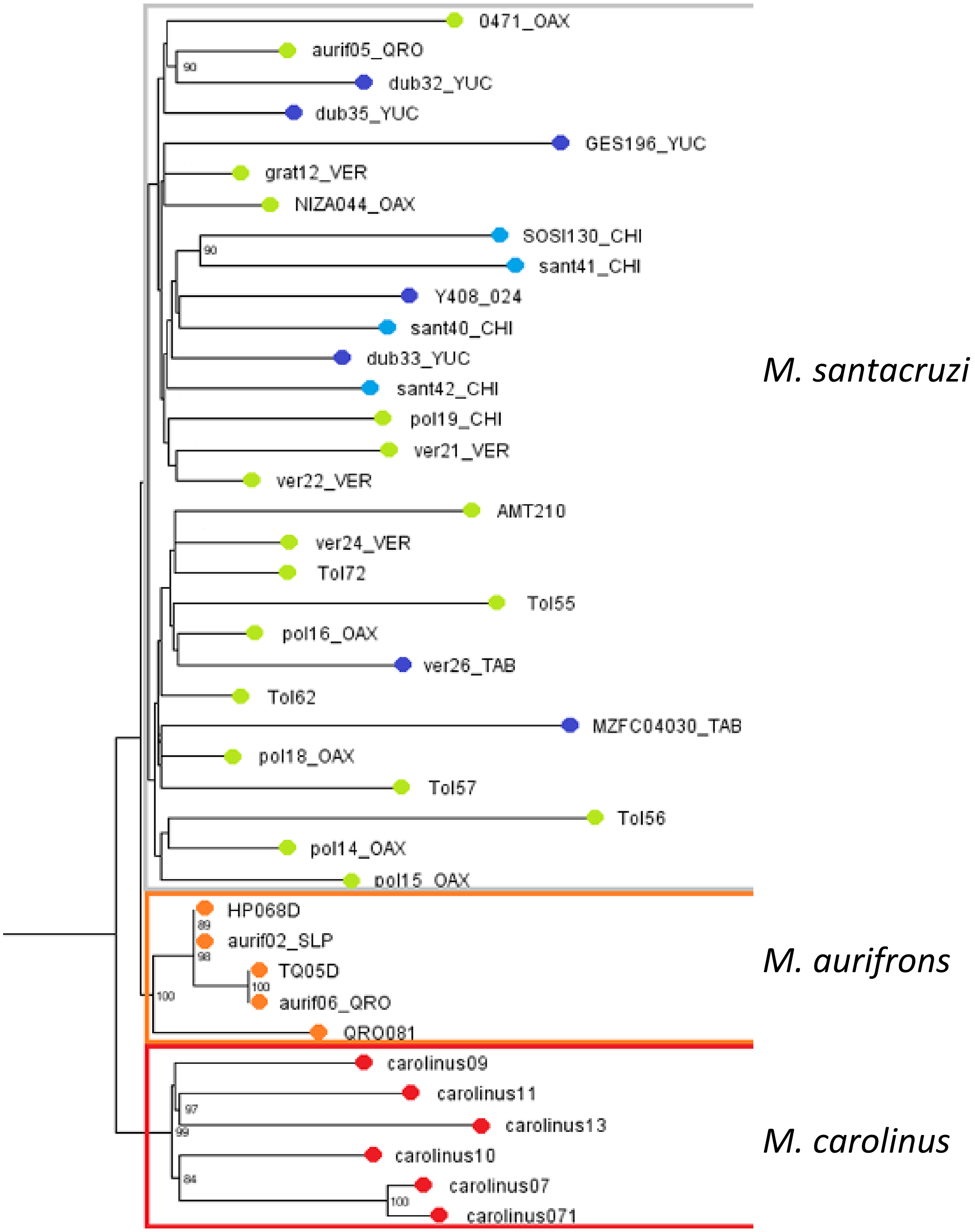


Fig. 3. Maximum-likelihood phylogenetic tree estimated using IQ-Tree. Bootstrap values lower than 85% are not shown. From Llanes-Quevedo et al. (2022).

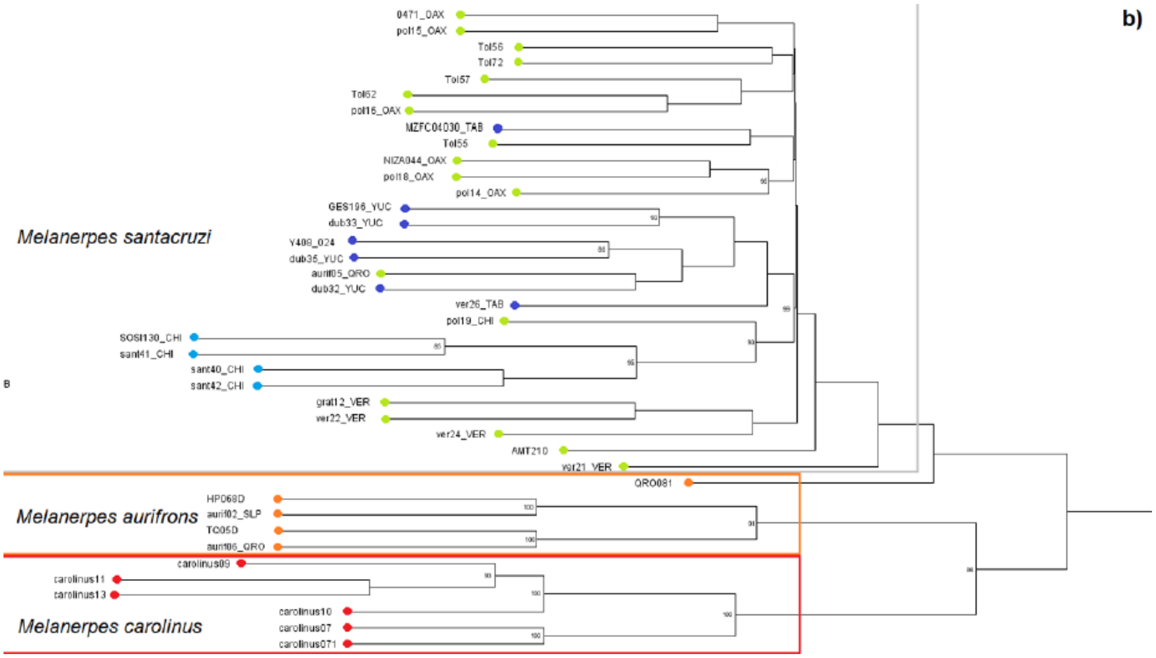


Fig. 4. Coalescent-based phylogenetic tree determined using SVDQuartets. Key bootstrap values, when blown up into legibility, are 100% for the *M. carolinus* clade, 91% for the 4 of 5 samples of *M. aurifrons* that form a clade, 86% for the clade uniting *M. carolinus* and 4/5 *M. aurifrons*, and <85% for monophly of *M. santacruzi*. Bootstrap values lower than 85% are not shown. From Llanes-Quevedo et al. (2022).

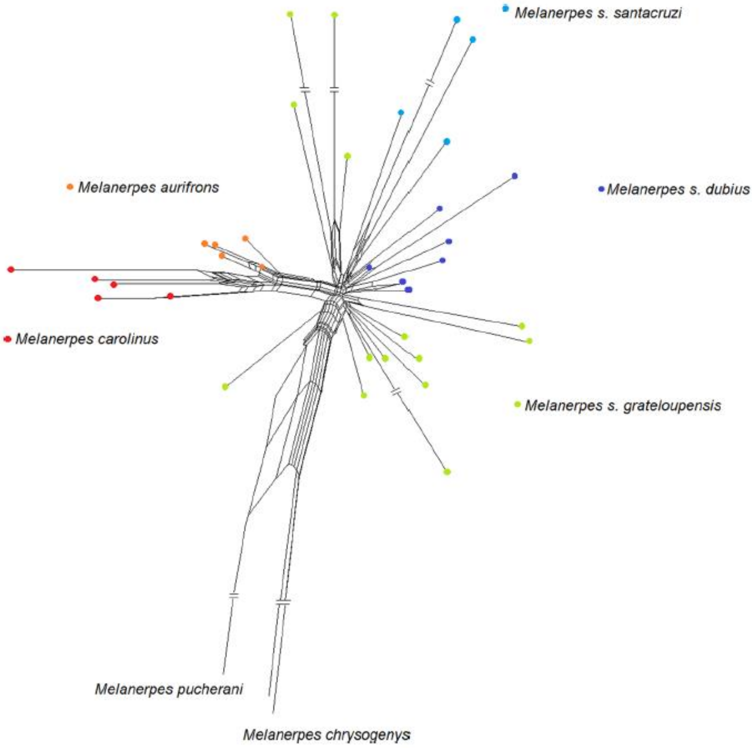


Fig. 5. Phylogenetic network constructed using SplitsTree using unlinked SNPs (from Llanews-Quevedo et al. 2022)

K=5), both of which had similar support based on the entropy criterion. The plot using K=2 showed that one group consisted of all individuals of *M. carolinus* whereas the other group consisted of all *M. aurifrons* + *M. santacruzi*. The plot using K=5 resulted in the following groups: *M. carolinus*, *M. aurifrons*, *M. s. grateloupensis*, *M. s. dubius*, and *M. s. santacruzi*. Note that there is a great deal of admixture between groups when K=5, including between *M. aurifrons* and *grateloupensis*. Llanes-Quevedo et al. also plotted their individuals on a map showing the geographical distribution of admixture as reflected by the structure-like plots (Fig. 7). One point apparently not discussed in their paper (at least we didn't see it) but evident from the map is that most of their samples of *M. aurifrons* are from the southeastern part of the distribution, close to the range of *grateloupensis.*

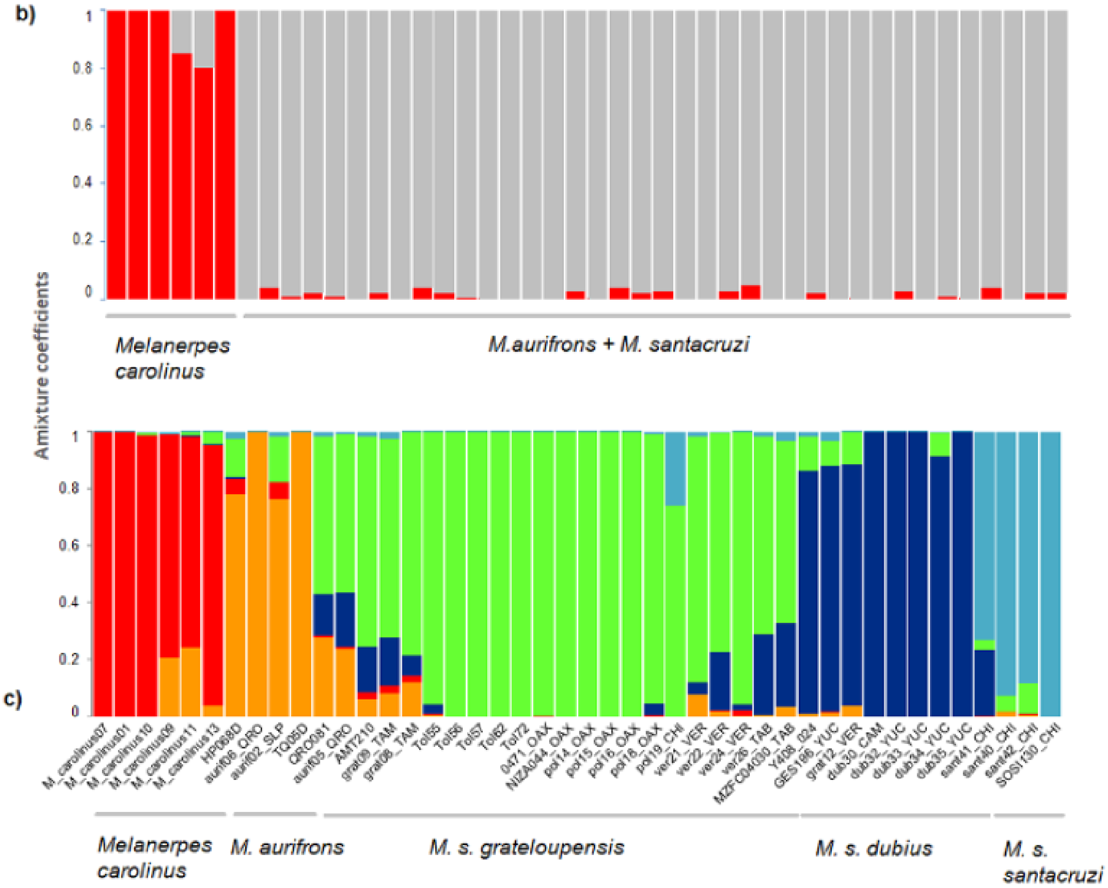


Fig. 6. Structure-like plots based on K=2 (top) and K=5 (below), the two most likely clusterings of the sequenced individuals.

Pairwise F_{ST} between *M. carolinus* and *M. aurifrons* was 0.223, whereas that between *M. santacruzi* and *M. aurifrons* was 0.068 and that between *M. santacruzi* and *M. carolinus* was 0.138. Estimates of gene flow using Treemix inferred gene flow between *M. aurifrons* and *M. s. grateloupensis*, largely from *aurifrons* to *grateloupensis*, and a smaller amount of gene flow between *M. carolinus* and *M. aurifrons.* Patterson's D-tests inferred significant gene flow between *aurifrons* and *grateloupensis*, as well as between *M. s. dubius* and *M. s. grateloupensis*, but not between *M. carolinus* and *M. aurifrons*. Llanes-Quevedo et al. (2022) concluded that their data "support the existence of bidirectional gene flow between *M. aurifrons* and adjacent populations of *M. santacruzi* (*M. s. grateloupensis*) along the Sierra Madre Oriental in northeastern Mexico."

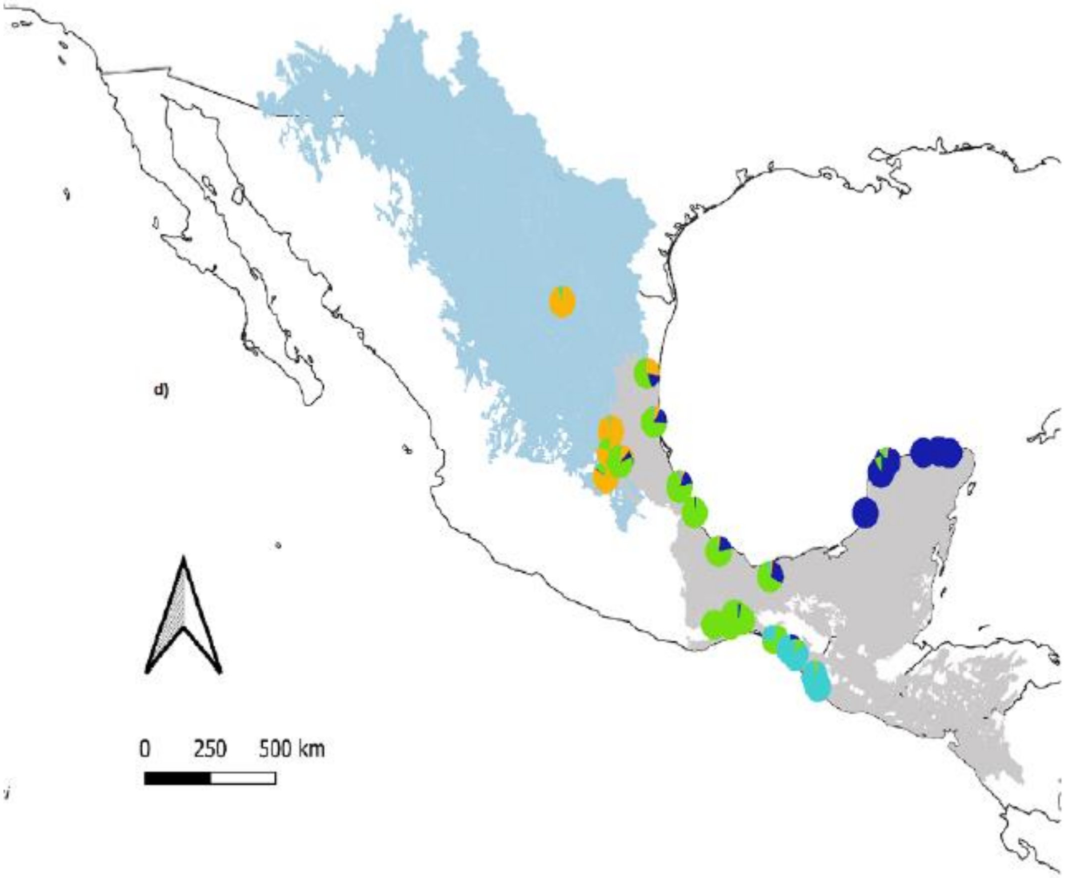


Fig. 7. Map of samples used in Llanes-Quevedo et al. (2022), showing the extent of admixture in each individual. Colors are the same as in Fig. 6.

Vocalizations:

Nathan Pieplow's previous proposal on this issue discussed differences in the calls of *santacruzi* and *aurifrons*. Note that the following excerpt is from 2013 and that many more recordings are now available online:

> Online audio recordings show that at least one call type appears to differ consistently between the two clades. Northern birds give a single-syllable "gaf" call not unlike that of *M. carolinus*, whereas southern birds give a distinctive two-noted "CHUCK-a" call. The sample size is not particularly large, but the vocal differences appear to consistently follow the geographic boundaries between the clades.
>
> The single available recording of *polygrammus* sounds almost exactly like "CHUCK-a" calls from the *santacruzi* group. The few available recordings of

dubius suggest that in this subspecies the call is slightly different, more of a "chuck-trrr", sometimes shortened to a single-noted "chuck" rather like the call of *aurifrons*.

List of recordings available online:

aurifrons (1-noted "gaf"):
http://xeno-canto.org/109193
(Rio Grande Village, Brewster County, Texas)
http://xeno-canto.org/5773
(NABA Park, Hidalgo County, Texas)
http://macaulaylibrary.org/audio/23117
(17 km north of Valles, San Luis Potosi, Mexico)

***santacruzi* group (2-noted "chuck-a"):**
http://xeno-canto.org/118430
(Amatlan, Veracruz, Mexico)
http://macaulaylibrary.org/audio/23102
(near Lake Catemaco, Veracruz)
http://xeno-canto.org/33955
(Minatitlan, Veracruz, Mexico)
http://xeno-canto.org/118429
(near Tehuantepec, Oaxaca, Mexico –ssp. *polygrammus*)
http://macaulaylibrary.org/audio/137684
(Suchitepequez, Guatemala)
http://macaulaylibrary.org/audio/20912
(Morazan, El Salvador)

***dubius* (2-noted "chuck-trrr," sometimes shortened to "chuck"):**
http://macaulaylibrary.org/audio/23110
(near Hopelchen, Campeche, Mexico)
http://macaulaylibrary.org/audio/23111
(near Carrillo Puerto, Quintana Roo, Mexico)
http://macaulaylibrary.org/audio/103346
(Calakmul, Campeche, Mexico – including single-note versions)

[*Note:* Broken links for two recordings from the Ohio State collection have been deleted.]

Recommendation:

We lean against recognizing *M. santacruzi* as a separate species, but this is not a strong opinion (both of us have doubts). One thing that's very clear is that the simple picture from the mitochondrial data of *carolinus* + *aurifrons* as sister taxa with *santacruzi* sister to them (i.e., a paraphyletic *aurifrons* of *santacruzi* is included) is not a simple picture in the nuclear analyses, which are ambiguous about the relationships among the groups. Analyses that seem to contradict the mtDNA tree are the IQ-Tree analysis, in which *aurifrons* and *santacruzi* are sister taxa (although with unknown but not great support bootstrap support); the fact that 1 of the 5 samples of *aurifrons* does not group with the rest in the SVD-Quartets tree, but instead is sister to *santacruzi*; the DAPC and Structure-type analyses, in which *aurifrons* and *santacruzi* form one group and *carolinus* a different one under k=2 and in the DAPC, and in which *carolinus*, *aurifrons*, and 3 subspecies of *santacruzi* form groups in k=5 (i.e., none of the preferred k values have proposed species *M. santacruzi* as a separate group); the Fst values, which are much lower between *santacruzi* and *aurifrons* than between *carolinus* and *aurifrons* (or *carolinus* and *santacruzi*); and the finding of significant gene flow between *aurifrons* and *santacruzi grateloupensis* but not between *carolinus* and *aurifrons* (although some gene flow was found between these species, which are known to hybridize a bit).

Analyses that might favor species status for *M. santacruzi* include the relationships in the SVD-Quartets tree (if the aberrant *aurifrons* sample is ignored), and the phylogenetic network, in which *aurifrons* and *carolinus* cluster to the exclusion of *santacruzi* (although *santacruzi* is a bit all over the place). One thing that concerns us, however, is the preponderance of samples of *aurifrons* from near the zone of contact with *santacruzi*. We don't know the exact effect of this on the analyses, but it presumably compromises them to some unknown extent. Nevertheless, every individual sampled in this region (and somewhat beyond as well) appears to have admixed DNA.

A key question, it seems to us, is whether *santacruzi* and *aurifrons* mainly mate assortatively in the contact zone and, despite all the interesting analyses and results, we don't know that the Llanes-Quevedo paper can answer that question, and we're reluctant to separate the species without further information.

Better sampling of the three groups (*aurifrons*, *santacruzi* and *carolinus*) with information on phenotype would help resolve the relationships among them and better characterize the zone of contact. On the other hand, the difficulty of using the color patterns and morphometrics to distinguish these groups also makes it difficult to generate a hypothesis about the recognition of *santacruzi* as a separate species from *M. aurifrons*.

English names

If the split is accepted, then a separate proposal on English names will be required.

References:

Benites, P., M. D. Eaton, E. A. García-Trejo, and A. G. Navarro-Sigüenza. 2020. Environment influences the geographic phenotypic variation in Velazquez's Woodpecker (*Centurus santacruzi*). Journal of Ornithology 161:621–634.

Dufort, M. J. 2016. An augmented supermatrix phylogeny of the avian family Picidae reveals uncertainty deep in the family tree. Molecular Phylogenetics and Evolution 94:313–326.

García-Trejo, E. A., A. E. De Los Monteros, M. C. Arizmendi, and A. G. Navarro-Sigüenza. 2009. Molecular systematics of the Red-bellied and Golden-fronted woodpeckers. Condor 111:442–452.

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Navarro-Sigüenza, A.G., H. Vázquez-Miranda, G. Hernández-Alonso, E. A. García-Trejo, and L. A. Sánchez-González. 2017. Complex biogeographic scenarios revealed in the diversification of the largest woodpecker radiation in the New World. Molecular Phylogenetics and Evolution 112:53–67.

Ridgway, R., 1914. The birds of North and Middle America. Bulletin of the United States National Museum 506, 65–88.
Selander, R. K., and D. R. Giller. 1963. Species limits in the woodpecker genus *Centurus* (Aves). Bull. Am. Mus. Nat. History, 124, article 6.
Short, L. L. 1982. Woodpeckers of the World. Delaware Museum of Natural History, Greenville.

Submitted by: Blanca Hernández and Terry Chesser

Date of Proposal: 3 Feb. 2023

Treat (a) *Sclerurus obscurior* and (b) *S. pullus* as separate species from Tawny-throated Leaftosser *S. mexicanus*

Note: This is a modified version of SACC proposal 752, which was an update of SACC 603 (see https://www.museum.lsu.edu/~Remsen/SACCprop752.htm). This proposal is meant to be considered sequentially (i.e., Part 1 must be approved to consider Part 2). Of the parts relevant to NACC, SACC passed Part 1 by an 8-2 vote and Part 2a 7-3, although the latter was only a provisional vote given that neither of the proposed species occurs in South America. (Part 2b proposed treating the South American taxa as three species [*obscurior*, *andinus*, and *macconnelli*], and Part 3 further proposed treating *macconnelli* as two species. Part 2b failed on a 6-4 vote, and Part 3 failed 2-8.)

PART 1: Treat *Sclerurus obscurior* as a separate species from *S. mexicanus*

Effect on NACC:

Sclerurus mexicanus would be split into two species that are assumed to be parapatric in the Darién Gap. All North American populations would remain as *S. mexicanus* but the distribution of this species would be modified; all South American populations would become *S. obscurior*.

Background:

The genus *Sclerurus* currently contains six widespread, polytypic species. *Sclerurus mexicanus* has the broadest distribution of any *Sclerurus*, with seven subspecies occurring from northern Mexico to southern Brazil (Cooper and Barragan 2017; Fig. 1). Despite the recognized diversity and broad distribution, differences are minimal (Remsen 2003) and subspecies distributions are still incompletely known (Cooper and Barragan 2016; Cooper and Cuervo 2017).

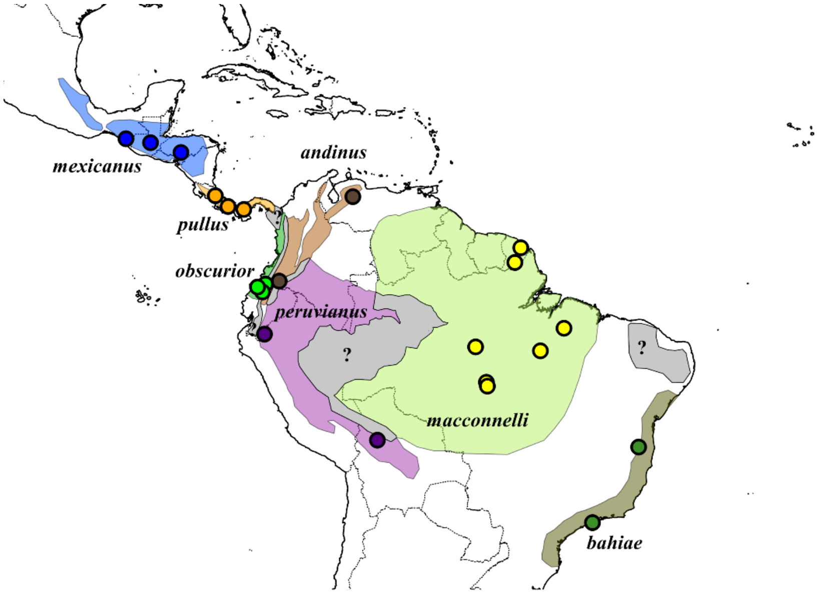


Figure 1. A map of subspecific distributions within *Sclerurus mexicanus*. Points represent localities from which vocalizations were sampled. Figure from Cooper and Cuervo (2017).

New Information:

d'Horta et al. (2013) found that *Sclerurus mexicanus* is not monophyletic as currently defined. Rather, three major clades were discovered that form a polytomy in the rufous-throated leaftosser clade: (1) *S. mexicanus* (subspecies *mexicanus* and *pullus*) in North America; (2) *S. rufigularis*; and (3) *S. mexicanus* (subspecies *obscurior*, *andinus*, *macconnelli*, and *peruvianus*) in South America (Fig. 2).

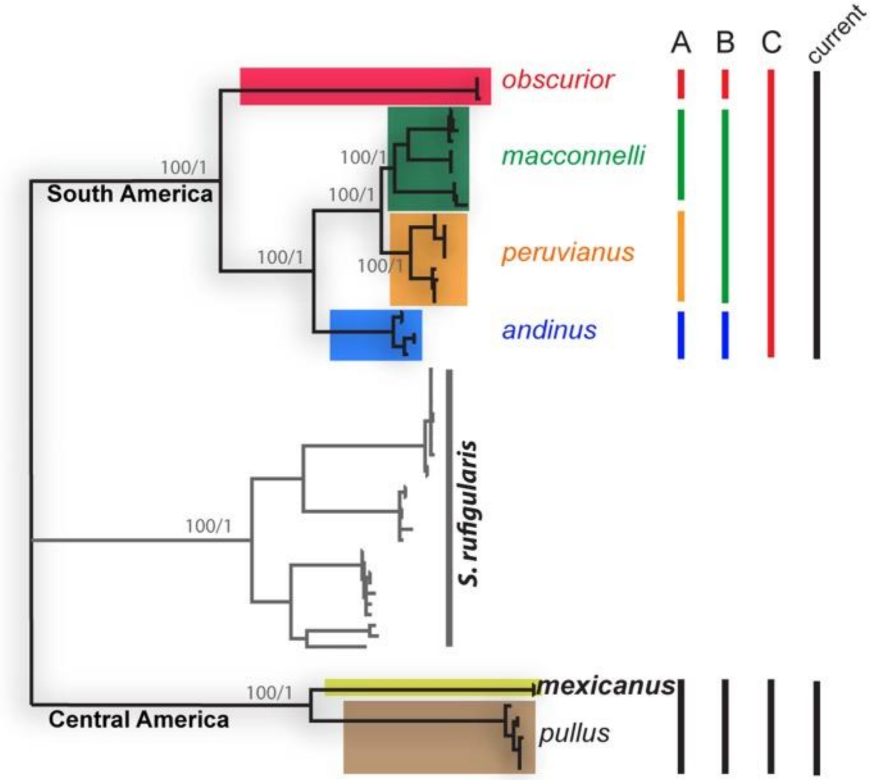


Fig. 2. Combined tree based on phylogenetic analyses of nuclear and mitochondrial DNA for *S. mexicanus* by d'Horta et al. 2013. Bars at the right indicate possible species-level groupings of this complex. Figure from Cooper and Cuervo (2017).

New Information:

The suboscine study of Harvey et al. (2020) included five individuals of *S. mexicanus* and one of *S. rufigula*. Their results (Fig. 3) indicated that the three samples from South America formed a clade and that *S. rufigula* was sister to them, and that the two samples from North America (*mexicanus* from Guatemala and *pullus* from Costa Rica) formed a clade sister to the *rufigula* + SA *S. mexicanus* clade. Thus, the polytomy in d'Horta et al. (2013) was resolved such that *S. mexicanus* constituted a paraphyletic group.

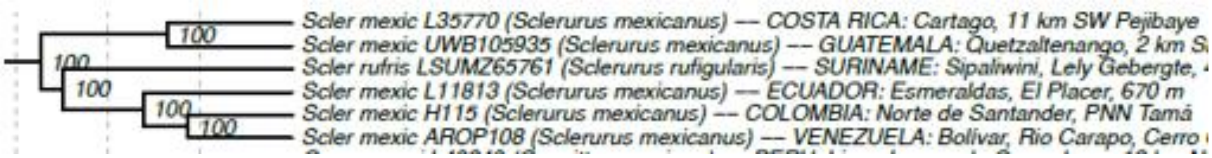


Fig. 3. Excerpt from the Harvey et al. (2020) suboscine phylogeny based on UCEs and exons.

Vocalizations

Cooper and Cuervo (2017) conducted vocal analyses of *S.mexicanus* and *S. rufigula*. Here are sonograms and PCAs from this paper:

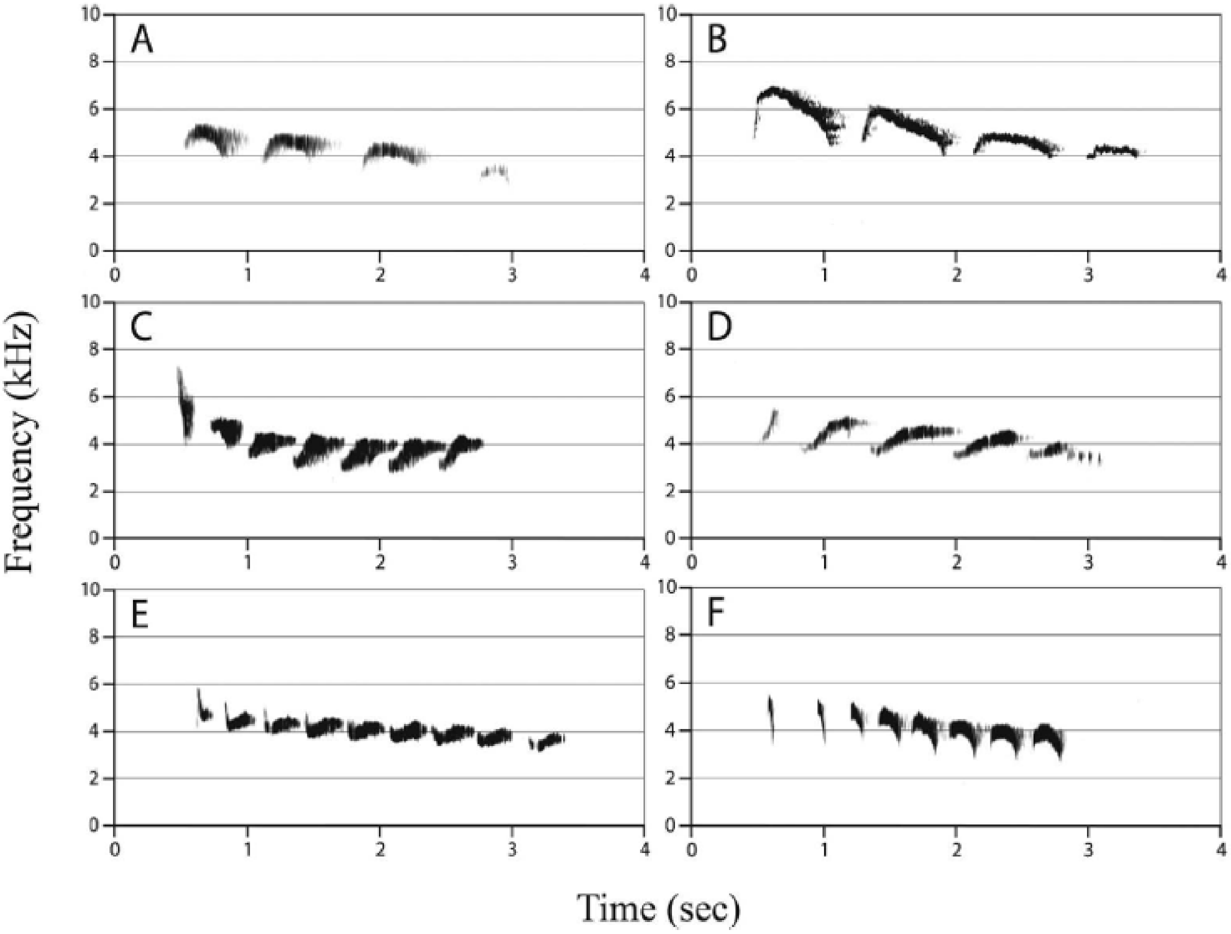


Fig. 4. Primary Songs of principal vocal groups recovered in Cooper and Cuervo (2017). (A) *S. m. mexicanus*, Francisco Morazan, Honduras (XC185348); (B) *S. m. pullus*, Cocle, Panama (XC3301); (C) *S. m. obscurior*, Ecuador (84_Esm07); (D) *S. m. andinus*, Lara, Venezuela (XC41899); (E) *S. m. macconnelli*, Cayenne, French Guiana (XC64999); (F) *S. rufigularis*, Mato Grosso, Brazil (XC39469).

Cooper and Cuervo (2017) concluded that songs of *S. mexicanus* could be divided into two groups, a slower Central American group and a faster South American group. DFAs of songs recovered this primary grouping, although calls of *S. rufigularis* were erroneously clustered with the South American group of *S. mexicanus*. Analyses of songs highlighted the uniqueness of *S. m. pullus*, whereas analyses of calls separated *S. m. mexicanus* from all other groups:

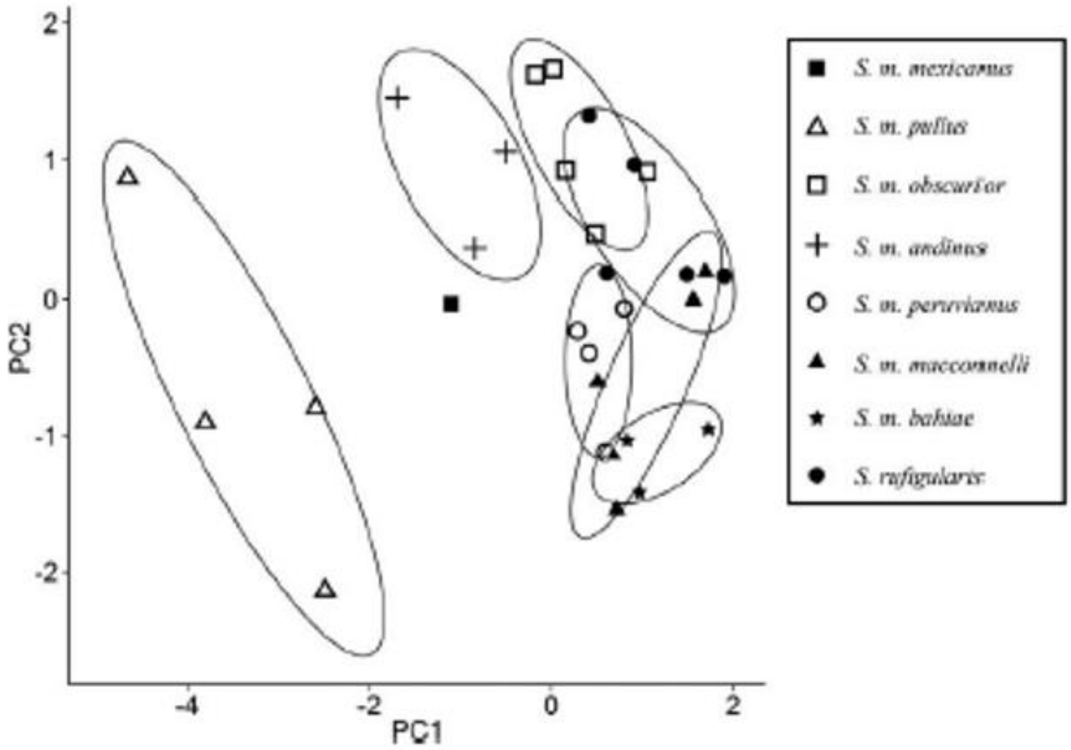


Fig. 5. PCA of songs of *Sclerurus rufigularis* and subspecies of *S. mexicanus*. Each point represents the song of a single individual. Subspecies of *S. mexicanus* are listed in the legend from north to south. From Cooper and Cuervo (2017).

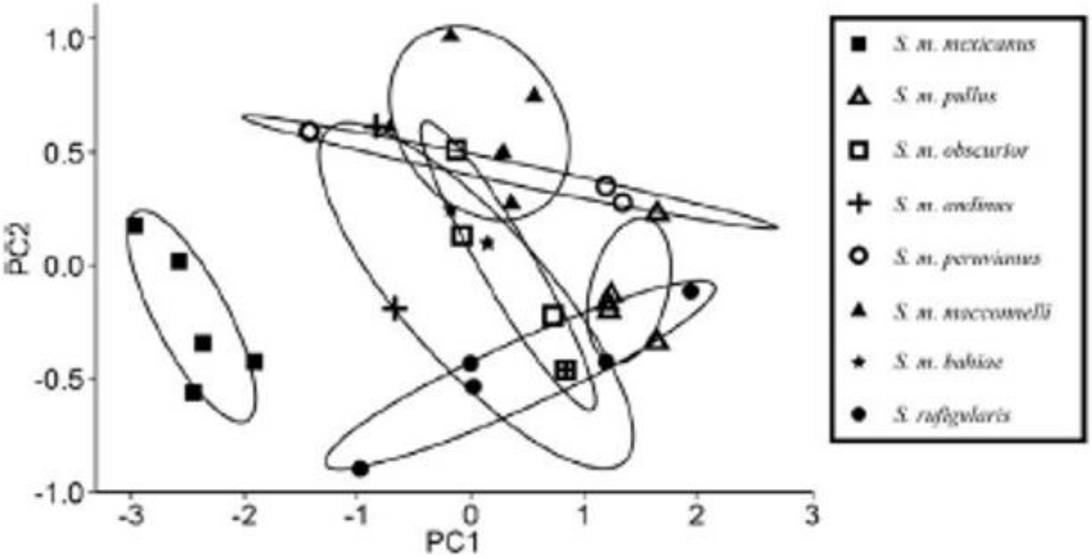


Fig. 6. PCA of calls of *Sclerurus rufigularis* and subspecies of *S. mexicanus*. Each point represents the call of a single individual. Subspecies of *S. mexicanus* are listed in the legend from north to south. From Cooper and Cuervo (2017).

Within the *S. mexicanus* group, North and South American populations appear wholly allopatric, diagnosably monophyletic (d'Horta et al. 2013), and vocally distinct (Cooper and Cuervo 2017). Unless all rufous-throated leaftossers (including *S. rufigularis*) are considered a single species, the most prudent decision is to split *S. mexicanus* into two taxa with no known geographic overlap:

1. ***Sclerurus mexicanus*** (Sclater 1856). Suggested English name: Central American Leaftosser. Type locality: Cordoba, Veracruz, Mexico. This species contains two subspecies: *mexicanus* (from northern Nicaragua north to east Mexico) and *pullus* (from northern Costa Rica south to southern Panama). This includes *certus* (Chubb 1919, from Guatemala), which is considered a synonym of *mexicanus* (Hellmayr 1925).

2. ***Sclerurus obscurior*** (Hartert 1901). Suggested English name: Dusky Leaftosser. Type locality: Lita, Esmeralda, Ecuador (ca. 600m). This species contains five subspecies: *obscurior* (the Choco lowlands), *andinus* (the mid-montane Andes of Colombia, Ecuador, and Venezuela), *peruvianus* (the eastern foothills of the Andes and western Amazonia in Peru, Ecuador, Colombia, and probably Brazil), *macconnelli* (eastern Amazonia and the Guianan shield), and *bahiae* (the Atlantic Forest of Brazil).

Part 2A: **Treat *Sclerurus pullus* as a separate species from *S. mexicanus***

Effect on NACC:

Both proposed species occur in North America, so this would add a species to the checklist.

Background:

Despite limited vocal data, differences were recovered between *S. m. mexicanus* and *S. m. pullus*. As noted above, the PCAs indicate that *pullus* is distinct from all other taxa in songs, and that *mexicanus* is distinct from all other taxa in songs (Cooper and Cuervo 2017). Populations of these taxa are also reciprocally monophyletic (d'Horta et al. 2013). A split of these two taxa is therefore warranted.

Sclerurus pullus (Bangs 1902). Suggested English name: Isthmian Leaftosser (thus altering *S. mexicanus* to Tawny-throated or Mexican Leaftosser). Type locality: Boquete, Panama. Distributed from northern Costa Rica through the Darién in Eastern Panama. This species may occur in the Darién and Urabá regions of Colombia, and may exist parapatrically with *S. obscurior*. This species includes the synonym *anomalus* (Bangs and Barbour 1922), which has erroneously been synonymized with *andinus* in the past (Peters 1951).

Recommendation:

We recommend that the committee vote in favor of both parts of this hierarchical proposal:

(a) Part 1. Treat *Sclerurus obscurior* as a separate species from *S. mexicanus*.

(b) Part 2a. Treat *Sclerurus pullus* as a separate species from *S. mexicanus*.

English names:

SACC has adopted English names based on treating *S. mexicanus* and *S. obscurior* as separate species: Central American Leaftosser (as proposed above) and South American Leaftosser (rather than Dusky), respectively. These names have also been adopted by

Clements. The rationale for these unexciting names is that they are placeholders pending further splits – see https://www.museum.lsu.edu/~Remsen/SACCprop860.htm.

The IOC list has chosen to use different names, retaining Tawny-throated Leaftosser for *S. mexicanus* and adopting Dusky Leaftosser for *S. obscurior*. Note, however, that "Dusky" was the name formerly used by Ridgway and Cory & Hellmayr for *S. m. pullus.*

Proposed English names if *S. pullus* is treated as separate from *S. mexicanus*, as indicated above, are Isthmian Leaftosser and either Tawny-throated Leaftosser or Mexican Leaftosser, respectively. Dusky and Mexican were names previously used for these taxa when they were named as subspecies.

References:

Cooper, J. C. & A. M. Cuervo. 2017. Vocal variation and species limits in the *Sclerurus mexicanus* complex. *The Wilson Journal of Ornithology* 129:13-24.

Cooper, J. C. & Barragán, D. 2017. Tawny-throated Leaftosser *Sclerurus mexicanus*. Neotropical Birds Online <http://neotropical.birds.cornell.edu/>.

d'Horta, F. M., A. M. Cuervo, C. C. Ribas, R. T. Brumfield & C. Y. Miyaki. 2013. Phylogeny and comparative phylogeography of *Sclerurus* (Aves: Furnariidae) reveal constant and cryptic diversification in an old radiation of rain forest understory specialists. *Journal of Biogeography* 40:37-49.

Harvey, M. G., G. A. Bravo, S. Claramunt, A. M. Cuervo, G. E. Derryberry, J. Battilana, G. F. Seeholzer, J. S. McKay, B. C. Faircloth, S. V. Edwards, J. Pérez-Emán, R. G. Moyle, F. H. Sheldon, A. Aleixo, B. T. Smith, R. T. Chesser, L. F. Silveira, J. Cracraft, R. T. Brumfield, and E. P. Derryberry. 2020. The evolution of a tropical biodiversity hotspot. *Science* 370: 1343-1348.

Submitted by: Jacob C. Cooper & Andres M. Cuervo, modified for NACC by Terry Chesser

Date of Proposal: May 2017 (SACC proposal), modified on 5 February 2023

SACC comments on Proposal 752 (the previous proposal on this topic, SACC 603, can be found at https://www.museum.lsu.edu/~Remsen/SACCprop603.htm):

Comments from Jaramillo: "Part I – YES, data look solid to me, and include multiple independent sets of data. Note that Central American Leaftosser does not work for me.

"Part IIA – YES, assuming it eventually is found in Colombia.

"Part IIB – YES, I find it powerful that obscurior and andinus are syntopic, and replace each other elevationally. It is unfortunate that bahiae was not sampled molecularly, as it may shift the tree perhaps?

Part III – NO, unresolved as noted in the proposal. Data needed for bahiae, as well as no reliable way to identify taxa in field!"

Comments from Stiles: "YES to part 1. YES to part 2. The split between mexicanus and pullus is deep, suggesting isolation across the Nicaraguan gap in mountain habitats. YES to part 3, given the genetic and vocal data and the likelihood of parapatry (or even sympatry?) at intermediate elevations. NO to part 4: data are not sufficient for this split at this time."

Comments from Claramunt: " NO. Quoting Cooper & Cuervo (2017:13): "…revising species limits in the group is complicated by subtle phenotypic variation between lineages and an incomplete understanding of the limits of their distribution." I fully agree and this exactly what is missing in this proposal: a better understanding of phenotypic geographic variation. We know that there is important geographic variation in plumage (Remsen 2003), mitochondrial DNA (d'Horta et al. 2013), and vocalizations (Cooper & Cuervo 2017). What we don't know yet is whether that variation is just geographic variation in a widespread species or indicative of multiple species. In particular, a strong match between genetic and phenotypic subdivisions would suggest reproductive isolation in differentiated lineages, thus species status. What we observe here is a general correlation between the different sets of data but I don't see evidence of a strong match across traits.

"For example, affinities of the birds from E Panama are uncertain; plumage suggests affinities with the South American clade: birds there have been referred to obscurior and andinus (Wetmore1972, Remsen 2003). On the other hand, the bird included in d'Horta et al. from E Panama carried a Central American haplotype (it is identified as pullus in the paper, but I don't know if that was based on plumage or a posteriori, based on DNA). Songs from this region were not analyzed by Cooper & Cuervo (2017), but a song from this region in xeno-canto sounds to me like a perfect intermediate between those of Central America and NW South America. So, right now, we don't know if this pattern reflects primary intergradation of traits, a hybrid zone, or sympatry of two isolated lineages.

"Similarly, birds from the Pantepui region have been assigned to andinus but carry a macconnelli mtDNA, and birds from W Brazilian Amazonia have been referred to peruvianus but carry macconnelli mtDNA. Thus, it seems that there are broad mismatches between mitochondrial and plumage variation, thus suggesting that we are seeing the vagaries of polymorphic traits within a large and geographically structured population, rather than discrete lineages evolving independently. A detailed analysis of plumage variation would be very informative.

"Song variation is also complex and, aside from a general large-scale correspondence, I don't see evidence that it matches either plumage or mtDNA, and the statistical design used by Cooper & Cuervo is problematic in several respects. First, they did not analyze songs from both sides of putative contact zones, like Darién Chocó (pullus-obscurior), the W foothills of the W Andes (obscurior-andinus, all songs of andinus are from the E slopes of E cordilleras) or Amazonian Andes forelands (peruvianus-macconnelli). Therefore, the possibility of finding intermediate songs and mismatches was minimized. Second, univariate pairwise comparisons of song traits was problematic for two reasons: 1) differences in group means do not prove that groups are discrete units (cannot distinguish clines from discrete variation), and 2) incurred in a serious problem of multiple testing (Appendix 2 contains 196 P-values; standard methods for adjusting P-values for multiple test result in none of the pairwise tests being statistical significant! Note that none of the P-values are particularly low). Therefore, no statistical evidence there. The discriminant analysis does provide some support for one of the proposed taxonomies, but again, the lack of samples near putative contact zones may have biased the analysis towards good levels of discrimination. Finally, from the perspective of the biological species concept, there is no information regarding the potential effect of the geographic variation in song on reproductive isolation. Actually, birds seem to respond to songs from distantly related subspecies and they can sometimes switch to a song that is more similar to that of other subspecies (Cooper & Cuervo 2017:16); this kind of information is usually taken as evidence of conspecificity under the biological species concept.

"Finally, the phylogeny of d'Horta et al. (2013) raises the possibility that mexicanus is not monophyletic, but the evidence is weak (no statistical support either way). In sum, I can't find the evidence for the existence of multiple species within mexicanus."

Comments from Zimmer: "YES. I think that the genetic and vocal differences of all Central American populations north and west from the highlands of western Panama from those of South America provide strong evidence for at least a two-way split in this complex. Part IIA. Split Sclerurus mexicanus into S. mexicanus and S. pullus. YES (tentatively). Again, I think that the genetic differences are persuasive, and a split here would fit an established biogeographic pattern of differentiation across the inter-montane gap between Nicaragua and the Talamanca-Chiriqui highlands. However, my YES vote comes with the caveat that the situation in the Darién of eastern Panama really muddles the overall picture. The Proposal treats the birds of eastern Panama as being referable to S. [m.] pullus, but other authors (e.g. Remsen in HBW Volume 8) have characterized the situation in eastern Panama as being one of elevational parapatry, with andinus inhabiting the lowlands, and obscurior replacing it in the highlands. Looking at this from the perspective of biogeography, the typical pattern of taxon-replacement that we see in eastern Panama, is for Talamanca-Chiriqui highland birds to drop out in the isolated mountains of central Panama (e.g. Coclé-Panama provincial border region), and for lowland birds to extend eastward at least to the Bayano River valley before being replaced in the lowlands of Darién by taxa typical of the Chocó region of Colombia and northwestern Ecuador, with taxa occupying the Darién highlands either unique to that region, or, showing affinities to Andean taxa in Colombia. To me, the obvious break in vocal characters among all "Tawny-throated Leaftossers" is between Central American birds (verifiable east/south to the highlands of western Panama) and South American birds east of the Andes. It doesn't make much sense to me that the leaftossers from eastern Panama would be referable to pullus. The scenario that Van proposed in HBW (andinus in the lowlands and obscurior in the highlands) for eastern Panama makes more sense to me, and if accurate, the apparent elevational parapatry and pattern of taxon replacement would argue for splitting andinus and obscurior from one another, a split that would probably be supported by plumage differences. I am not familiar with the voices of the eastern Panamanian mexicanus, and it doesn't appear that Cooper & Cuervo (2017) included vocal samples from the region in their vocal analysis, so I have no confidence that the distributional boundaries of pullus, andinus and obscurior are being accurately portrayed. Because of this, and taking into consideration Santiago's well-reasoned arguments regarding the lack of clarity as regards phenotypic variation and congruence of the different data sets, I'm not willing to go further in splitting up this complex until we know more. I would echo Santiago's calls for better vocal sampling and analysis from both sides of putative contact zones. So, for now at least, I'm a NO on Part IIB, and Part III of this proposal."

Comments from Pacheco: "NO. As stressed by Santiago and Kevin, I consider for the moment that data (vocal, genetic) of some populations are still unavailable so that they can have a more robust understanding of the specific limits in this complex.

"There is no assurance that the birds of eastern Panama are "pullus". There is no definition about the affiliation of the populations of the Pantepui (despite being the type-locality of macconnelli) and the Atlantic Forest. My opinion is that the geographic coverage and the number of song samples is not enough to guarantee the proposed taxonomic suggestions. More importantly, vocal analysis did not find perfect congruence with genetics. Tentatively, I vote YES only for Part I."

Comments from Remsen: "YES to all proposed splits. Although I strongly appreciated the well-reasoned conservative comments of Santiago and others, I am strongly influenced by handling specimens of all these taxa and by the likely elevational separation of taxa that for me is a nail-in-coffin piece of evidence for species rank. The differences among S. mexicanus populations sensu lato are greater than those between Amazonian populations of S. mexicanus and S. rufigularis. Continued maintenance of all of these taxa as a single species masks a lot of what I would consider species-level biodiversity. Philosophically, in this group repairing and refining problems in species limits of all taxa recommended as splits in the proposal (as in taxon rank of bahiae) are secondary concerns compared to maintenance of broad mexicanus."

Comments from Robbins: "Clearly Part 1 is straightforward, thus a "YES", for splitting Sclerurus mexicanus into at least two species, S. mexicanus and S. obscurior.

Part IIA. Given this is outside of our region, I presume we are not voting on this. Nonetheless, genetic data clearly show there is a deep split between mexicanus and pullus (as compared to other taxa in this group), so despite similarity in plumage and vocalizations pullus should be recognized at species level.

I believe d' Horta et al. (2013) and Cooper and Cuervo have provided good rationale for recognizing obscurior, andinus, and macconnelli as species, so a " YES " to Part IIB.

Following Cooper and Cuervo's recommendation, at least for now, I vote "NO" for part III.

Comments from Stotz: "I. YES. This seems straightforward to me with several datasets showing corresponding separation between these taxa.

"IIA. I am inclined to say YES on this split, but it is not a case we actually have to consider given the currently known distribution of the taxa. However, the North American committee should probably consider this issue, especially given that it appears SACC will at very least split obscurior from mexicanus.

"IIB. YES.

"III. NO. I can see no reason not to follow the recommendation of the authors of the proposal based on our current knowledge of the situation.

Revise the taxonomy of *Amaurospiza* seedeaters: (a) split *Amaurospiza relicta* from Blue Seedeater *A. concolor*, and (b) lump *A. concolor* and *A. carrizalensis* with *A. moesta*; or (c) split *A. aequatorialis* from *A. concolor*; or (d) lump the five taxa as subspecies of *A. moesta*

Description of the problem:

This proposal seeks to revise the taxonomy of *Amaurospiza* seedeaters and contribute to the efforts of the Working Group on Avian Checklists (WGAC) in reconciling global checklists. The genus *Amaurospiza*, as currently recognized, is comprised of five taxa of blue seedeaters that show minor differences in plumage coloration and body measurements. Recognition of the five taxa as species or subspecies, including the species to which a subspecies belongs, varies among global avian checklists (Table 1). Howard & Moore and eBird/Clements coincide in the three species they recognize (*concolor*, *carrizalensis*, *moesta*), HBW-BL recognizes two species (*relicta*, *moesta*), and IOC recognizes four species (*concolor*, *aequatorialis*, *carrizalensis*, *moesta*). Classification by the NACC and the SACC agrees with Howard & Moore and eBird/Clements.

Table 1. Current taxonomy of *Amaurospiza* seedeaters in four global avian checklists. Classification by the NACC and the SACC agrees with Howard & Moore and eBird/Clements.

Taxa	**Howard & Moore + eBird/Clements**	**HBW-BL**	**IOC**
relicta (Griscom, 1934)	*A. concolor relicta*	*A. relicta*	*A. concolor relicta*
concolor Cabanis, 1861	*A. concolor concolor*	*A. moesta concolor*	*A. concolor concolor*
aequatorialis Sharpe, 1888	*A. concolor aequatorialis*	*A. moesta aequatorialis*	*A. aequatorialis*
carrizalensis Lentino & Restall, 2003	*A. carrizalensis*	*A. moesta carrizalensis*	*A. carrizalensis*
moesta (Hartlaub, 1853)	*A. moesta*	*A. moesta moesta*	*A. moesta*

The five taxa in the genus *Amaurospiza* are allopatric, distributed from central Mexico to northeastern Argentina (Table 2). Two of the three subspecies within *A. concolor* (*relicta* and *concolor*) occur in the area covered by the NACC, from central Mexico to Panama. The third subspecies of *A. concolor* (*aequatorialis*), and the species *A. carrizalensis* and *A. moesta*, are found in South America, and, therefore, are under the jurisdiction of the SACC.

Table 2. Geographic distribution of *Amaurospiza* seedeaters.

Taxa	**Distribution**	**NACC**	**SACC**
relicta	Mts. of s Mexico (s Jalisco to Guerrero, Morelos and Oaxaca)	*A. concolor* Blue Seedeater	
concolor	Mts. of s Mexico (Chiapas) to Nicaragua, Costa Rica and Panama	*A. concolor* Blue Seedeater	
aequatorialis	Mountains of sw Colombia (Nariño) to n Peru (Cajamarca)		*A. concolor* Blue Seedeater
carrizalensis	N Venezuela (lower Río Caroni in Bolívar)		*A. carrizalensis* Carrizal Seedeater
moesta	Locally from se Paraguay to e Brazil and ne Argentina (Misiones)		*A. moesta* Blackish-blue Seedeater

Background:

Amaurospiza seedeaters are Neotropical resident species generally associated with bamboo thickets and dense understory (Lopes et al. 2011). They feed on arthropods and bamboo seeds, flowers, petioles, and buds (Areta et al. 2023); in Costa Rica they prefer greener and healthier leaves (Figure 1, Pablo-Castillo 2018).

***Figura 2.** Macho adulto alimentándose de Chusquea sp. ZP Río Tiribí. Fotografía por Eddy Chacón.*

Figure 1. Male of *Amaurospiza concolor* feeding on bamboo leaves in Costa Rica (Pablo-Castillo 2018).

The taxa within the genus *Amaurospiza* have a convoluted history. Here is a brief summary of the five *Amaurospiza* taxa:

<u>concolor</u>

The genus *Amaurospiza* was described along with the species *A. concolor* based on specimens from Costa Rica (Cabanis 1861). Ridgway (1901) measured one Panamanian specimen from the Salvin-Godman collection; he noted that the species was found in both Costa Rica and Panama.

Griscom (1934) recognized three subspecies within *concolor*: *concolor* from northwestern Costa Rica (Miravalles and Tenorio); and two additional subspecies that he proposed: *grandior* from the humid Caribbean forest of eastern Nicaragua, and *australis* from southwestern Costa Rica to western Panama. Griscom provided measurements of *relicta* (placed in *Amaurospizopsis*) and the three taxa within *concolor* (*grandior*, *concolor*, *australis*). He found overlap among most of the measurements with the exception of the wing of *Amaurospizopsis*, which was larger than in any of the *concolor* taxa (Table 3).

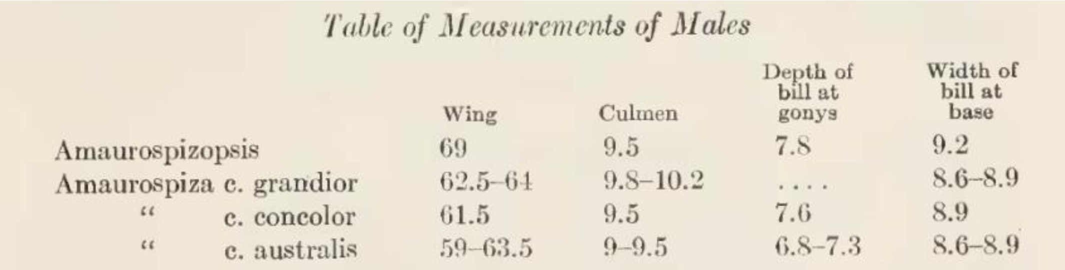
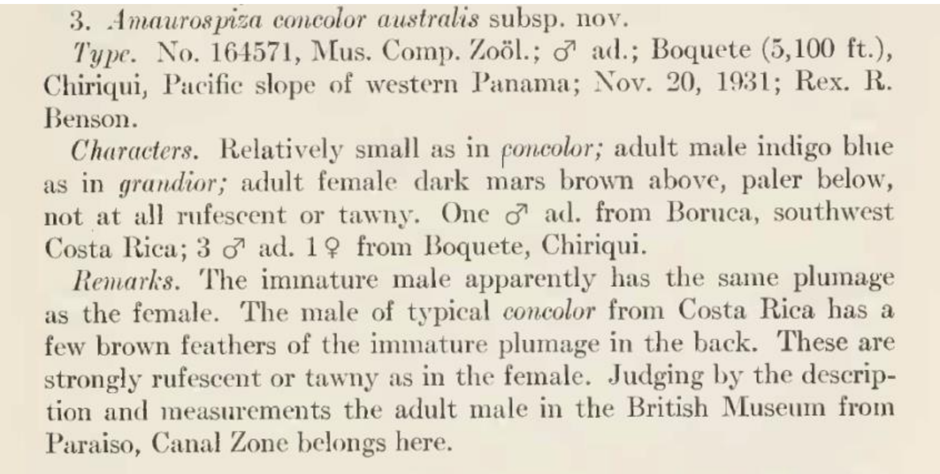


Table of Measurements of Males

	Wing	Culmen	Depth of bill at gonys	Width of bill at base
Amaurospizopsis	69	9.5	7.8	9.2
Amaurospiza c. grandior	62.5–64	9.8–10.2	. . . .	8.6–8.9
" c. concolor	61.5	9.5	7.6	8.9
" c. australis	59–63.5	9–9.5	6.8–7.3	8.6–8.9

Table 3. From Griscom (1934), morphometric measurements of male *Amaurospizopsis* and *Amaurospiza* seedeaters.

Hellmayr (1938) noted that *grandior* was indistinguishable in color from *concolor*, and that only one of three specimens had a slightly longer bill, suggesting that *grandior* was not maintainable as a separate taxon. The *australis* group has not been reassessed since the original description by Griscom (1934), from which it appeared that the main difference between *australis* and *concolor* was the plumage coloration of the immature male (Figure 2). The two taxa *grandior* and *australis* are not recognized by any of the four global checklists; they are currently grouped within *concolor concolor* (Ramos-Ordóñez et al. 2020).



3. *Amaurospiza concolor australis* subsp. nov.

Type. No. 164571, Mus. Comp. Zoöl.; ♂ ad.; Boquete (5,100 ft.), Chiriqui, Pacific slope of western Panama; Nov. 20, 1931; Rex. R. Benson.

Characters. Relatively small as in *concolor;* adult male indigo blue as in *grandior;* adult female dark mars brown above, paler below, not at all rufescent or tawny. One ♂ ad. from Boruca, southwest Costa Rica; 3 ♂ ad. 1 ♀ from Boquete, Chiriqui.

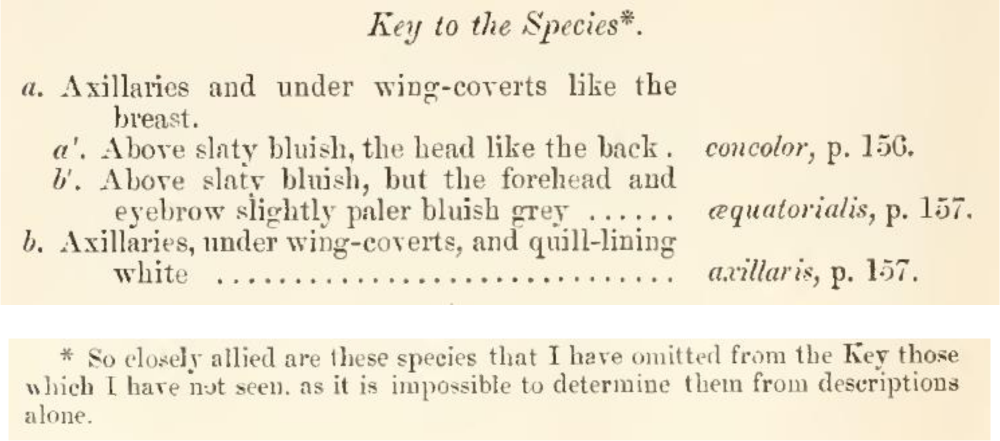
Remarks. The immature male apparently has the same plumage as the female. The male of typical *concolor* from Costa Rica has a few brown feathers of the immature plumage in the back. These are strongly rufescent or tawny as in the female. Judging by the description and measurements the adult male in the British Museum from Paraiso, Canal Zone belongs here.

Figure 2. Original description of *Amaurospiza concolor australis* by Griscom (1934).

moesta

The taxon *moesta* was described as *Sporophila moesta* with a type from Brazil (Hartlaub, 1853). Orr and Ray (1945) noted that Hellmayr (1904) found *S. moesta* to be identical to *Amaurospiza axillaris* (Sharpe 1888). From then on, *axillaris* and *moesta* were synonymized and have been considered part of the genus *Amaurospiza*. Sharpe, in a key to the *Amaurospiz*a species, differentiated this taxon by its white axillaries, underwing coverts, and quill-lining (Figure 3) [see below, that Hellmayr´s assessment indicates that the immature male type of *aequatorialis* lacks white underwing coverts as indicated by Sharpe, but that an adult male has white underwing coverts, setting *aequatorialis* apart from *concolor*; also see Table 4 in Areta et al. 2023]. However, Sharpe also noted that taxa within *Amaurospiza* are very closely allied, making it impossible to distinguish them from descriptions alone. The taxon *moesta* is mainly found in the

Atlantic Forest, although records in pre-Amazonian wooded habitats are recently increasing (Rising et al. 2020).



Key to the Species.*

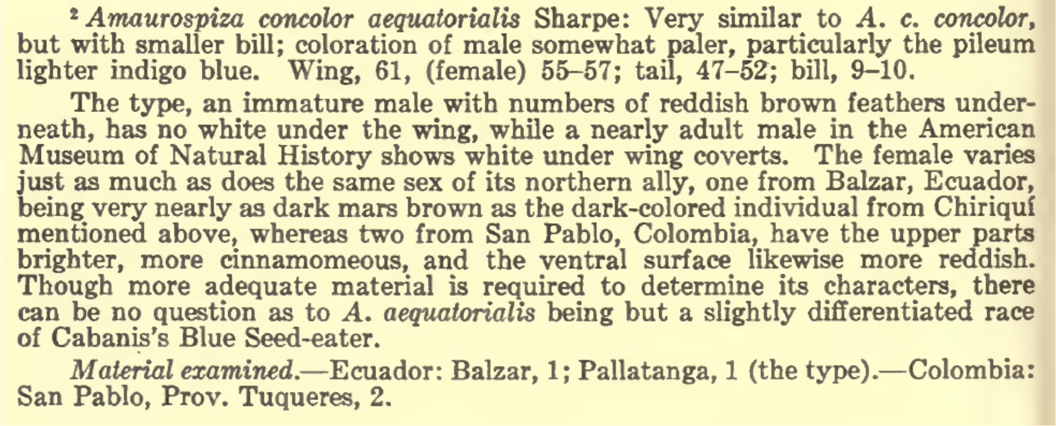
a. Axillaries and under wing-coverts like the breast.
a'. Above slaty bluish, the head like the back . *concolor*, p. 156.
b'. Above slaty bluish, but the forehead and eyebrow slightly paler bluish grey …… *æquatorialis*, p. 157.
b. Axillaries, under wing-coverts, and quill-lining white ………………………… *axillaris*, p. 157.

* So closely allied are these species that I have omitted from the Key those which I have not seen, as it is impossible to determine them from descriptions alone.

Figure 3. Key to *Amaurospiza* species from Sharpe (1888).

aequatorialis

Sharpe (1888) described *A. aequatorialis*, a species from the western foothills of the Andes of Ecuador, as a separate species from *concolor* and *moesta* (under the name *A. axillaris*). This taxon is similar to *concolor* but the forehead and eyebrows are slightly paler bluish gray and the bill is smaller. Hellmayr (1938) treated *aequatorialis* as a subspecies within *concolor* after examination of four specimens, two from Ecuador and two from Colombia, and noted that *aequatorialis* was slightly smaller and paler than *concolor* (Figure 4).



[2] *Amaurospiza concolor aequatorialis* Sharpe: Very similar to *A. c. concolor*, but with smaller bill; coloration of male somewhat paler, particularly the pileum lighter indigo blue. Wing, 61, (female) 55–57; tail, 47–52; bill, 9–10.

The type, an immature male with numbers of reddish brown feathers underneath, has no white under the wing, while a nearly adult male in the American Museum of Natural History shows white under wing coverts. The female varies just as much as does the same sex of its northern ally, one from Balzar, Ecuador, being very nearly as dark mars brown as the dark-colored individual from Chiriquí mentioned above, whereas two from San Pablo, Colombia, have the upper parts brighter, more cinnamomeous, and the ventral surface likewise more reddish. Though more adequate material is required to determine its characters, there can be no question as to *A. aequatorialis* being but a slightly differentiated race of Cabanis's Blue Seed-eater.

Material examined.—Ecuador: Balzar, 1; Pallatanga, 1 (the type).—Colombia: San Pablo, Prov. Tuqueres, 2.

Figure 4. Note about *Amaurospiza concolor aequatorialis* by Hellmayr (1938).

AOU/AOS considers *aequatorialis* as part of the group *A. c. concolor* (AOU 1983; AOU 1998). Although *aequatorialis* is not mentioned explicitly in the checklist, the geographic distribution of *A. c. concolor* encompasses southwestern Colombia and northwestern Ecuador. Recently, the taxon *aequatorialis* has also been recorded from northwestern Peru (Angulo Pratolongo et al. 2012; Sánchez et al. 2012).

relicta

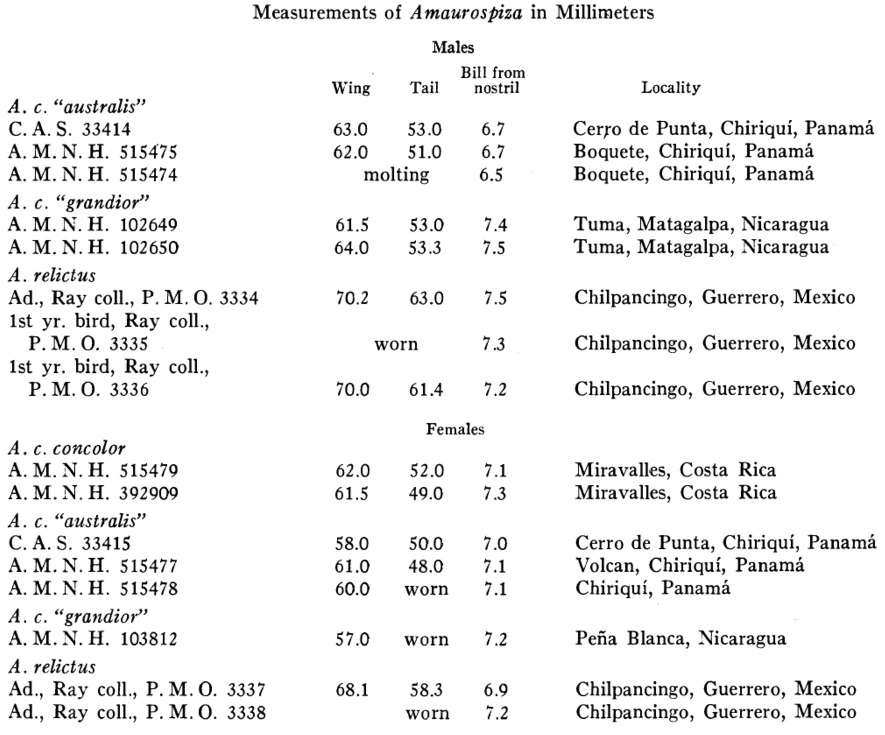
Griscom (1934) described a new species within a new genus, *Amaurospizopsis relictus*, based on a specimen from Chilpancingo, Guerrero, Mexico.

Hellmayr (1938) suggested that *relictus* could be a northern race of *concolor*, both of them very similar in coloration, *relictus* slightly larger with a deeper, stubbier bill.

Orr and Ray (1945) compared *Amaurospizopsis* and *Amaurospiza*, concluded that the differences were not sufficient to warrant separate genera, and proposed that *Amaurospizopsis* be considered a synonym of *Amaurospiza*. Griscom, in a letter from 1944, concurred with Orr and Ray, mentioning that his views on avian genera had changed since he proposed the genus *Amaurospizopsis*.

Orr and Ray (1945) tentatively considered *relictus* as a separate species, mainly due to the geographic hiatus between *relictus* and *concolor*, and the absence of intergradation in the specimens they examined. They noted that in the length of the wing and the tail there is no overlap between *A. relictus* and *A. concolor*, although the length of the bill is the same for both species (Table 4). They reported that the color in the adult male of *relictus* is grayer and duller than the adult males of *concolor*.

Table 4. From Orr and Ray (1945), morphometric measurements of *Amaurospiza* seedeaters.



Measurements of *Amaurospiza* in Millimeters

	Wing	Tail	Bill from nostril	Locality
Males				
A. c. "australis"				
C. A. S. 33414	63.0	53.0	6.7	Cerro de Punta, Chiriquí, Panamá
A. M. N. H. 515475	62.0	51.0	6.7	Boquete, Chiriquí, Panamá
A. M. N. H. 515474	molting		6.5	Boquete, Chiriquí, Panamá
A. c. "grandior"				
A. M. N. H. 102649	61.5	53.0	7.4	Tuma, Matagalpa, Nicaragua
A. M. N. H. 102650	64.0	53.3	7.5	Tuma, Matagalpa, Nicaragua
A. relictus				
Ad., Ray coll., P. M. O. 3334	70.2	63.0	7.5	Chilpancingo, Guerrero, Mexico
1st yr. bird, Ray coll., P. M. O. 3335	worn		7.3	Chilpancingo, Guerrero, Mexico
1st yr. bird, Ray coll., P. M. O. 3336	70.0	61.4	7.2	Chilpancingo, Guerrero, Mexico
Females				
A. c. concolor				
A. M. N. H. 515479	62.0	52.0	7.1	Miravalles, Costa Rica
A. M. N. H. 392909	61.5	49.0	7.3	Miravalles, Costa Rica
A. c. "australis"				
C. A. S. 33415	58.0	50.0	7.0	Cerro de Punta, Chiriquí, Panamá
A. M. N. H. 515477	61.0	48.0	7.1	Volcan, Chiriquí, Panamá
A. M. N. H. 515478	60.0	worn	7.1	Chiriquí, Panamá
A. c. "grandior"				
A. M. N. H. 103812	57.0	worn	7.2	Peña Blanca, Nicaragua
A. relictus				
Ad., Ray coll., P. M. O. 3337	68.1	58.3	6.9	Chilpancingo, Guerrero, Mexico
Ad., Ray coll., P. M. O. 3338		worn	7.2	Chilpancingo, Guerrero, Mexico

Miller et al. (1957) noted under *A. concolor relicta*: "Measurements of *relicta* … essentially bridge the size gap between this form and *A. c. concolor* of Central America and the color differences appear to be of a magnitude frequent in races."

AOU/AOS considers *relicta* as a group within *A. concolor* (AOU 1983; AOU 1998). The sixth edition (AOU 1983) noted: "The two groups are sometimes recognized as distinct species, *A. relicta* (Griscom, 1934) [Slate-blue Seedeater] and *A. concolor* [Blue Seedeater]". The seventh edition (AOU 1998) mentioned the two groups without referring to the possible recognition of two distinct species.

Some authors treat *relicta* as a separate species (Eisenmann 1955; Davis 1972; Howell and Webb 1995). The song of *relicta* is described as similar to *concolor* but slightly higher and faster (Howell and Webb 1995). Lentino and Restall (2003), considering bill shape, size, color, and song differences, suspected that *relicta* might represent a separate species from *concolor*.

HBW-BL split *A. relicta* from *A. concolor* based on the following rationale:

> [*relicta*] commonly treated as conspecific with *A. concolor*; differs (in this analysis rictal bristles and nostrils accorded equivalence of plumage characters) by its slate-blue vs. dark blue plumage in male (2); longer rictal bristles (Griscom 1934) (allow 1); operculate nostrils (Griscom 1934) (allow 1); shorter, deeper bill (allow 1); longer wing and tail (mean of 3 male tails 57.7 mm vs mean of 5 males 50.8; allow 2); "slightly higher and faster" song (Howell and Webb 1995) (at least 1).

<u>*carrizalensis*</u>

The taxon *carrizalensis* was described by Lentino and Restall (2003) based on specimens collected on the river island Carrizal in eastern Venezuela. The authors measured their specimen series and specimens from the other taxa within the genus (Table 5). They found that *carrizalensis* has the longest bill and most pointed wing of all the taxa within *Amaurospiza*. Lentino and Restall diagnosed *carrizalensis* as "separable from other members of the genus by the density of coloration and black flammulations on the breast, overall size, wing formula, volume and shape of the bill, and general measurements". Lentino and Restall suggested that *carrizalensis* should be considered a separate species, which was accepted by the SACC due to the large range disjunction and morphological differences from *concolor* and *moesta* (Proposal 74, https://www.museum.lsu.edu/~Remsen/SACCprop74.htm). Subsequently, the English name Carrizal Seedeater was adopted by the SACC (Proposal 92, https://www.museum.lsu.edu/~Remsen/SACCprop92.htm).

Table 5. From Lentino and Restall (2003), morphometric measurements of *Amaurospiza* seedeaters.

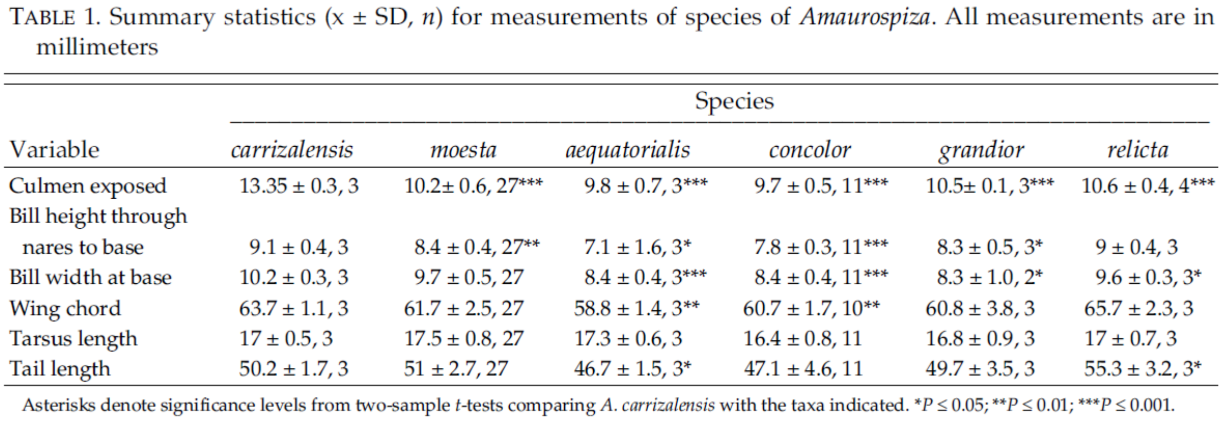


TABLE 1. Summary statistics (x ± SD, *n*) for measurements of species of *Amaurospiza*. All measurements are in millimeters

	Species					
Variable	*carrizalensis*	*moesta*	*aequatorialis*	*concolor*	*grandior*	*relicta*
Culmen exposed	13.35 ± 0.3, 3	10.2± 0.6, 27***	9.8 ± 0.7, 3***	9.7 ± 0.5, 11***	10.5± 0.1, 3***	10.6 ± 0.4, 4***
Bill height through nares to base	9.1 ± 0.4, 3	8.4 ± 0.4, 27**	7.1 ± 1.6, 3*	7.8 ± 0.3, 11***	8.3 ± 0.5, 3*	9 ± 0.4, 3
Bill width at base	10.2 ± 0.3, 3	9.7 ± 0.5, 27	8.4 ± 0.4, 3***	8.4 ± 0.4, 11***	8.3 ± 1.0, 2*	9.6 ± 0.3, 3*
Wing chord	63.7 ± 1.1, 3	61.7 ± 2.5, 27	58.8 ± 1.4, 3**	60.7 ± 1.7, 10**	60.8 ± 3.8, 3	65.7 ± 2.3, 3
Tarsus length	17 ± 0.5, 3	17.5 ± 0.8, 27	17.3 ± 0.6, 3	16.4 ± 0.8, 11	16.8 ± 0.9, 3	17 ± 0.7, 3
Tail length	50.2 ± 1.7, 3	51 ± 2.7, 27	46.7 ± 1.5, 3*	47.1 ± 4.6, 11	49.7 ± 3.5, 3	55.3 ± 3.2, 3*

Asterisks denote significance levels from two-sample *t*-tests comparing *A. carrizalensis* with the taxa indicated. $^{*}P \leq 0.05$; $^{**}P \leq 0.01$; $^{***}P \leq 0.001$.

Additional notes that involve more than one of the five taxa

Hellmayr (1938) recognized three species: *Amaurospizopsis relictus*, *Amaurospiza concolor* (including *grandior*, *concolor*, *aequatorialis*), and *Amaurospiza moesta*.

Orr and Ray (1945) proposed that two races of *Amaurospiza concolor* should be recognized: *concolor* from Central America and *aequatorialis* from northern South America. They added that further collecting efforts may show *relictus* as a large, pale, northern race of *concolor*.

Monroe (1968) noted that, in Honduras, *concolor* is a rare resident of the Caribbean lowlands, where it inhabits open rain forests, forest edges, and second growth. Monroe examined a series of *relicta* and noted that the Honduran exemplars of *concolor* are not conspecific with Mexican *relicta*. Honduran *concolor* and *relicta* differ in morphology and habitat, given that *relicta* inhabits mountain ranges. However, the currently known elevational range of *concolor* in Central America is 600-2500 m (Howell and Webb 1995), which includes elevations similar to those inhabited by *relicta*.

Paynter (1970) recognized two species: *Amaurospiza concolor* (*relicta*, *concolor*, *aequatorialis*) and *A. moesta*.

Lentino and Restall (2003) suggested that based on wing formula, plumage and morphological differences, and geographic distribution, *aequatorialis* could be a distinct species from *concolor* (Figure 5).

Notes from HBW-BL: “plumage and mensural differences are all minor, with the possible exception of the larger bill of *carrizalensis*; moreover, new records from Brazil as far N as Maranhão suggest that populations of *Amaurospiza* may generally be more widespread and less disjunct than range maps indicate, as seems often the case with bamboo specialists. “

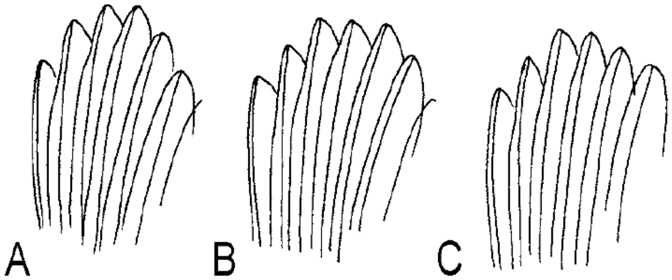


FIG. 6. Comparative wing formulae of *Amaurospiza*. (A) *carrizalensis* 7=6,5=8,9=4, (B) *grandior*, *concolor*, *relicta* and *moesta* 7=6=5,8=4,9, and (C) *aequatorialis* 7,6,5,9,8,4/(7=6=5)8,9,4/6,7=5,8,9,4 (see text for explanation of variances).

Figure 5. Comparative wing formulae of *Amaurospiza* as described by Lentino and Restall (2003).

Howell and Dyer (2022) commented on the similarity in morphology and voice of the taxa within the genus *Amaurospiza*. However, they noted that *relicta* is a distinctive taxon, endemic to

Mexico, and that it has been considered a separate species. They also considered *concolor* and *aequatorialis* to be conspecific.

New information:

Genetics

Bryson et al. (2014) studied the diversification of the "blue cardinals" across the New World. They generated multilocus sequence data from one mitochondrial gene (ND2) and three nuclear introns (ACO1, MYC, FGB-I5) and estimated time-calibrated species trees. The authors included four *Amaurospiza* taxa, all except for *relicta*. The mtDNA phylogeny recovered two main clades: a first clade consisting of *concolor* (*concolor*) from southern Mexico and Central America, and a second clade formed by the South American subspecies of *concolor* (*aequatorialis*), *moesta*, and *carrizalensis* (Figure 6). Therefore, *Amaurospiza concolor* was not recovered as a monophyletic taxon, although only one sample from *concolor aequatorialis* was included, and as noted before, *concolor relicta* was not included. Support for the node uniting *moesta* and *carrizalensis* was a middling PP ≥0.70, whereas support for all others was ≥0.95.

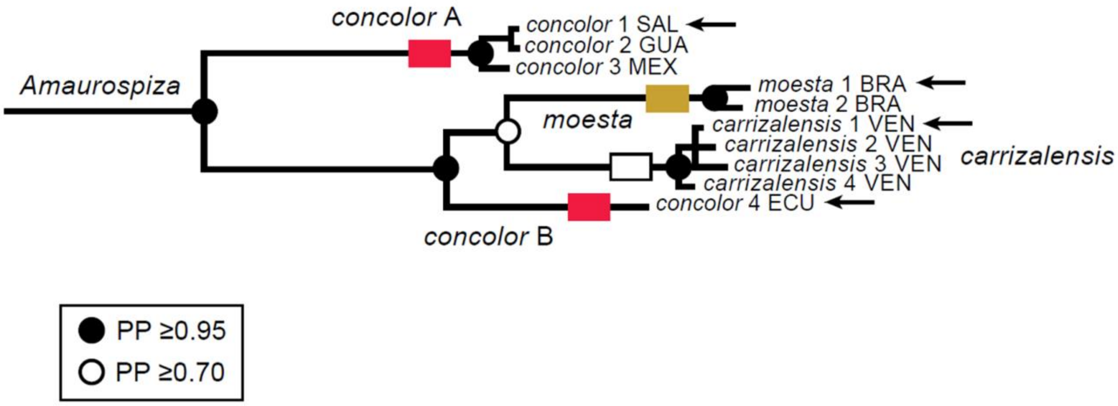


Figure 6. Relevant part of Figure 2 of Bryson et al. (2014), mitochondrial ND2 Bayesian phylogeny.

The multilocus phylogeny from Bryson et al. (2014) included a smaller sample size, one individual per *Amaurospiza* taxa: *concolor A* (*concolor*), *concolor B* (*aequatorialis*), *moesta*, and *carrizalensis*. However, the authors noted that it was not possible to obtain any nuclear data for *concolor B* (*aequatorialis*), and this individual was represented only by mtDNA. The divergence between Central American *concolor* and South American *aequatorialis*, *moesta*, and *carrizalensis* was supported by a PP ≥0.95 (Figure 7). The nodes within the South American clade had lower support (PP ≥0.70). Branch lengths in *Amaurospiza* were comparable to intraspecific divergence in -*Cyanocompsa parellina* and *C. cyanoides*, although branch length between *P. ciris* and *P. versicolor* was shorter, and the branch length between *Cyanoloxia* and "*Cyanocompsa*" *brissonii* was comparable to *Amaurospiza*.

Genetic evidence, based solely on mitochondrial DNA, suggests that *concolor* is more distantly related to *aequatorialis* than the latter is to *carrizalensis* and *moesta*; therefore, the authors suggested that the geographically and genetically distinctive *aequatorialis* be elevated to species status (Bryson et al. 2014).

The IOC list split *aequatorialis* based on Bryson et al. 2014.

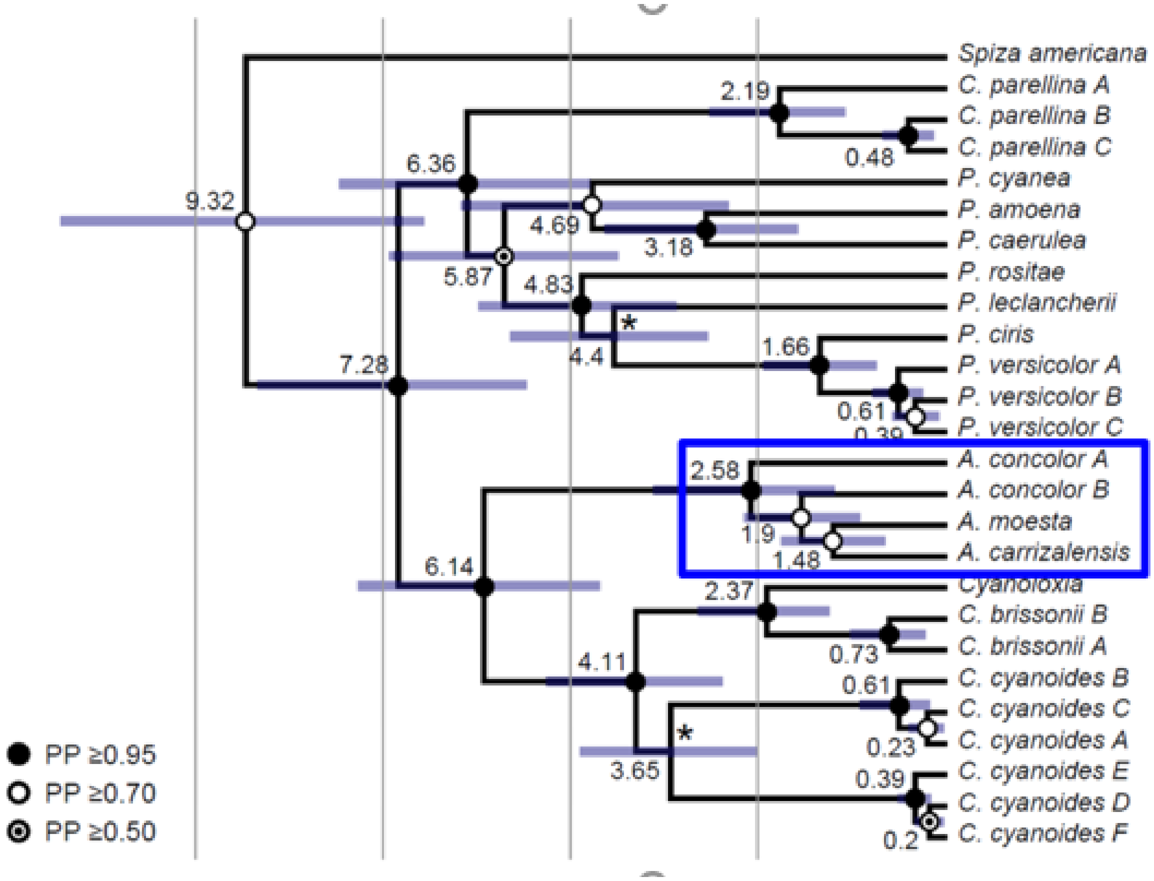


Figure 7. Multilocus *BEAST phylogeny from Bryson et al. (2014).

The SACC assessed the split of *aequatorialis* in 2016, analyzing the new phylogenetic information from Bryson et al. The split was rejected mainly because vocal data were not published (Proposal 728, https://www.museum.lsu.edu/~Remsen/SACCprop728.htm).

Areta et al. (2023) developed the first phylogenetic analysis that included multiple samples from each of the five taxa within the genus *Amaurospiza*. The mitochondrial gene ND2 was sequenced for all 19 ingroup samples, and three nuclear introns (ACO1, FGB5, MB) for a subset of samples (one sample per taxon, with the exception of *relicta*). ND2 and multilocus phylogenetic analyses confirmed the monophyly of the genus *Amaurospiza*, recovered *A. moesta* and *A. carrizalensis* as sister species, and supported the relationship of *aequatorialis* as sister to the *moesta-carrizalensis* clade, thus confirming the paraphyly of *A. concolor* (Figure 8). ND2 haplotypes of *relicta* were recovered as monophyletic, either within a polytomy of *concolor* haplotypes in the ND2 gene tree or as sister to *concolor* in the BEAST tree. The relationship of *concolor+relicta* (ND2) or *concolor* (multilocus) was recovered as sister to all the other taxa.

Additionally, Areta et al. (2023) estimated mean ND2 pairwise distances, showing that the distances between *concolor* and *aequatorialis* were greater (8.3%) than those between *moesta* and *carrizalensis* (5.7%). The two *relicta* samples diverged on average by 1.0% from nominate *concolor*. Importantly, the authors uncovered low levels of intraspecific genetic differentiation between geographically distant populations, which contrasts with the deep divergences between allopatric species. Divergence times estimated from ND2 suggest that the Central and South

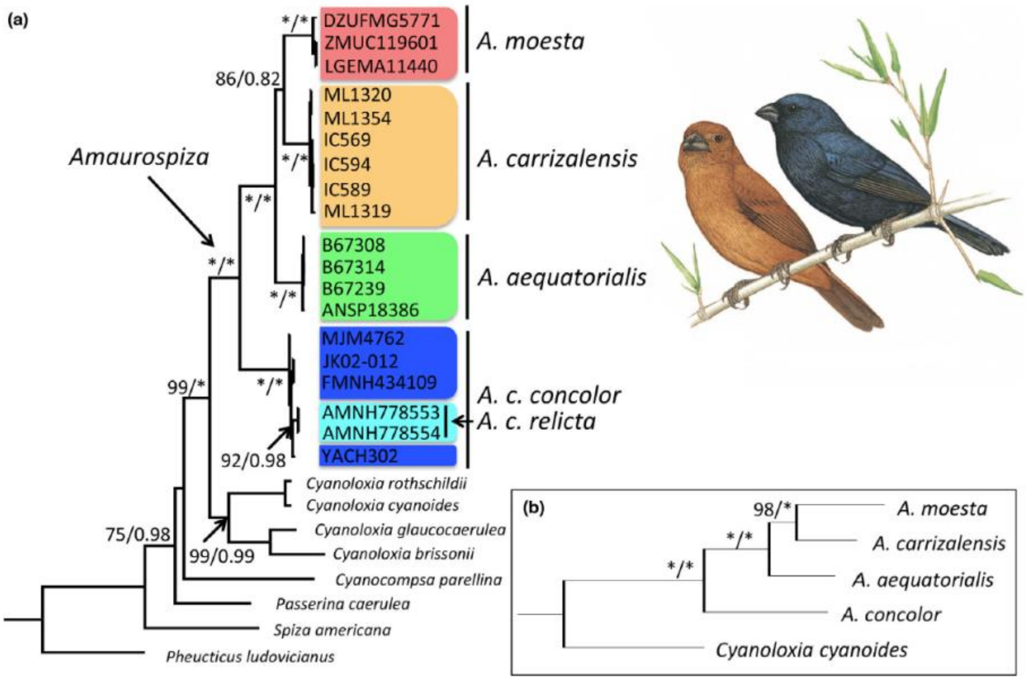


Figure 8. Phylogenetic hypothesis of relationships within the genus *Amaurospiza* from Areta et al. (2023). (a) mtDNA and (b) multilocus datasets. Numbers on nodes represent maximum likelihood bootstrap (* 100%) / Bayesian posterior probabilities (* 1.0).

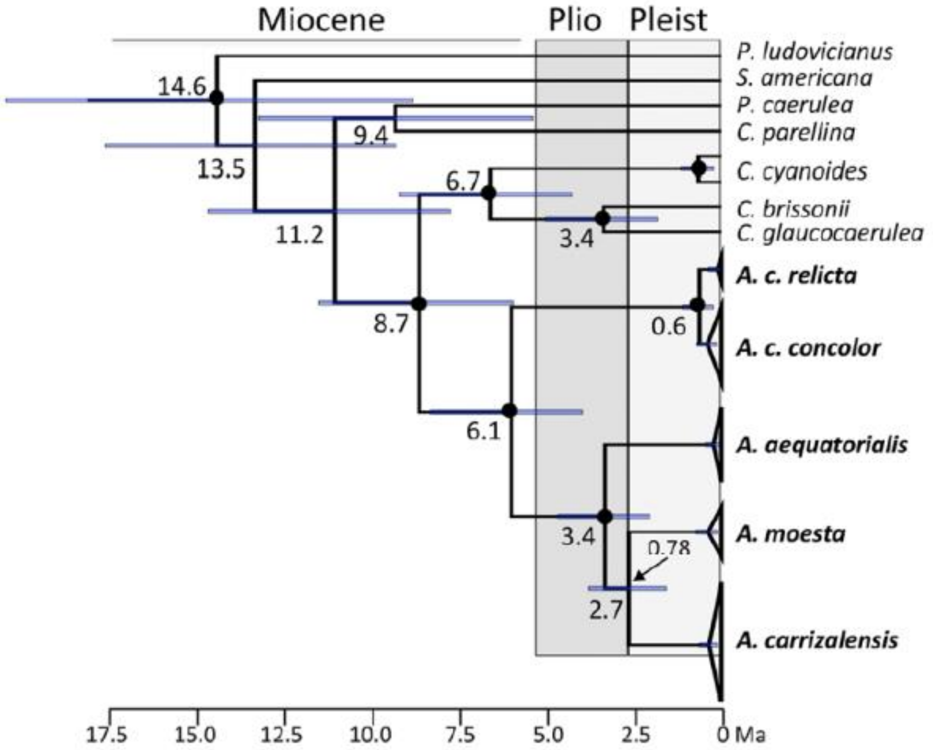


Figure 9. Bayesian phylogenetic reconstruction of *Amaurospiza* based on ND2 data from Areta et al. (2023).

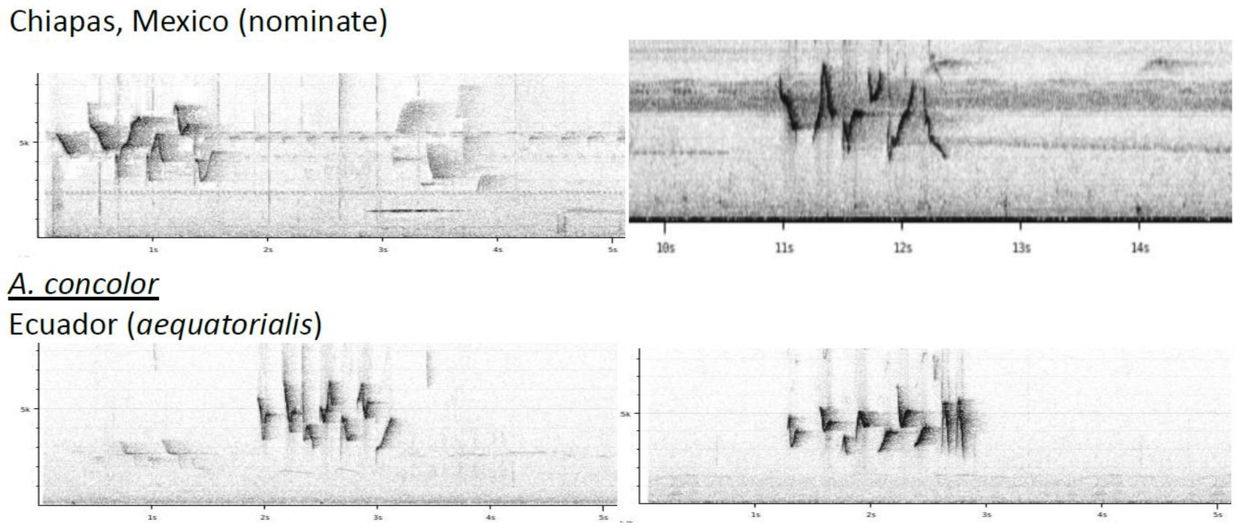
American groups diverged 6.1 Ma, that populations of *relicta* diverged from *concolor* about 1 million years ago, and that the differentiation of South American lineages started about 3.4 Ma (Figure 9).

Vocalizations

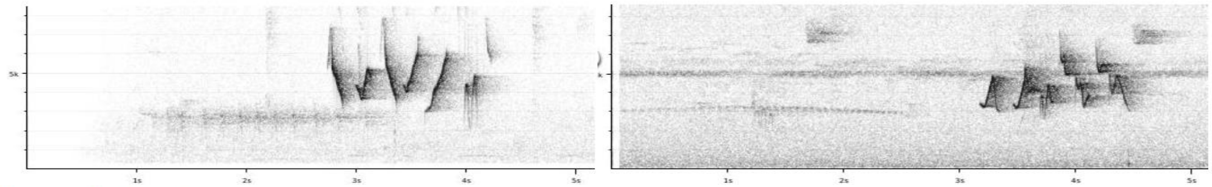
Boesman (2016), using songs available in Xeno Canto (XC), analyzed and compared the voices of *concolor* (including *concolor* and *aequatorialis*), *moesta*, and *carrizalensis*. The taxon *relicta* was not included; there are no songs available in XC or the Macaulay Library (only calls in XC). Boesman concluded that the "song of all three species is very similar, given the range of variation within each species". He added:

> "All basic sound parameters have a largely overlapping range (min. frequency, max. frequency, number of notes, note length, phrase length,...). Note shapes are also quite similar, with many about identical between species.
> Other features that may allow differentiation such as e.g. at start or end of a song phrase could not be found.
> It is probably impossible to assign any recording with a reasonable level of confidence to any species. A multivariate statistical analysis may allow to separate song of the different taxa (once more recordings become available), but in any case differences will be small, and will not lead to scores higher than e.g. 1 + 1 applying Tobias criteria."

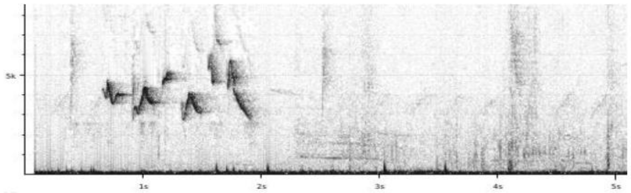
Sample of the sonograms included by Boesman (2016):



A. moesta



A. carrizalensis



Notes from HBW-BL: while *relicta* is here separated as a full species, the other taxa appear to be very weakly differentiated: available acoustic evidence reveals identical songs (Boesman 2016).

Areta et al. (2023) performed a quantitative vocal analysis that included the five taxa within the genus *Amaurospiza*. They showed that vocalizations are quite conserved in the group, but that they also provide taxonomically useful information. The authors found consistent differences between the Central and the South American clades: the number of inflections/second exhibited a stepped pattern, with *concolor* and *relicta* on the lower end and *carrizalensis*, *aequatorialis*, and *moesta* on the upper end; the South American taxa averaged more inflections per note than *concolor* and *relicta* (Table 6). A linear discriminant analysis using nine acoustic variables correctly assigned all 62 songs to the correct taxon (but note that there were single recordings for *relicta* [most similar to nominate *concolor*] and *carrizalensis* [most similar to *moesta*]. The first linear discriminant consisted mainly of maximum frequency, peak frequency average of all notes per song, and song duration on the first three notes; this first linear discriminant separated the South American taxa from the Central American taxa (Figure 10).

Table 6. From Areta et al. (2023), quantitative characterization of the inflections in the songs of *Amaurospiza* seedeaters.

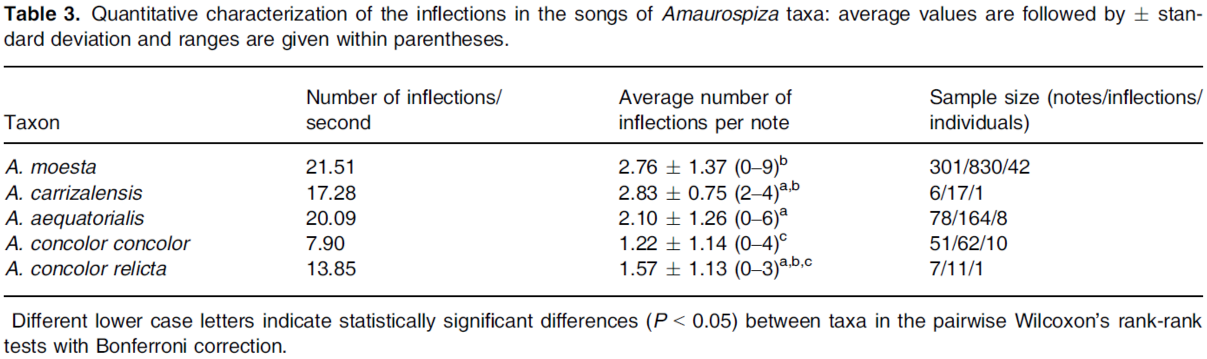


Table 3. Quantitative characterization of the inflections in the songs of *Amaurospiza* taxa: average values are followed by ± standard deviation and ranges are given within parentheses.

Taxon	Number of inflections/ second	Average number of inflections per note	Sample size (notes/inflections/ individuals)
A. moesta	21.51	2.76 ± 1.37 (0–9)^{b}	301/830/42
A. carrizalensis	17.28	2.83 ± 0.75 (2–4)^{a,b}	6/17/1
A. aequatorialis	20.09	2.10 ± 1.26 (0–6)^{a}	78/164/8
A. concolor concolor	7.90	1.22 ± 1.14 (0–4)^{c}	51/62/10
A. concolor relicta	13.85	1.57 ± 1.13 (0–3)^{a,b,c}	7/11/1

Different lower case letters indicate statistically significant differences ($P < 0.05$) between taxa in the pairwise Wilcoxon's rank-rank tests with Bonferroni correction.

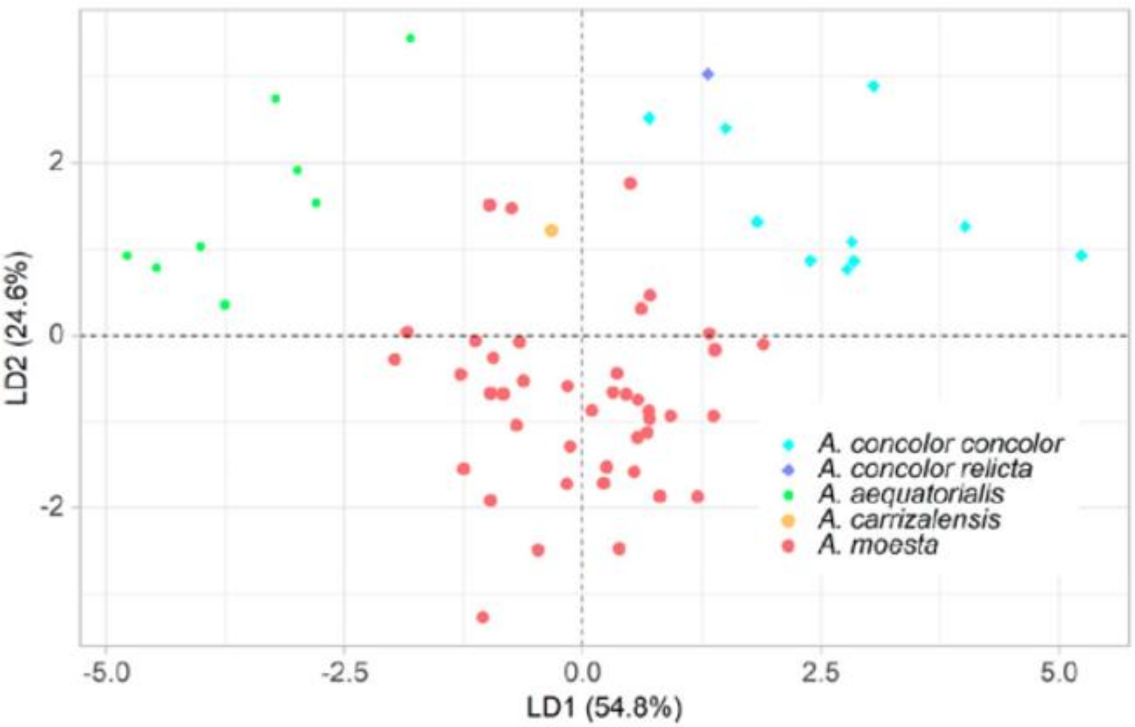


Figure 10. Linear discriminant analysis of songs of *Amaurospiza* seedeaters from Areta et al. (2023). Note the distinctive cluster of *aequatorialis*, and the placement of the single recordings of *relicta* (close to nominate *concolor*) and *carrizalensis* (close to *moesta*).

Recommendation:

Species limits in *Amaurospiza* seedeaters are a complex issue mainly due to their morphological similarity and allopatric distributions. Each of the five *Amaurospiza* taxa is considered a subspecies in at least one of the four global avian checklists, and each has also been considered a separate species at some point in history. Total evidence should be considered to reconcile the taxonomy of these seedeaters. They all are allopatric with no evidence of intergradation, show morphological differences, have similar but distinctive songs, and are phylogenetically closely related. The recent integrative study by Areta et al. (2023), which analyzed phylogenetic data, vocalizations, morphology, and plumage, suggested that four species should be recognized within the genus *Amaurospiza*: *A. concolor* (*relicta* + *concolor*), *A. aequatorialis*, *A. carrizalensis*, and *A. moesta*.

We present four separate subproposals to revise the taxonomy of *Amaurospiza* seedeaters:

(a) Split *Amaurospiza relicta* from Blue Seedeater *A. concolor.*
(b) Lump two subspecies of *A. concolor* (*concolor* + *aequatorialis*) and *A. carrizalensis* with *A. moesta*.
(c) Split *A. aequatorialis* from *A. concolor*.
(d) Lump the five taxa (*relicta*, *concolor*, *aequatorialis*, *carrizalensis*, *moesta*) as subspecies of *Amaurospiza moesta*.

Approval of subproposals (a) and (b) would reconcile NACC (and SACC) with HBW-BL. Approval of subproposal (c) would reconcile NACC (and SACC) with IOC and follows the recommendation by Areta et al. (2023). Approval of (a) and (c) would result in five species; conversely, approval of subproposal (d) would lump the five taxa in a single species, *A. moesta*.

We recommend the following votes:

(a) NO, different lines of evidence (genetics, plumage, morphology, and vocalization) suggest that *relicta* should not be given species status but considered a subspecies of *A. concolor*. However, Areta et al. 2023 recommend more rigorous studies on the taxonomic status of *relicta*.
(b) NO, neither Bryson et al. 2014 nor Areta et al. 2023 provide phylogenetic support for this lump. HBW-BL considers *concolor*, *aequatorialis*, *carrizalensis*, and *moesta* as subspecies within *A. moesta*, leaving *A. relicta* as a separate species. However, the two large clades (*relicta*, *concolor* / *aequatorialis*, *carrizalensis*, *moesta*) supported by phylogenetic data do not correspond with that classification.
(c) YES, all evidence support *aequatorialis* as a separate species from *A. concolor*, *aequatorialis* is more closely related to *carrizalensis* and *moesta* than to *concolor*, and also differs from the latter in having white underwing coverts (at least in adult males) and in song. Considering *aequatorialis* as a separate species requires a change in the geographic distribution of *A. concolor* to include only the area from Mexico to Panama (eliminating Colombia and Ecuador).
(d) NO, phenotypic and genotypic data do not support the lump of the five taxa within a single species.

English names:

Similarly to taxonomic treatment for *Amaurospiza* seedeaters, there is no consensus in English names among global avian checklists (Table 7).

Table 7. English names currently used for *Amaurospiza* seedeaters in four global avian checklists.

	Howard & Moore	**eBird/Clements**	**HBW-BL**	**IOC**
relicta	Blue Seedeater	Blue Seedeater (Slate-blue)	Slate-blue Seedeater	Cabanis's Seedeater
concolor	Blue Seedeater	Blue Seedeater (Blue)	Blue Seedeater	Cabanis's Seedeater
aequatorialis	Blue Seedeater	Blue Seedeater (Equatorial)	Blue Seedeater	Ecuadorian Seedeater
carrizalensis	Carrizal Seedeater	Carrizal Seedeater	Blue Seedeater	Carrizal Seedeater
moesta	Blackish-blue Seedeater	Blackish-blue Seedeater	Blue Seedeater	Blackish-blue Seedeater

Therefore, according to passing subproposals, please consider the following:

- If (a) passes and *relicta* is separated, Slate-blue Seedeater could be used.
- If (b) passes and *concolor* (*concolor* + *aequatorialis*), *carrizalensis*, and *moesta* are merged, the name Blue Seedeater could continue to be used or a new name could be proposed.
- If (c) passes and *aequatorialis* is separated, Areta et al. (2023) suggested the English name Ecuadorian Seedeater because most of its range occurs in Ecuador, whereas the previously proposed name, Equatorial Seedeater, could suggest a lowland distribution rather than the montane range that the species occupies. If you vote YES on (c), please vote either for Ecuadorian Seedeater or Equatorial Seedeater.

- If (d) passes and the five taxa become subspecies within *A. moesta*, a new English name should be proposed.
- If (a) and/or (c) pass, the name Blue Seedeater could continue to be used for *concolor* or a new name could be proposed.

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Submitted by: Rosa Alicia Jiménez**,** Universidad de San Carlos de Guatemala; Terry Chesser; and Juan I. Areta, Instituto de Bio y Geociencias del Noroeste Argentino

Proposal date: 4 February 2023

Treat *Pipilo socorroensis* as a separate species from Spotted Towhee *P. maculatus*

Background:

The Spotted Towhee (*Pipilo maculatus*) is a polytypic species with as many as 20 extant subspecies recognized (Figure 1, Bartos Smith and Greenlaw 2020). Subspecies vary in plumage coloration, morphology (body and bill size), and extent of spotting on both the body and tail. Vocal differences (trill rate and presence/absence of introductory notes) also are pronounced between some populations (e.g., Borror 1975, Cicero et al. unpublished). Although the entire complex is interesting for a variety of reasons, this proposal is focused on the status of *socorroensis* – a taxon (hereafter called “Socorro Towhee”) endemic to Isla Socorro which is a small volcanic island off the western coast Mexico. This island is the largest of four islands of the Revillagigedo Archipelago and is home to a number of endemic bird species or subspecies (Jehl and Parkes 1982). Jehl and Parkes (1982) noted a marked population decline in towhees on the island and the taxon is now considered endangered.

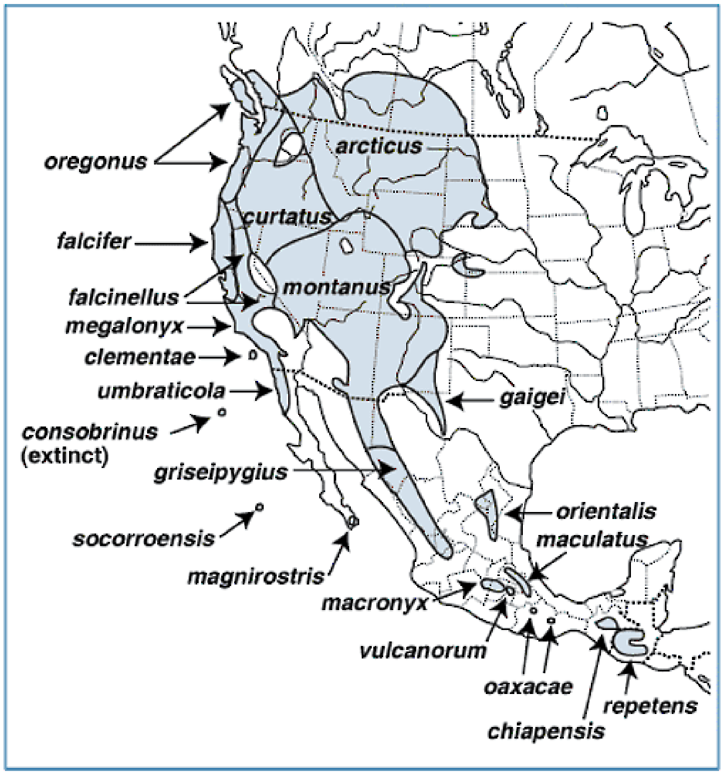

Figure 1. Map of Spotted Towhee subspecies, from Bartos Smith and Greenlaw (2020).

Pipilo socorroensis was originally described as a new species by Colonel A. J. Grayson in 1867. This description was published in the “California Farmer and Journal of Useful Sciences” (vol. 28, October 24), which at the time was used as a medium for communicating new discoveries. I was able to find that publication online but not the particular issue describing the Socorro Towhee. However, Taylor (1951) provided a nice summary of the history including the original description (excerpt #1 below).

The main reason that Taylor (1951) focused on the Socorro Towhee is because of a subsequent publication by Lawrence (1871, excerpt #2 below) in which he also described the Socorro Towhee but gave it the specific name *Pipilo carmani*. Type specimens were collected by Grayson and are in the USNM collection. Apparently, the name *P. carmani* was given by Spencer Fullerton Baird and retained by Lawrence, and both were unaware of the earlier description by Grayson, who had died in 1869, of the same taxon (Taylor 1951).

The Socorro Towhee continued to be recognized as a distinct species until 1970, when it was lumped with the Rufous-sided Towhee and subsequently the Spotted Towhee after that taxon was split from the Eastern Towhee (AOU 1995). Peter's Check-list of Birds of the World (Paynter 1970) recognized *P. socorroensis*, but in the same year Mayr and Short (1970) merged *socorroensis* into *erythrophthalmus* (including *maculatus*) with the following comment: "The Socorro Island subspecies *socorroensis* is also distinctive, but the extensive hybridization between the more divergent *ocai* and *maculatus* groups suggests that *socorroensis* is conspecific with *erythrophthalmus*." AOU (1998) treated *soccoroensis* as a group within *P. maculatus* with the note that it had been treated formerly as a distinct species.

Current treatments are mixed. Birds of the World (Bartos Smith and Greenlaw 2020) and Clements Checklist (2022) retain *socorroensis* as a subspecies of *P. maculatus,* although editions of the Clements Checklist through 2007 recognize *P. socorroensis* (see Avibase link below). Handbook of the Birds of the World (HBW) Alive had *socorroensis* as a subspecies in 2015 but as a species in 2017. This change follows del Hoyo et al. (2016) who provided the following rationale: "Usually treated as conspecific with *P. maculatus*, but differs in its much smaller size (wing and tail 70.2 and 71.6 mm vs mean of one of each subspecies of *P. maculatus* 89.4 and 95.8; at least 3); dark brown vs blackish head, breast and back (2); greatly reduced white spotting on wings (1); smaller white tips to tail (1)."

The species-level treatment is followed by HBW and Bird Life International, with the following taxonomic note at the Bird Life International Data Zone: "*Pipilo maculatus* and *P. socorroensis* (del Hoyo and Collar 2016) were previously lumped as P*. maculatus* following AOU (1998 and supplements); Stotz *et al*. (1996)."

http://datazone.birdlife.org/species/factsheet/socorro-towhee-pipilo-socorroensis
https://avibase.bsc-eoc.org/species.jsp?avibaseid=26AB0890

New Information:

There isn't really any new data to shed light on this issue. Although there are morphological differences, I am not aware of any genetic or vocal data that compares *socorroensis* with mainland *maculatus* subspecies. I also was unable to find any recordings at either Xeno-canto or Macaulay Library. Thus, the only reason to consider splitting *socorrensis* is the smaller size plus some plumage differences. However, those differences by themselves are insufficient in my opinion to justify a split, especially without a comprehensive quantitative morphological and vocal (and ideally also genetic) comparison with other subspecies of Spotted Towhee.

Recommendation:

I recommend a NO vote on treating *socorroensis* as a separate species from *maculatus*, pending additional study. If a split is adopted, then it makes sense to use the historic English name of "Socorro Towhee."

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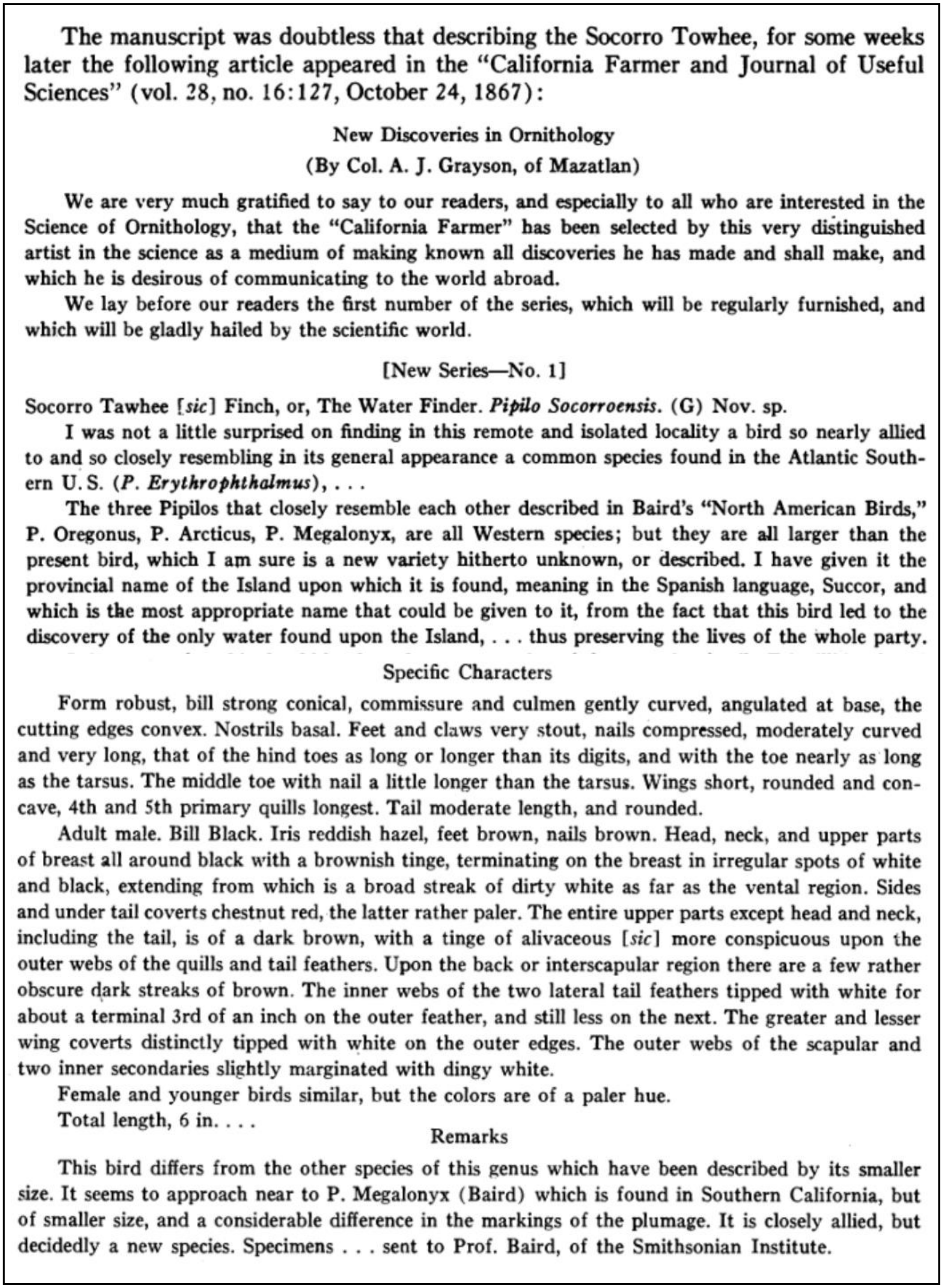
Submitted by: Carla Cicero

Date of Proposal: 8 February 2023

Excerpts on following pages:

1. Original description of *P. socorroensis* Grayson 1867 extracted from Taylor (1951).
2. Original description of *P. carmani* (= *socorroensis*) Lawrence 1871.

Excerpt #1



The manuscript was doubtless that describing the Socorro Towhee, for some weeks later the following article appeared in the "California Farmer and Journal of Useful Sciences" (vol. 28, no. 16:127, October 24, 1867):

New Discoveries in Ornithology

(By Col. A. J. Grayson, of Mazatlan)

We are very much gratified to say to our readers, and especially to all who are interested in the Science of Ornithology, that the "California Farmer" has been selected by this very distinguished artist in the science as a medium of making known all discoveries he has made and shall make, and which he is desirous of communicating to the world abroad.

We lay before our readers the first number of the series, which will be regularly furnished, and which will be gladly hailed by the scientific world.

[New Series—No. 1]

Socorro Tawhee [*sic*] Finch, or, The Water Finder. ***Pipilo Socorroensis.*** (G) Nov. sp.

I was not a little surprised on finding in this remote and isolated locality a bird so nearly allied to and so closely resembling in its general appearance a common species found in the Atlantic Southern U. S. (***P. Erythrophthalmus***), . . .

The three Pipilos that closely resemble each other described in Baird's "North American Birds," P. Oregonus, P. Arcticus, P. Megalonyx, are all Western species; but they are all larger than the present bird, which I am sure is a new variety hitherto unknown, or described. I have given it the provincial name of the Island upon which it is found, meaning in the Spanish language, Succor, and which is the most appropriate name that could be given to it, from the fact that this bird led to the discovery of the only water found upon the Island, . . . thus preserving the lives of the whole party.

Specific Characters

Form robust, bill strong conical, commissure and culmen gently curved, angulated at base, the cutting edges convex. Nostrils basal. Feet and claws very stout, nails compressed, moderately curved and very long, that of the hind toes as long or longer than its digits, and with the toe nearly as long as the tarsus. The middle toe with nail a little longer than the tarsus. Wings short, rounded and concave, 4th and 5th primary quills longest. Tail moderate length, and rounded.

Adult male. Bill Black. Iris reddish hazel, feet brown, nails brown. Head, neck, and upper parts of breast all around black with a brownish tinge, terminating on the breast in irregular spots of white and black, extending from which is a broad streak of dirty white as far as the vental region. Sides and under tail coverts chestnut red, the latter rather paler. The entire upper parts except head and neck, including the tail, is of a dark brown, with a tinge of alivaceous [*sic*] more conspicuous upon the outer webs of the quills and tail feathers. Upon the back or interscapular region there are a few rather obscure dark streaks of brown. The inner webs of the two lateral tail feathers tipped with white for about a terminal 3rd of an inch on the outer feather, and still less on the next. The greater and lesser wing coverts distinctly tipped with white on the outer edges. The outer webs of the scapular and two inner secondaries slightly marginated with dingy white.

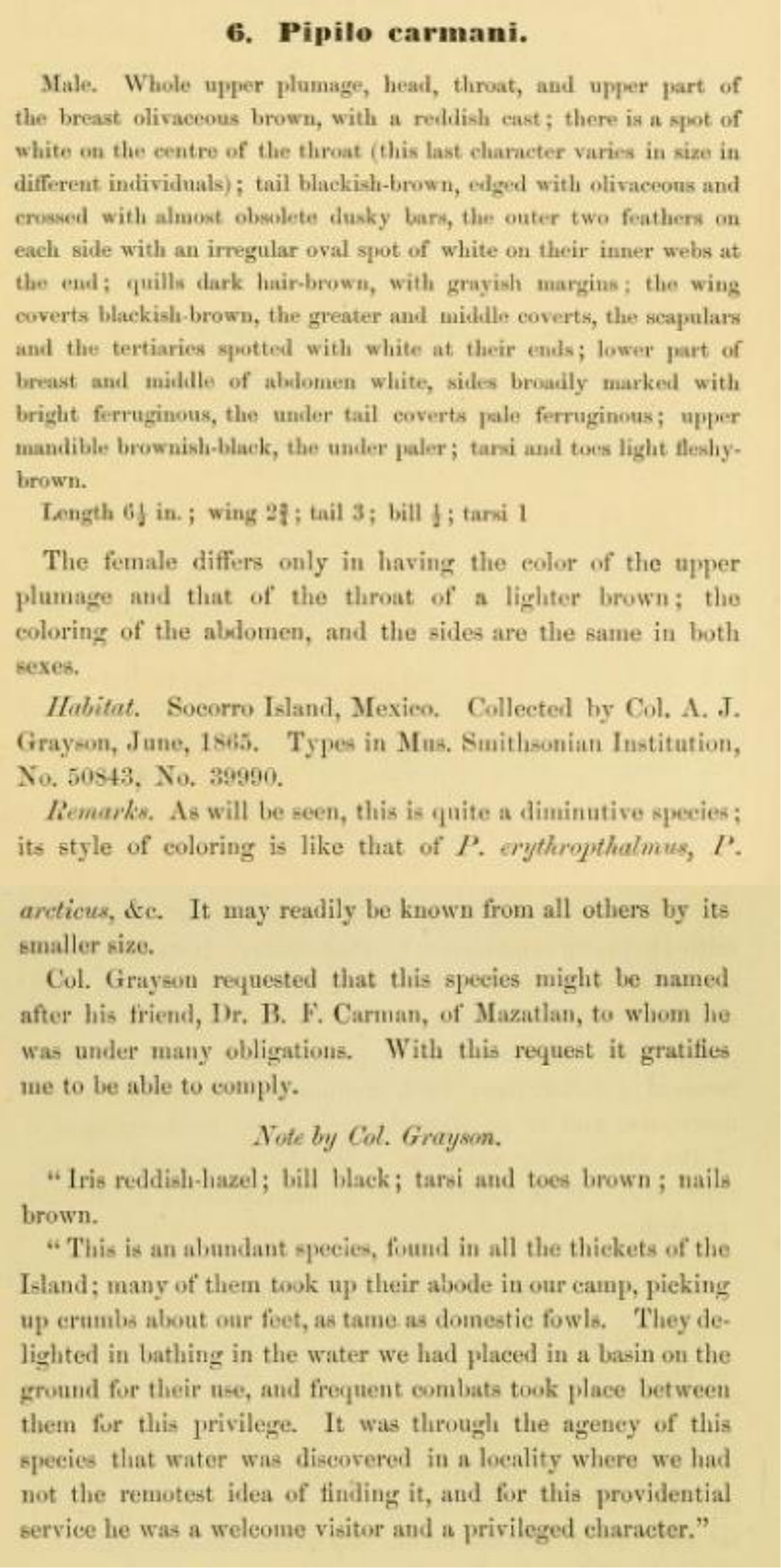
Female and younger birds similar, but the colors are of a paler hue.

Total length, 6 in. . . .

Remarks

This bird differs from the other species of this genus which have been described by its smaller size. It seems to approach near to P. Megalonyx (Baird) which is found in Southern California, but of smaller size, and a considerable difference in the markings of the plumage. It is closely allied, but decidedly a new species. Specimens . . . sent to Prof. Baird, of the Smithsonian Institute.

Excerpt #2



6. Pipilo carmani.

Male. Whole upper plumage, head, throat, and upper part of the breast olivaceous brown, with a reddish cast; there is a spot of white on the centre of the throat (this last character varies in size in different individuals); tail blackish-brown, edged with olivaceous and crossed with almost obsolete dusky bars, the outer two feathers on each side with an irregular oval spot of white on their inner webs at the end; quills dark hair-brown, with grayish margins; the wing coverts blackish-brown, the greater and middle coverts, the scapulars and the tertiaries spotted with white at their ends; lower part of breast and middle of abdomen white, sides broadly marked with bright ferruginous, the under tail coverts pale ferruginous; upper mandible brownish-black, the under paler; tarsi and toes light fleshy-brown.

Length 6½ in.; wing 2¾; tail 3; bill ½; tarsi 1

The female differs only in having the color of the upper plumage and that of the throat of a lighter brown; the coloring of the abdomen, and the sides are the same in both sexes.

Habitat. Socorro Island, Mexico. Collected by Col. A. J. Grayson, June, 1865. Types in Mus. Smithsonian Institution, No. 50843, No. 39990.

Remarks. As will be seen, this is quite a diminutive species; its style of coloring is like that of *P. erythropthalmus*, *P. arcticus*, &c. It may readily be known from all others by its smaller size.

Col. Grayson requested that this species might be named after his friend, Dr. B. F. Carman, of Mazatlan, to whom he was under many obligations. With this request it gratifies me to be able to comply.

Note by Col. Grayson.

"Iris reddish-hazel; bill black; tarsi and toes brown; nails brown.

"This is an abundant species, found in all the thickets of the Island; many of them took up their abode in our camp, picking up crumbs about our feet, as tame as domestic fowls. They delighted in bathing in the water we had placed in a basin on the ground for their use, and frequent combats took place between them for this privilege. It was through the agency of this species that water was discovered in a locality where we had not the remotest idea of finding it, and for this providential service he was a welcome visitor and a privileged character."

Revise generic limits among *Rhodothraupis*, *Periporphyrus*, and *Caryothraustes*, and adopt a new linear sequence for these taxa

Background:

Rhodothraupis celaeno (Deppe, 1830) is a dichromatic understory cardinalid of the lowlands of northeastern Mexico, the males being largely dark red with a solid black head and dark back, whereas the females have the red replaced by yellowish olive (Brewer 2020b). This overall plumage pattern is shared by *Periporphyrus erythromelas* ("Gmelin, JF", 1789) of northeastern South America and the southeastern Amazon Basin, although that species is brighter red (males) or yellow (females), especially on the back, and has a larger bill (Brewer 2020a, eBird records). After being placed in various 'catchall' genera (e.g., *Loxia*, *Fringilla*) in the 19th century, *Rhodothraupis celaeno* bounced around between the monotypic genus *Rhodothraupis* Ridgway 1898, *Periporphyrus* Reichenbach 1850, *Caryothraustes* Reichenbach 1850, and *Pitylus* Cuvier 1829 (Ridgway 1901, Hellmayr 1938), whereas *Periporphyrus erythromelas* moved between its current genus and *Pitylus* Cuvier 1829 (Hellmayr 1938). Molecular data have now shown *Pitylus* to be part of *Saltator* in the Thraupidae, but the remaining three genera are closely related and part of the Cardinalidae (Barker et al. 2015). *Parkerthraustes humeralis* (Lawrence 1867) was previously considered a *Caryothraustes* until molecular data showed it belonged in the Thraupidae (Demastes and Remsen 1994). In the current treatment of NACC/SACC, *Caryothraustes* contains two species: *poliogaster* of Mexico and Central America and *canadensis* of northeastern South America, southeastern Brazil, and eastern Panama (Clements et al. 2022). Both species of *Caryothraustes* are monochromatic, largely arboreal lowland species. Both *Rhodothraupis celaeno* and *Periporphyrus erythromelas* are mostly understory / midstory species, and at least *Periporphyrus* will join mixed flocks (Brewer 2020a).

All four species in this group give leisurely whistled songs in short but widely separated strophes (i.e., typical cardinalid songs), although the pattern differs between species. The two *Caryothraustes* also give a variety of "loud and arresting" calls when flocking, described as a "zzzrt", "tree-dreek", or "chew-chew-chew" (Gulson 2020). *Rhodothraupis* and *Periporphyrus* both give more subtle calls; a "high, clear, penetrating slurred 'sseeuu'" in *Rhodothraupis* and a "high-pitched, sharp 'spink'" in *Periporphyrus* (Brewer 2020a, 2020b).

The last major generic revision of this group was that of Ridgway (1901), resulting in the treatment followed by most subsequent authors, with *Rhodothraupis* and *Periporphyrus* each being monotypic, and *Caryothraustes* with two species (e.g. Dickinson and Christidis 2014, Gill et al. 2020, Clements et al. 2022, Chesser et al. 2023). Paynter (1970) lumped *Caryothraustes poliogaster* with *canadensis* but that treatment was not followed by subsequent authors. SACC recently considered a proposal to split *Caryothraustes canadensis*, which did not pass. In addition to whether the species were dichromatic or monochromatic, Ridgway (1901) used the following structural characters to delimit genera: *Periporphyrus* with a culmen longer than the tarsus, concave mandibular tomium, and a "broad truncated prominence" at the base of the tomium (i.e. a "toothed" tomium), *Rhodothraupis* with a relatively longer tail and narrower bill, and *Caryothraustes* with a relatively shorter tail and broader bill. We now know that bill shape is extremely labile in the Cardinalidae, with a particularly drastic example being "*Guiraca*" [=*Passerina*] *caerulea*.
del Hoyo et al. (2016) transferred both *Rhodothraupis* and *Periporphyrus* to *Caryothraustes* but provided no rationale for this action. Both *Periporphyrus* and *Caryothraustes* were described in the same volume by Reichenbach (Reichenbach 1850), but I am unable to locate a copy of this

volume to review the genus descriptions. Hellmayr (1938) lists the two genera as being described on sequential plates 77 (*Periporphyrus*) and 78 (*Caryothraustes*). My interpretation is that these genera were therefore simultaneously published, and that in transferring *Periporphyrus* to *Caryothraustes*, del Hoyo et al. (2016) should be considered the First Revisers when they selected *Caryothraustes* as having priority.

New Information:

Barker et al. (2015) used a supertree approach to estimate a phylogeny for the 9-primaried oscines which resulted in many genus and family level rearrangements that have since been adopted by NACC, SACC, and other authorities. This tree was based primarily on the mitochondrial genes Cyt-B and ND2, augmented by four nuclear genes for representatives of most genera. Below I have reproduced a portion of the tree showing most of the Cardinalidae, including the species relevant to this proposal (Figure 1). Of note is that *Rhodothraupis*, *Periporphyrus*, and *Caryothraustes* form a clade sister to *Cardinalis*. *Rhodothraupis* and *Periporphyrus* are sister taxa, separated by about 5 Ma (right-most dashed line in Figure 1). A more recent phylogenetic analysis of *Caryothraustes* (Tonetti et al. 2017; with *Rhodothraupis* and *Periporphyrus* as outgroups) using the mitochondrial locus ND2 found similar branch lengths and topology as Barker et al. (2015).

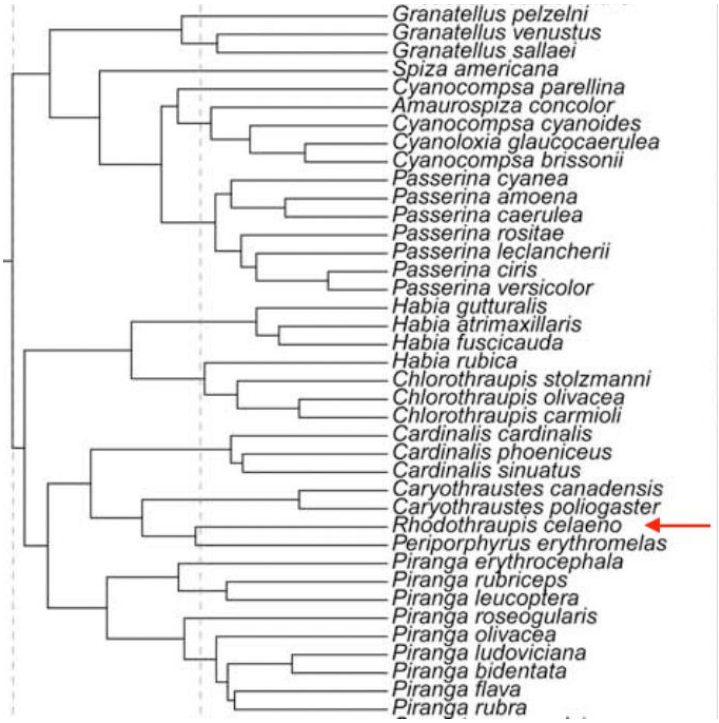


Figure 1. A portion of the Cardinalidae phylogeny from Barker et al. (2015). The two vertical dashed lines correspond to 10 Ma (left-hand line) and 5 Ma (right-hand line). *Rhodothraupis celaeno* is indicated with a red arrow.

A more recent study on sister relationships of multiple complexes of Amazonian and Atlantic Forest taxa (Bocalini et al. 2021) included all subspecies of *Caryothraustes* and both *Rhodothraupis* and *Periporphyrus* as outgroups. They estimated a coalescent-based species tree from 3,826 UCE SNPs, which I have reproduced below (Figure 2). As an aside, Bocalini et al. (2021) found that *Caryothraustes canadensis simulans* of eastern Panama was sister to *C.*

poliogaster, rather than to the remainder of *C. canadensis*, so a species-level taxonomic change should be considered for *simulans*, either considering it a separate species or transferring it to *C. poliogaster*.

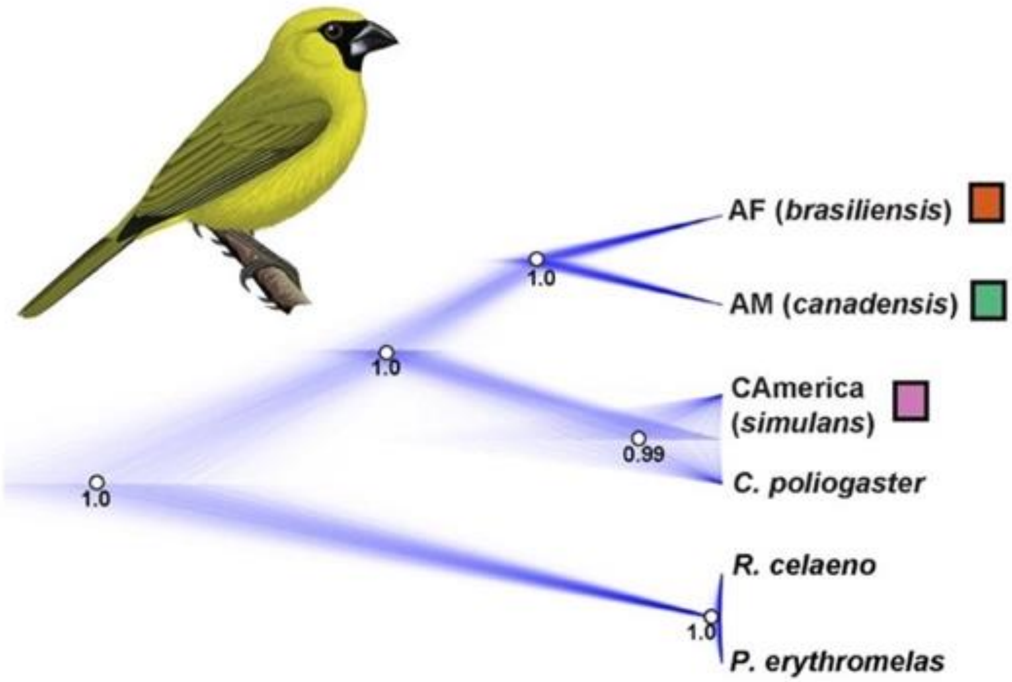


Figure 2. The phylogeny of *Caryothraustes* and two outgroups, estimated in SNAPP. From Bocalini et al. (2021).

The topology of the phylogenies in Barker et al. (2015) and Bocalini et al. (2021) are concordant, but the branch lengths are extremely different. Most notably, the UCE tree in Bocalini et al. (2021) found extremely low divergence between *Rhodothraupis* and *Periporphyrus* (far less than the divergence within *Caryothraustes*), although I note that this is a coalescent-based analysis, which in my experience often recovers lower divergence estimates than maximum likelihood methods like those used in Barker et al. (2015). The Barker et al. (2015) study was based on many fewer loci, which may also explain the different branch lengths between the two studies.

A series of specimens of the relevant species in this group are shown on below, courtesy of Terry Chesser. Within each species, males are on the left and females on the right, and the species from left to right are: *Rhodothraupis celaeno*, *Periporphyrus erythromelas*, *Caryothraustes poliogaster*, and *Caryothraustes canadensis*.

Effect on AOS-CLC area:

Merging *Rhodothraupis* into *Periporphyrus* would result in a name change from *Rhodothraupis celaeno* to *Periporphyrus celaeno*. Merging all species into *Caryothraustes* (following del Hoyo et al. 2016) would result in name changes for *Rhodothraupis celaeno* and *Periporphyrus erythromelas* in the following linear sequence: *Caryothraustes celaeno*, *C. erythromelas*, *C. poliogaster*, *C. canadensis*.

Recommendation:

The two major clades in this group have the same number of species (2), and *Rhodothraupis celaeno* is the northern-most member of the group, so regardless of any genus-level transfers *celaeno* should go first in the linear sequence. I recommend adopting a new linear sequence (see below), which differs only slightly from the current NACC treatment.

The ~5 Ma divergence between *Rhodothraupis* and *Periporphyrus* in Barker et al. (2015) is less than that shown by most related cardinalid genera, and the very low divergence between the two species found by Bocalini et al. (2021) suggests that these two species are very closely related. The bill size / shape differences are best not considered genus-level characters in the Cardinalidae, and I find the wing and tail length differences to not be drastically different. Combined with the broadly similar red-and-black (male) and green-and-black (female) plumages of *Rhodothraupis* and *Periporphyrus*, I think *Rhodothraupis celaeno* is best transferred to *Periporphyrus*.

Based solely on relative branch lengths in Barker et al. (2015), the divergence between *Caryothraustes* and *Rhodothraupis* + *Periporphyrus* is roughly comparable to some other genus-level divergences in the Cardinalidae, such as those among *Amaurospiza*, *Cyanoloxia*, and *Cyanocompsa*. These similar genus-level clade ages, combined with the differing plumage dimorphism (monochromatic in *Caryothraustes* vs. dichromatic in *Rhodothraupis* and *Periporphyrus*), and a more canopy-dwelling habit and differing calls of *Caryothraustes*, are sufficient in my view to keep *Caryothraustes* and *Periporphyrus* as separate genera. Although I minimized the importance of the bill shape differences in advocating for the merger of *Rhodothraupis* and *Periporphyrus*, the two *Caryothraustes* do have a notably wide bill. *Caryothraustes* do also look superficially like females of *Rhodothraupis* and *Periporphyrus*, albeit with restricted black on the head. That said, I don't think that a merger of *Caryothraustes* and *Periporphyrus* is necessary, although it would maintain a monophyletic grouping.

Please vote on the following:

A. Adopt the following linear sequence: *celaeno*, *erythromelas* (extralimital), *poliogaster*, *canadensis*.
B. Transfer *Rhodothraupis celaeno* to *Periporphyrus*
C. Transfer *Rhodothraupis celaeno* and *Periporphyrus erythromelas* to *Caryothraustes* (only if B passes)

I recommend a **YES** on A and B, and a **NO** on C.

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Submitted by: Oscar Johnson, The University of Texas at El Paso

Date of proposal: 17 February 2023

Treat *Pachyramphus uropygialis* as a separate species from Gray-collared Becard *P. major*

Effect on NACC:

Splitting *Pachyramphus uropygialis* from *P. major* would result in an additional species in the AOS area.

Background:

Pachyramphus major currently consists of five described subspecies and occurs from the mountains of northwestern and northeastern Mexico south into Central America, including the Yucatan Peninsula, as far south as northern Nicaragua. The five subspecies consist of two groups: a western group composed of *uropygialis*, and an eastern group composed of *major*/*matudai*/*itzensis*/*australis*. All taxa are allopatric (del Hoyo et al. 2022): *P. m. uropygialis* occurs in western Mexico from Sonora/Chihuahua south to the highlands of Oaxaca on the Pacific slope, whereas taxa of the eastern group occur on the Atlantic slope or south of the Isthmus of Tehuantepec. The species frequents forest, especially pine (*Pinus*) and oak (*Quercus*), although it can use a wide variety of habitats, including semihumid broadleaf, plantations, agricultural areas, and swampy lowlands, provided that trees are present (del Hoyo, et al. 2022). Since initially described in the late 1800's, *uropygialis* was considered to be a subspecies of *P. major* (Nelson 1898, 1899). Originally, only the male was described and, as the name suggests, the difference was in rump color, with *uropygialis* having a distinctly paler rump, nearly white on the lateral tail coverts, and paler underparts (Nelson 1899, Figure 1).

Figure 1: Specimens showing the paler rump *uropygialis*. The four specimens on the left are *uropygialis* (MLZ 12682, MLZ 58342, MLZ 28738, MLZ 12028), the middle four are *major* (MLZ 35017, MLZ 34479, MLZ 49820, MLZ 48293), and four on the right are *matudai* (MLZ 47702, MLZ 35265, MLZ 27293, MLZ 27291). Photo by Marky Mutchler/Moore Laboratory of Zoology.

Females of *uropygialis*, described later, differ in their rufous crown (other subspecies of *P. major* have a black crown), more lemon to the sides of the head, and underparts lacking cinnamon-buff. Although size reportedly differs (Ridgway 1907), larger sample sizes are needed to confirm this (del Hoyo et al. 2022).

Unfortunately, neither LSU nor the Moore Lab of Zoology had female *uropygialis*, although the photos linked below illustrate the variation among subspecies. In the eastern group, depending on subspecies, underpart coloration varies from cinnamon with a solid black crown, e.g.,
https://macaulaylibrary.org/asset/448531801
https://macaulaylibrary.org/asset/383712751
https://macaulaylibrary.org/asset/355809961

to a buffy yellow
https://macaulaylibrary.org/asset/499958651

sometimes with some brown in the crown
https://macaulaylibrary.org/asset/339580581

A more intermediate individual of *P. m. major* from the Atlantic slope of Oaxaca (*uropygialis* is found on the Pacific slope of Oaxaca) shows a combination of traits including brown throughout the crown and paler yellow underparts
https://search.macaulaylibrary.org/catalog?taxonCode=grcbec1&subId=S93651505

In contrast, *uropygialis* shows pale yellow underparts with a solid brown crown, e.g.,
https://macaulaylibrary.org/asset/300015411
https://macaulaylibrary.org/asset/529688551

The one-species treatment has been the prevailing treatment since the description of *uropygialis*. It has been thought to be closely related to and possibly conspecific with *P. albogriseus* (Hellmayr 1929), but I can find no mention historically of treating *uropygialis* as a separate species. More recently, *uropygialis* has been proposed to be a separate species using the ESC (Navarro-Sigüenza and Peterson 2004) based on the differing crown pattern of the females. Navarro-Sigüenza & Peterson (2004) also suggested that more splits within the group may be warranted under an ESC treatment. This treatment has been followed by the Handbook Birds of the World (del Hoyo et al. 2017) based on differences in the male rump pattern and the differences in crown and underpart pattern of females mentioned above.

New Information:

A handful of recent papers investigating the genetic relationships of Tityrinae and *Pachyramphus* have included a couple of samples of both the western and eastern groups of *P. major*, although none has investigated *P. major* in depth.

Musher and Cracraft (2018) used the PSC to delineate evolutionarily distinct taxa of *Pachyramphus*. They considered the two groups of *P. major* to be evolutionarily distinct and included single samples of *P. m. australis* and *P. m. itzenis* (although they only referenced them as *P. major*) and two of *uropygialis.* Both groups were only included in their mtDNA tree (Figure 2). They tested the two groups using Bayesian Phylogenetics and Phylogeography (BPP) to estimate the probability of speciation and found strong support in 2/3 of the runs.

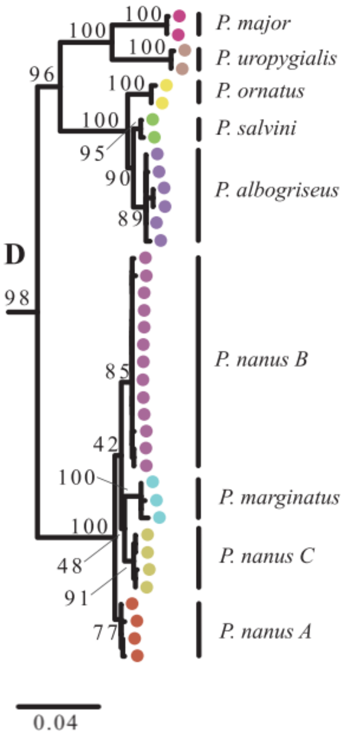

Figure 2: ML tree based on mtDNA of clade D of Musher and Cracraft (2018) showing boot strap values. Scale bar is substitutions per site.

In a broad study on why Amazonia is a source of biodiversity using Tityrinae as a case study, Musher et al. (2019) included single samples of *itzenis* and *uropygialis* and estimated they had diverged .32 Ma. Below is their Figure 1b, a UCE time-calibrated phylogeny for Tityrinae (Figure 3).

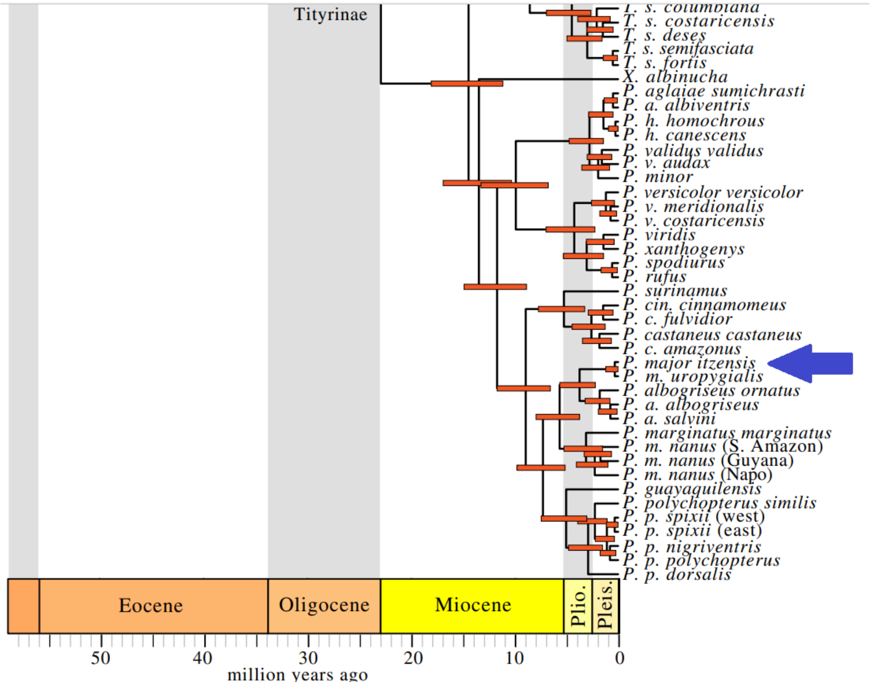

Figure 3: A UCE time-calibrated phylogeny for Tityrinae from Musher et al. (2019) with the addition of a blue arrow to highlight the two samples of P. major. The Orange bars represent 95% HPD for nodes and black bars represent the calibration priors applied.

Musher et al. (2023) in a study of *Pachyramphus albogriseus sensu lato* included a new sample of *itzenis* and *uropygialis* for a phylogenetic tree based on concatenated nuclear (UCE) data (Figure 4) which found a similar topology to the previous work.

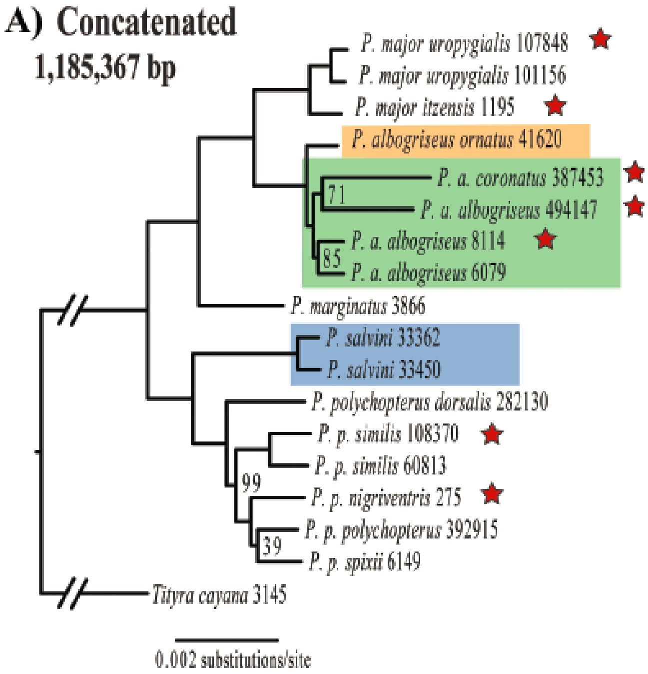

Figure 4: UCE concatenated tree with *P. major* at top (Musher et al. 2023). Red Stars denote samples new to this study.

Vocalizations reportedly do not differ (del Hoyo, et al. 2022) and in listening to recordings online, most vocalizations seemed to overlap between populations, though I found one potential slight difference in one call:

Eastern: https://macaulaylibrary.org/asset/103322

Western: https://macaulaylibrary.org/asset/288736281

Any difference will need a formal analysis comparing homologous vocalizations combined with reciprocal playback experiments.

Recommendation:

I recommend a NO vote given recent divergence times between allopatric populations, with a close sister relationship between *P. m. uropygialis* and *australis*/*itzenis*, and a lack of published vocal differences. Nominate *major* and *matudai*, whose range are geographically closest to *uropygialis*, have yet to be included in genetic studies of *Pachyamphus* and would need to be included before any taxonomic revisions can be made, along with a rigorous analysis of the vocalizations.

Acknowledgment:

Many thanks to Marky Mutchler and the Moore Laboratory of Zoology for the photo.

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Submitted by: David Vander Pluym, Louisiana State University

Date of proposal: 17 February 2023

Treat *Chlorospingus hypophaeus* as a separate species from Yellow-throated Chlorospingus *C. flavigularis*

Background:

The Yellow-throated Chlorospingus (*Chlorospingus flavigularis*) consists of three subspecies. Subspecies *hypophaeus* is found in western Panama, mainly on the Caribbean slope, and there is also an isolated population of this subspecies on Cerro Tacarcuna, in NW Colombia on the border with Panama (Renjifo et al. 2017). This subspecies is allopatric from the other two: *C. f. flavigularis* occurs in the Andes of central Colombia, south through the eastern slope of Andes in Ecuador and Peru; and *C. f. marginatus* occurs on the western slope of western Andes in Colombia south to southwestern Ecuador. All three subspecies differ in iris color and plumage.

As a side note, *C. f. marginatus* is similar in throat color to a different species, *C. parvirostris*, but the ranges do not overlap*. Chlorospingus parvirostris* is now considered separate species from *C. flavigularis*, but *C. parvirostris* was previously considered a subspecies of *C. flavigularis*.

This proposal considers whether the northern subspecies of the Yellow-throated Chlorospingus (*C. f. hypophaeus*) should be considered a separate species from the two more southern subspecies (*C. f. flavigularis* and *C. f. marginatus*). This form was initially described as a species by Sclater and Salvin 1868 (https://www.biodiversitylibrary.org/item/91104#page/483/mode/1up).

With the exception of del Hoyo and Collar (2016), current taxonomies (e.g., Clements et al. 2022, Sibley and Monroe 1990, Storer 1970, Dickinson 2003, Gill et al. 2023) and field guides (e.g., Ridgely and Tudor 1989, Ridgely and Greenfield 2001, Ridgely and Gwynne 1989, Hilty 2021) consider all three subspecies as belonging to the same species. Despite this, a few sources suggest that more than one species is involved, based on plumage differences. Some examples are below:

Ridgely and Gwynne (1989): "The form found in Panama is geographically disjunct from the other races of this species, and stands apart in plumage as well (dark brown as opposed to pale amber or hazel iris, buff as opposed to gray breast, etc.). It may deserve full species status."

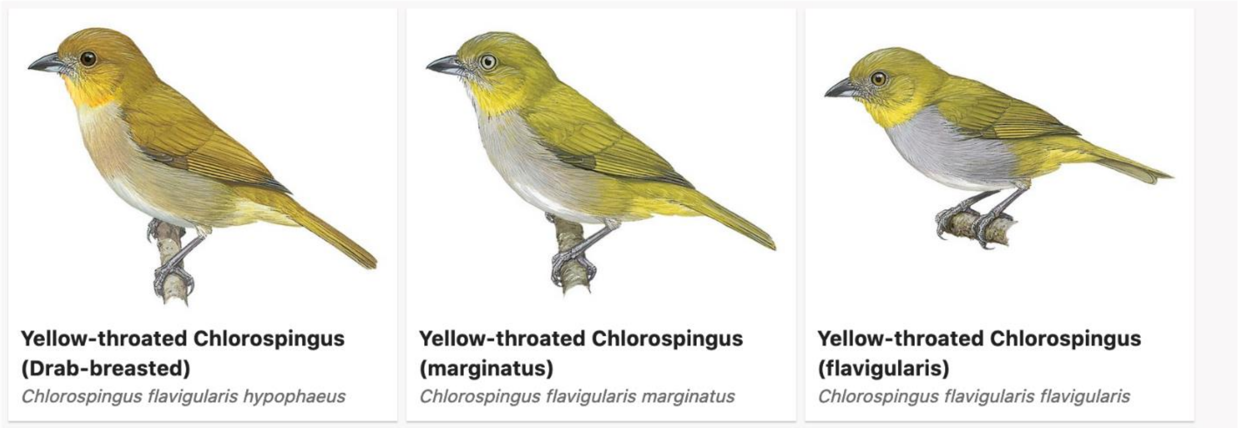
AOU (1983), 6th edition of the checklist: "Differences in eye color and behavior suggest that the Panama form may represent a species *C. hypophaeus* Sclater and Salvin 1868 [Dark-breasted Bush-Tanager], different from South American *C. flavigularis*."

AOU (1998), 7th edition of the checklist: "Differences in iris color and behavior suggest the two groups may represent separate species (Isler and Isler 1987), *C. hypophaeus* Sclater and Savin, 1868 [Drab-breasted Bush-Tanager] and *C. flavigularis* [Yellow-throated Bush-Tanager]."

Isler and Isler (1987) described plumage and iris color differences and stated "..may prove to be a distinct species." In their section on foraging, they indicate that foraging observations in Panama are in middle to upper heights of the tree, and they cite Ridgely (1976). Their descriptions of foraging heights of other populations are generally lower. It’s hard to know if that’s just variation due to few observations or if the populations do have fixed differences in foraging behavior. Otherwise, I can’t find any references that talk about “differences in behavior” that is mentioned in past AOU checklists.

As far as I can tell, del Hoyo and Collar (2016) is the only taxonomy that currently treats the northern subspecies as separate species. The reasoning is based on iris color, plumage, and tail size: "Hitherto treated as conspecific with *C. flavigularis*, but differs in its dark vs pale iris (3); yellow-orange vs yellow throat (1); warm buff vs cold grey breast (2); lower underparts buffy-grey vs grey-green (ns1); smaller size, notably shorter tail (effect size for 8 males vs 10 male nominate *C. flavigularis* –2.9, score 2)."

I don’t have access to specimens, but these differences can be seen in the illustrations from Birds of the World online (Hilty et al. 2020), as well as from Isler and Isler (1987):

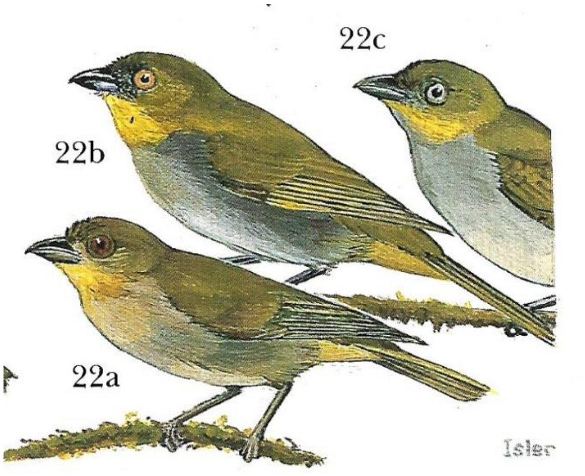


Yellow-throated Chlorospingus (Drab-breasted)
Chlorospingus flavigularis hypophaeus

Yellow-throated Chlorospingus (marginatus)
Chlorospingus flavigularis marginatus

Yellow-throated Chlorospingus (flavigularis)
Chlorospingus flavigularis flavigularis

Illustrations from Birds of the World online (Hilty et al. 2020)



Isler and Isler’s (1987) illustrations. 22a: C. f. hypophaeus, 22b: C. f. flavigularis, 22c: C. v. marginatus

Note that although iris color is one of the traits used to split *C. f. hypophaeus* from *C. flavigularis*, all three subspecies differ in iris color: *C. f. flavigularis* (hazel iris), *C. f. marginatus* (grey), and *C. f. hypophaeus* (dark).

New Information:

There is no new information *per se*; this proposal is to provide feedback to WGAC which is working to reconcile all world lists. Nonetheless, I looked for any information I could find on genetics or vocalizations.

<u>Genetics</u>: As far as I can tell, samples of only one of the subspecies (a sample of *C. f. flavigularis* from Peru) has been sequenced (Klicka et al. 2014). This study looked at relationships among Passerellidae using mtDNA and 4 nuclear regions. *Chlorospingus flavigularis* was sister taxon to *C. parvirostris*. Levels of sequence divergence aren't provided; however, based on the phylogeny, these two species show fairly deep divergence that seems to be deeper than most other sister species of Passerellidae. As mentioned above, *C. parvirostris* itself used to be considered a subspecies of *C. flavigularis*.

<u>Vocalizations</u>: The song is not described for *C. f. hypophaeus*, and there aren't many vocalizations available for any of the subspecies in question. Macaulay Library only has only three recordings from Panama, all of similar sounding call notes. These should be *C. f. hypophaeus* based on locality. Xeno-canto only has two recordings, and I think these are actually the same as two that are on Macaulay. The recordings of the call notes do sound really different to me than the ones I listened to from the other subspecies. However, the other two subspecies also differ in vocalizations from each other, so it's hard to know what to make of these differences without a formal analysis.

Recommendation:

From what I can tell, the only information we have is plumage and iris color differences and differences in tail length and a disjunct distribution. I'm intrigued by the deep split between *C. flavigularis* and *C. parvirostris*. Compared to *C. f. hypophaeus*, *C. parvirostris* seems to be more similar in plumage *to C. f. flavigularis* and *C. f. marginatus*. Therefore, it would not surprise me if *C. f. hypophaeus* turns out to be genetically pretty different and a separate species. Nevertheless, at this time I don't think there is enough information to call these two biological species, so I recommend a "no" vote. More research is clearly warranted for all three subspecies of *C. flavigularis*. Personally, I've seen Yellow-throated Chlorospingus in Peru, but not in Panama. Admittedly, someone with more first-hand experience with both forms might have more insight.

English names:

If we were to decide to split them, there is some discrepancy in the English name being used for *C. f. hypophaeus*. del Hoyo and Collar (2016) use Orange-throated Bush-tanager, whereas other sources recommend Drab-breasted Bush-Tanager (AOU 1998, Ridgely and Gwynne 1989) or Dark-breasted Bush-Tanager (AOU 1983, Isler and Isler 1987). Of course, there is also the issue of using Bush-Tanager vs. Chlorospingus. We have been using Chlorospingus for English names of species in this genus.

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Submitted by: Kevin J. Burns, San Diego State University

Date of Proposal: 20 February 2023

Treat *Melozone occipitalis* as a separate species from White-eared Ground-Sparrow *M. leucotis*

Background:

White-eared Ground-Sparrow, *Melozone leucotis*, as recognized by the AOS *Check-List*, is comprised of three subspecies with disjunct distributions from southern Chiapas south to Costa Rica. These three subspecies are currently divided into two main groups by the Clements Checklist (Clements et al. 2022), with the nominate *leucotis* group also including the subspecies *nigrior*, with these two distributed from Nicaragua to Costa Rica. The taxon *occipitalis*, the "Gray-crowned Ground-Sparrow," occurs along the Pacific coast of southern Mexico in southern Chiapas south to Guatamala and El Salvador, and is separated from the nearest population of *nigrior* by at least 370 km. Salvin in 1878 described it as the species *Pyrgisoma occipital*e, which was maintained as a separate species by Ridgway (1901) before it was included within a broader *Melozone leucotis*, a treatment that has generally been followed by most authorities (Hellmayr 1938, Paynter 1970, Howell and Webb 1995, Dickinson and Christidis 2014, Clements et al. 2022, Gill et al. 2023). del Hoyo and Collar (2016), using the Tobias et al. (2010) scoring criteria for species delimitation, split *occipitalis* on the basis of plumage differences, noting: "its dull grey (sometimes black-lined) crown-stripe (3); broader, longer yellow postocular eye-line (2); black-centred white *vs* black upper breast (3); more chestnut tone to upperparts and tail (ns[1]); possibly slightly larger size (unmeasured)."

New Information:

Sandoval et al. (2017a) measured plumage, morphometric, and vocal differences among the three subspecies of White-eared Ground-Sparrow. In their analyses, they found that all three subspecies were distinguishable using both morphometric and plumage characteristics, and that *occipitalis* was most distinct, including in spectrophotometry analyses. As noted above, *occipitalis* has a gray crown stripe, broader yellow line on the side of the neck, and a small black breast spot compared to *leucotis/nigrior,* which are similar but do show some minor differences in plumage (Fig. 1). In spectrophotometry analyses, *occipitalis* had the throat, breast, and forehead significantly more saturated in the ultraviolet region compared to *leucotis*/*nigrior*, and with *occipitalis* also having the highest saturation values in the crown patch. In addition to saturation, *occipitalis* also had significantly higher brightness values in the breast, crown, and forehead patches than *leucotis/nigrior* (Fig. 2) Sandoval et al. (2017a) also found that *occipitalis* had shorter tarsi and a longer tail than the southern *leucotis/nigrior* group, with *leucotis/nigrior* also having a larger bill (Table 1). In pairwise diagnosability tests, only breast and crown patch color differences were diagnosably different between *occipitalis* and *nigrior*. Models based on plumage performed well in assigning birds to the correct subspecies, and performed better than expected by chance, assigning 92% of individuals correctly.

In their analysis of vocal differences, which looked at calls (49 *leucotis*, 7 *nigrior*, and 5 *occipitalis* individuals), male solo songs (46 *leucotis*, 7 *nigrior*, and 3 *occipitalis* individuals), and duets (47 *leucotis*, 9 *nigrior*, and 6 *occipitalis* pairs), Sandoval et al. (2017a) found that *occipitalis* had significantly lower maximum amplitude frequencies, as well as significantly longer songs than *leucotis/nigrior* for male solo songs (Table 2). Models were able to accurately classify 93% of male solo songs accurately, including 3/3 of *occipitalis* songs. Analyses of duets found that songs of *occipitalis* had lower maximum frequency, but models were unable to assign

Figure 1. From Sandoval et al. (2017a), photographs showing a specimen of each of the three taxa, *occipitalis* (left), *nigrior* (middle), and *leucotis* (right).

occipitalis songs accurately despite these differences. Calls were also significantly different in *occipitalis*, with higher minimum frequency and frequency of maximum amplitude (see Fig. 3). However, the low sample size could preclude some further conclusions to be drawn from these analyses, as earlier work by Sandoval et al. (2014) found that White-eared Ground-Sparrows studied in Costa Rica showed individual variation in song, with more variation between than within individuals. Sandoval et al. (2014) argued that there is enough variation in song to identify birds at both the individual and population level. No playback experiments have been done comparing responses between *occipitalis* and *leucotis/nigrior*; however, given the importance of song in this group (duets to maintain year-round territories in habitats where visual cues may be of limited use; Sandoval et al. 2015, 2016), the vocal differences identified may represent especially important differences between these taxa. Sandoval et al. (2017a) argued that the differences they identified in plumage, morphology, and vocalizations are similar to those identified in White-faced Ground- Sparrow (*Melozone biarcuata*) and Cabanis's Ground-Sparrow (*Melozone cabanisi*), which were split by NACC in 2017 (Chesser et al. 2017).

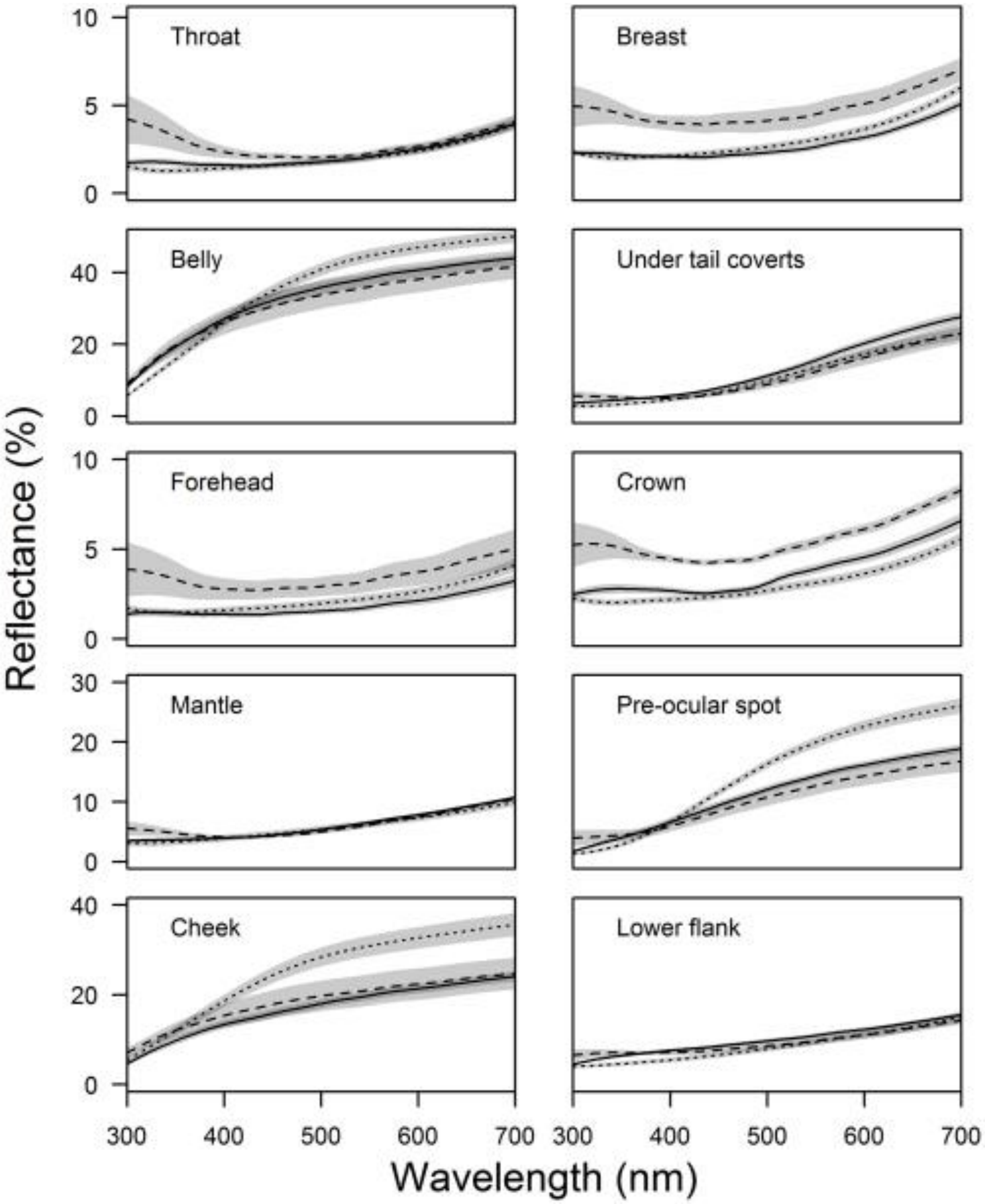

Figure 2. Mean reflectance spectra for different plumage patches for each of the three taxa (*leucotis* in solid line, *nigrior* in dotted line, and *occipitalis* in dashed line). From Sandoval et al. (2017a).

Female	***M. l. leucotis*** **(n = 28)**	***M. l. nigrior*** **(n = 8)**	***M. l. occipitalis*** **(n = 3)**
Tarsus (mm)	**28.1 ± 0.3**	**26.8 ± 0.5**	**26.1 ± 0.8**
Tail length (mm)	**68.2 ± 0.7**	**64.3 ± 1.2**	**76.0 ± 1.9**
Wing chord length (mm)	**76.2 ± 0.5**	**73.5 ± 0.8**	**77.0 ± 1.3**
Culmen length (mm)	**14.1 ± 0.1**	**14.5 ± 0.5**	**14.5 ± 0.4**
Beak width (mm)	9.6 ± 0.1	9.5 ± 0.1	9.5 ± 0.3
Beak depth (mm)	8.5 ± 0.1	8.7 ± 0.5	9.1 ± 0.2
Male	**(n = 45)**	**(n = 7)**	**(n = 5)**
Tarsus (mm)	**29.4 ± 0.2**	**28.4 ± 1.2**	**27.3 ± 0.5**
Tail length (mm)	**72.2 ± 0.5**	**71.0 ± 3.0**	**76.6 ± 1.6**
Wing chord length (mm)	**81.8 ± 0.4**	**81.9 ± 0.2**	**79.9 ± 1.0**
Culmen length (mm)	14.5 ± 0.1	14.4 ± 0.4	14.7 ± 0.3
Beak width (mm)	9.9 ± 0.1	9.5 ± 0.3	9.6 ± 0.3
Beak depth (mm)	10.5 ± 1.7	8.9 ± 0.2	9.6 ± 5.1
Plumage Pattern	**(n =16)**	**(n = 13)**	**(n = 9)**
Pre-ocular white spot (mm)	**5.8 ± 0.1**	**8.1 ± 0.2**	**6.4 ± 0.2**
Post-ocular white spot (mm)	8.6 ± 0.3	9.54 ± 0.3	8.7 ± 0.4
Height of breast spot (mm)	**21.4 ± 1.1**	**19.8 ± 1.2**	**11.8 ± 1.5**
Length of breast spot (mm)	**21.1 ± 0.8**	**26.6 ± 0.9**	**13.3 ± 1.1**
Throat patch length (mm)	21.3 ± 0.8	18.8 ± 0.7	20.8 ± 0.8
Crown length (mm)	**27.8 ± 0.6**	**31.1 ± 0.7**	**29.7 ± 0.8**

Table 1. Plumage pattern and morphological measurements of the three taxa. Values in bold represent significant differences between taxa. From Sandoval et al. (2017a).

	Minimum freq. (kHz)	Maximum freq. (kHz)	Freq. maximum amplitude (kHz)	Duration (s)	Number of elements
***Chip* calls**					
M. l. leucotis	**7341.7 ± 43.9**	12151.4 ± 93.8	**8294.3 ± 38.2**	0.078 ± 0.001	
M. l. nigrior	**7615.2 ± 101.7**	12349.2 ± 219.3	**9019.3 ± 213.6**	0.075 ± 0.003	
M. l. occipitalis	**8034.7 ± 273.5**	12237.1 ± 405	**8924.4 ± 447.2**	0.077 ± 0.005	
***Tseet* calls**					
M. l. leucotis	8102.7 ± 95.3	10595.1 ± 94.7	9263.6 ± 78.4	0.29 ± 0.01	
M. l. nigrior	8194.7	9892.9	9345.4	0.41	
M. l. occipitalis	8017 ± 142	11133.9 ± 178.4	8998.3 ± 160.3	0.35 ± 0.04	
Solo songs					
M. l. leucotis	3472.1 ± 587.6	11142 ± 704.3	**6064.6 ± 580.3**	**1.9 ± 0.2**	**7.7 ± 0.9**
M. l. nigrior	3725.7 ± 599.3	11032.4 ± 1009.4	**5904.3 ± 627.4**	**2.0 ± 0.1**	**11.0 ± 5.6**
M. l. occipitalis	3364.5 ± 978.4	10392.1 ± 1629.5	**5408.7 ± 479.3**	**2.2 ± 0.8**	**7.6 ± 1.2**
Duets					
M. l. leucotis	5093.2 ± 107.4	11547.4 ± 81.2	**7444.2 ± 170.7**	5.8 ± 0.2	
M. l. nigrior	5963.7 ± 225.7	10421.5 ± 246.9	**7497.5 ± 274.6**	5.8 ± 0.4	
M. l. occipitalis	5500.7 ± 214.8	11351.7 ± 226.5	**7168.7 ± 467.2**	5.8 ± 0.5	

Table 2. Acoustic characteristics of the three taxa. Values in bold represent significant differences. Note in particular the much lower minimum frequency amplitude of male solo songs for *occipitalis*, significantly longer duration of male song, and significantly lower minimum frequency of amplitude of the duets. From Sandoval et al. (2017a).

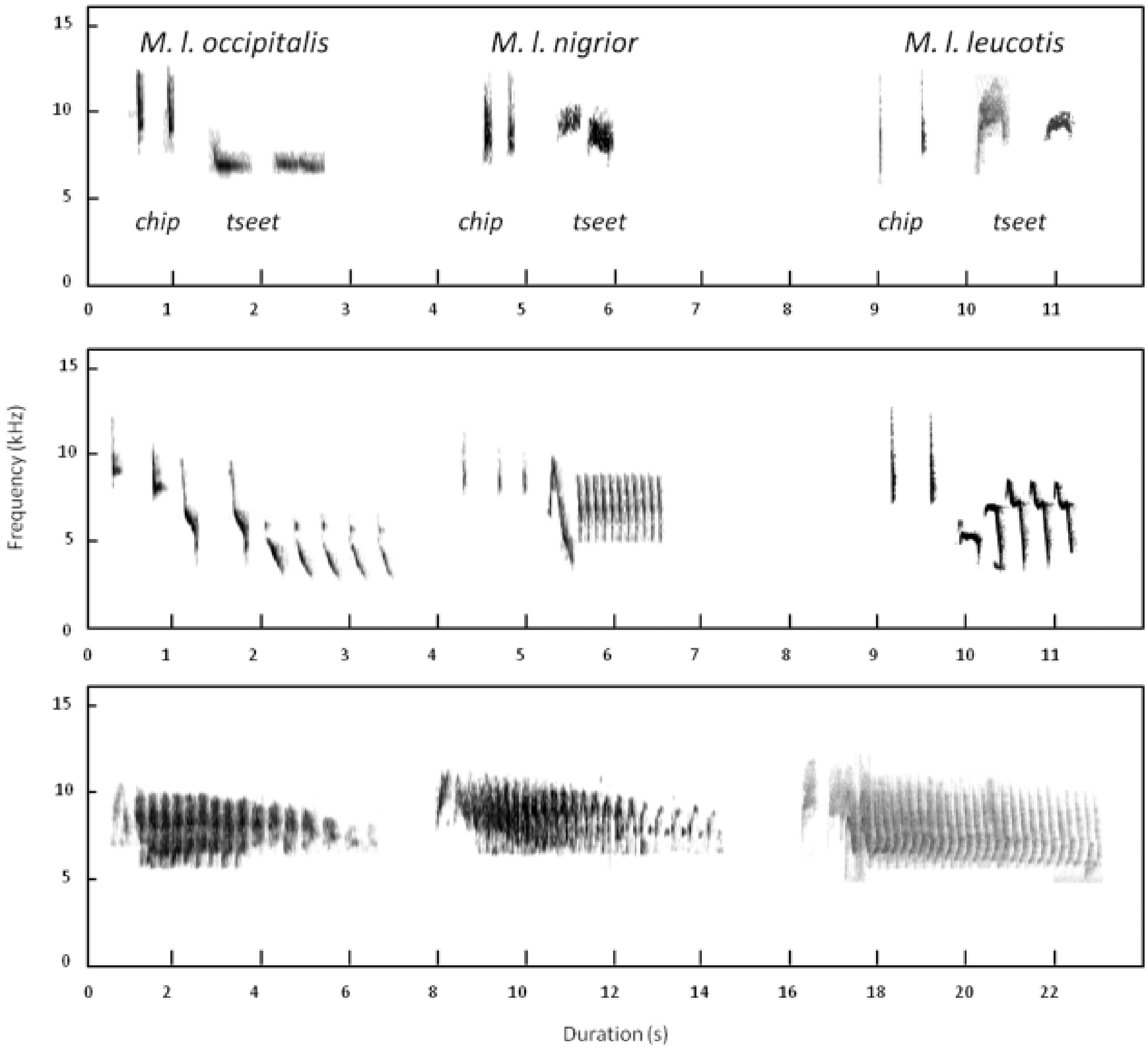

Figure 3. Spectrograms of the two call types (top panel), male solo song (middle panel), and duet song (bottom panel) for each of the three subspecies (*occipitalis* on left, *nigrior* in middle, and *leucotis* on right). From Sandoval et al. (2017a).

In addition to the morphological and vocal differences identified by Sandoval et al. (2017a), a phylogenetic analysis that included both nuclear and mitochondrial loci found *occipitalis* and *leucotis/nigrior* to be highly divergent, with an estimated divergence date of approximately 2 million years before present. In the phylogeny, 2 *occipitalis*, 1 *nigrior*, and 4 *leucotis* were included; the *occipitalis* samples were from Guatemala, the *nigrior* sample was from Nicaragua, and the *leucotis* samples were from Costa Rica. Together, these two groups appeared to be sister to White-faced Ground-Sparrow and Cabanis's Ground-Sparrow (Sandoval et al. 2017b; Fig. 4). The topology of the nuclear and mitochondrial trees were identical in the relationships recovered for *occipitalis, nigrior,* and *leucotis*, but their relationship to other species were slightly different (sister to *biarcuata/cabanisi* in nuclear DNA, and sister to most of the *Melozone/Aimophila* clade in mtDNA; Sandoval et al. 2017b).

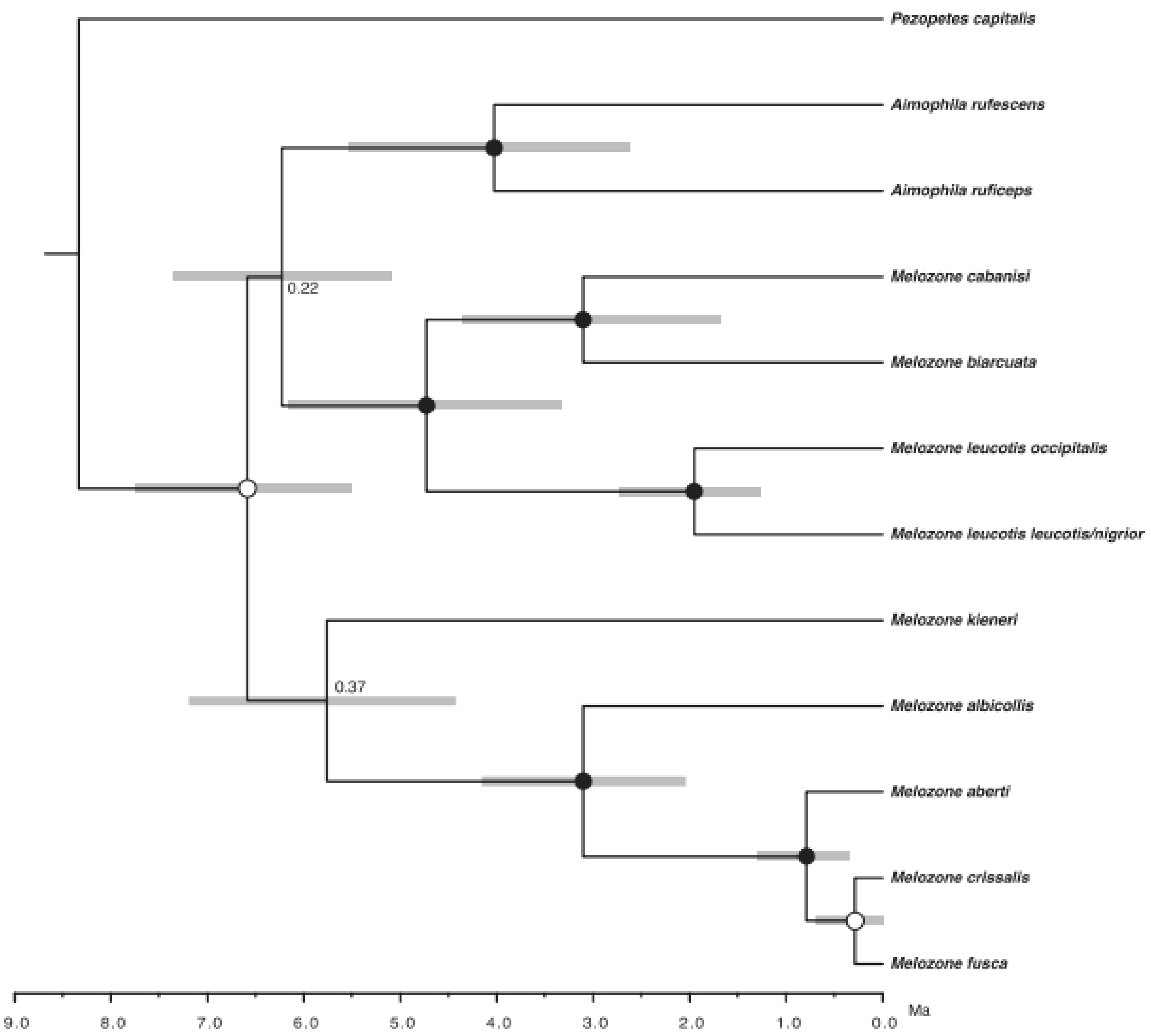

Figure 4. Time-calibrated phylogeny of *Melozone* and *Aimophila* using both mitochondrial and nuclear loci. Gray bars represent confidence interval (95% posterior density) around divergence date estimates. From Sandoval et al. (2017b).

Recommendation:

Based on the new analyses of Sandoval et al. (2017a, 2017b), and the similar levels of plumage, morphological, and vocal differences identified between other *Melozone* taxa that were recently split by NACC (Chesser et al. 2017), I recommend a YES vote for splitting *Melozone occipitalis* from *Melozone leucotis* (including both *leucotis* and *nigrior*). I recommend using the English names currently used for the two groups, with *leucotis* keeping White-eared Ground-Sparrow on account of its larger and more extensive distribution, and *occipitalis* being named Gray-crowned Ground-Sparrow (del Hoyo and Collar 2016, Clements et al. 2022).

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

Date: 20 February 2023

Treat *Granatellus francescae* as a separate species from Red-breasted Chat *G. venustus*

Effect on NACC:

If passed, this proposal would result in an additional species of *Granatellus* in the AOS area.

Background:

The genus *Granatellus* comprises three species of slender-billed cardinalids historically placed in Parulidae (albeit with some doubts; Chesser et al. 2009): Red-breasted Chat *Granatellus venustus* of western Mexico and far western Guatemala, Gray-throated Chat *G. sallaei* from the Yucatán Peninsula west to Veracruz, and Rose-breasted Chat *G. pelzelni* of Amazonia. All three have been considered to form a superspecies (AOU 1998). Within Red-breasted Chat, two subspecies are typically recognized: nominate *G. v. venustus* on the mainland, and *G. v. francescae* on the Tres Marías Islands (Islas Marías), off the coast of Nayarit, Mexico. (Birds from the northern part of the species's mainland distribution have been described as subspecies *melanotis* Van Rossem 1940 based on slight plumage color differences, but this is now typically synonymized with *venustus*; Gulson 2012, del Hoyo et al. 2018.) Subspecies *francescae* differs from nominate *venustus* in proportions, *francescae* having a significantly longer tail (averaging nearly 1 cm longer) and wing and somewhat longer tarsus than *venustus*, but with a slightly lower mass on average (Grant 1965). It also differs in some aspects of plumage coloration, including a reduced to absent black breast band (but see Grant 1965), more extensive white in the rectrices than *venustus*, and presence of a white hind collar (Curson et al. 1994, Howell and Webb 1995, Gulson 2012, del Hoyo et al. 2018).

Granatellus venustus francescae was first described (as *Granatellus francescæ**) by Baird (1865). Over the following century, it was variably treated as a species (e.g., by Ridgway 1902) or a subspecies of *G. venustus* (e.g., by Hellmayr 1935, Grant 1965, Blake et al. 1968). It has been considered conspecific with *venustus* (as a distinctive subspecies group) on the AOS Check-list since the Check-list's geographic coverage was expanded to cover Middle America (AOU 1983, 1998).

Del Hoyo et al. (2018), using the scoring system of Tobias et al. (2010), split Tres Marias Chat *G. francescae* from Red-breasted Chat based on the former's "lack of black breastband (3); white hindcollar formed by continuing white postocular stripe (at least 1); grey of crown extending over nape (1); tail with proportionately more white (ns[1]); pink of underparts generally slightly paler and less extensive (ns[1]); tail much longer (effect size 3.63, score 2)", a score of 7. (The same authors also treated ssp. *paraensis* of Rose-breasted Chat as a distinct species,

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*(Baird spelled the name *franciscæ* in the key on page 261 and *francescæ* on page 262; David et al. 2009, acting as First Revisers, selected *francescae* as the correct original spelling.)

Rose-bellied Chat *G. paraensis*, with a Tobias score of 8, increasing the number of species in the genus *Granatellus* from three to five.)

In addition to *G. v. francescae*, the Tres Marías Islands harbor roughly 23 additional endemic landbird taxa (Gómez de Silva et al. 2020, Clements et al. 2022), all of which are currently treated as conspecific with more widespread mainland species by AOS-NACC apart from Tres Marias Hummingbird *Cynanthus lawrencei*, split from Broad-billed Hummingbird *C. latirostris* by Chesser et al. (2022).

New Information:

There is little to no new data to bear on the (sub)specific status of *Granatellus* (*venustus*) *francescae*.

Gómez de Silva et al. (2020) scored several bird taxa endemic to the Tres Marías Islands using the Tobias et al. (2010) criteria, some previously scored for the HBW/BLI Illustrated Checklist and others not, and recommended treating the following taxa as separate species from their mainland counterparts: *Cynanthus lawrencei* (from Broad-billed Hummingbird *C. latirostris*), *Amazilia graysoni* (from Cinnamon Hummingbird *A. rutila*), *Forpus insularis* (from Mexican Parrotlet *F. cyanopygius*), *Pheugopedius lawrencii* (from Happy Wren *P. felix*), *Icterus graysonii* (from Streak-backed Oriole *I. pustulatus*), and *Granatellus francescae*. (They also scored the endemic subspecies of Golden Vireo *Vireo hypochryseus sordidus* and Blue Mockingbird *Melanotis caerulescens longirostris*, both of which fell short of the 7-point species cutoff, and recommended further study of endemic or near-endemic forms of White-tipped Dove *Leptotila verreauxi capitalis*, Rufous-backed Robin *Turdus rufopalliatus graysoni*, Tropical Parula *Setophaga pitiayumi insularis*, and Northern Cardinal *Cardinalis cardinalis mariae*.) In the case of *G. francescae*, Gómez de Silva et al. noted that, per Grant (1965), the presence/absence of a breast band is not completely diagnostic (so did not score it); considered del Hoyo et al.'s (2018) separate hind collar and crown scores to refer to the same character (although Gómez de Silva et al. scored this as 2, equalling the score for the separate characters [1+1] in del Hoyo et al.); and further gave a score of 2 to the difference in underparts color of immature males of the two taxa (little red in *francescae* vs. much red in *venustus*). These changes, among other scoring differences, led to a score of 8. (For the two hummingbirds, the only other taxa scored by both Gómez de Silva et al. and the HBW/BLI authors, the former set of authors' scores were likewise higher than those of the latter, rising from 7 to 8 for *Cynanthus lawrencei* and from 4 to 7 [crossing the Tobias et al. species threshold] for *Amazilia graysoni*.)

Vocal differences between *francescae* and *venustus* appear to have never been described or formally analyzed. There are only two recordings of the song of *francescae* in the Macaulay Library (and none in xeno-canto):
https://macaulaylibrary.org/asset/228954
https://macaulaylibrary.org/asset/228792

Comparing these with recordings of *venustus*, the songs of both taxa are similar, a series of sweet melancholy whistles often with a couple of similar introductory notes followed by some variably repeated phrases. There may be some differences in the structure of the notes/phrases in the second section of the song between *francescae* and *venustus*; however, the songs of both taxa appear to vary somewhat, and of course whether this eyeballed appraisal would hold with a larger sample of *francescae* recordings and an actual vocal analysis is unclear. (Nonetheless, these potential differences appear relatively subtle in comparison to the "striking" vocal differences reported between the two subspecies of Rose-breasted Chat by Boesman 2016.)

No published genetic data are available for *G. v. francescae*. Barker et al. (2015) did not sample this subspecies, and Scott (2022) sampled a toepad but the quality of the data was too poor to be useful. Scott (2022) successfully sampled nominate *venustus*, finding it sister to *G. sallaei*, with *G. pelzelni pelzelni* (+ *G. p. paraensis*) sister to the clade comprising the previous two species.

Recommendation:

Data supporting a split of *Granatellus francescae* from *G. venustus* (under the biological species concept followed by the Committee) are currently minimal. Vocalizations of the two taxa have not been analyzed; no published genetic data exist for *francescae*; and as for the plumage and structural differences between *francescae* and *venustus*, the relevance of at least some of these differences to reproductive isolation (were these taxa to meet) is not entirely clear. I therefore recommend a NO vote to a split of *Granatellus francescae* from *G. venustus* at this time.

In the event of a split, the previously used common name Tres Marias Chat is a logical choice for *Granatellus francescae*. The newly restricted *G. venustus*, with its vastly larger range, would keep the name Red-breasted Chat.

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