AOS Classification Committee – North and Middle America

Proposal Set 2020-B

27 January 2020

Transfer Buff-fronted Foliage-gleaner *Philydor rufum* to the genus *Dendroma* (as *D. rufa*)

Note: This proposal is a modified version of SACC Proposal 819.

New Information:

Derryberry et al. (2011) found *Philydor* to be polyphyletic. One of the problems is that *Philydor erythropterum* and *P. rufum* are sister to *Ancistrops strigilatus*, and together they are not closely related to other *Philydor* but closer to the *Clibanornis/Automolus* clade (see phylogenetic tree on next page).

Option A. One solution would be to resurrect the genus *Dendroma* Swainson, 1837, whose type (by subsequent designation) is *Sphenura poliocephala* Lichtenstein = *Dendrocopos rufum* Vieillot. This option will leave *A. strigilatus* in its own monotypic genus as usual. Because *Dendroma* is derived from the Greek *dendron* tree and -*dromos* –runner (Jobling) with a feminine suffix, the name is feminine in gender and the new combinations would be *Dendroma rufa* and *Dendroma erythroptera*.

Option B. Alternatively, these three species could be merged into the same genus. Although they lack the striped plumage of *strigilatus, erythropterum* and *rufum* share two traits that make the expanded genus cohesive: a bill with an apical hook (although not strongly developed in some subspecies of *rufum*), and rufous wings. *Philydor erythropterum* has also stripes on its crown. *Ancistrops strigilatus* and *P. erythropterum* are so similar that are easily confused in the field, although they forage in different microhabitats (Parker 1979). On the other hand, this expanded genus would be a very old genus compared to other genera of foliage gleaners, although there are other furnariid genera such as *Xenops*, *Dendrocincla*, the new *Sylviorthorhynchus*, *Geositta* and *Sclerurus* that are even older. In addition, because *Dendroma* Swainson, 1837, is older than *Ancistrops* Sclater, 1862, the former would be the name of the expanded genus and would result in additional nomenclatorial changes: the new combination *Dendroma strigilata*.

I recommend resurrecting the genus *Dendroma* only for *rufum* and *erythropterum* and keeping *strigilatus* in *Ancistrops* (Option A).

Recommendation:

Only one of these species occurs in the NACC area, and the recommendation is the same whether Option A or Option B is preferred: transfer *Philydor rufum* to *Dendroma*, where it would become *Dendroma rufa*.

Literature Cited:

Derryberry, E. P., S. Claramunt, G. Derryberry, R. T. Chesser, J. Cracraft, A. Aleixo, J. Pérez-Emán, J. V. Remsen, Jr., and R. T. Brumfield. 2011. Lineage diversification and

morphological evolution in a large-scale continental radiation: the Neotropical ovenbirds and woodcreepers (Aves: Furnariidae). *Evolution* 65: 2973-2986.

Jobling, J. A. 2010. The Helm dictionary of scientific bird names. Christopher Helm, London.

Parker, T. A., III. 1979. An introduction to foliage-gleaner identification. Continental Birdlife 1:32–37.

Submitted by: Santiago Claramunt

Date of Proposal: May 2019 (SACC proposal), modified for NACC on 16 October 2019
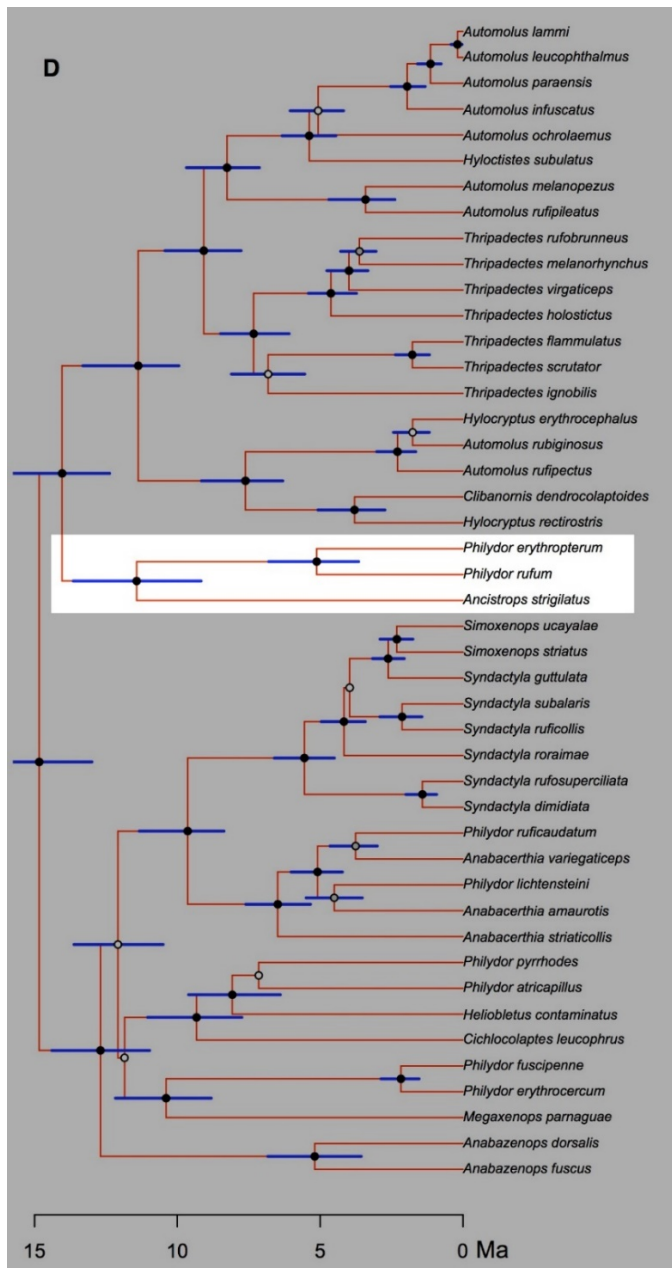
Votes and comments from SACC:

Note from Remsen on voting procedure: A YES vote is for Option A. A NO vote is for Option B or some other unspecified option.

Comments from Remsen: "YES. An arbitrary decision given phenotypic similarities among the three, but looking at the calibrated phylogeny above, treating *Ancistrops* as separate from *Dendroma* appears to me to be the better decision."

Comments from Stiles: "YES for reviving *Dendroma* for these two species, and leaving the more distantly related *Ancistrops* monospecific. (I note from the phylogeny that the genus *Philydor* remains polyphyletic, with two species probably in *Anabacerthia* and two other pairs of species, at least one of which might require a new name.. so here, over to Santiago!"

Comments from Robbins: "YES, given the branch length between *Ancistrops* and *erythropterum/rufum* and comparing to long-recognized genera, it seems the best course is to resurrect *Dendroma* for those two foliage-gleaners."

Comments from Pacheco: "YES. I consider the option to resuscitate *Dendroma* is a good solution to balance molecular and phenotypic data."

Comments from Zimmer: "YES" for Option A – retain *Ancistrops* and resurrect *Dendroma* for *rufa* & *erythroptera* (as they would then be called). *Ancistrops* is just a bit too different (in plumage pattern, bill morphology, vocalizations, and foraging behavior) from the other foliage-gleaners for me to be comfortable in lumping the three species into a single genus, and, as others have noted, the relative branch length of *Ancistrops* places it as older than just about all of the other foliage-gleaners."

Comments from Jaramillo: "A YES – resurrect *Dendroma* for these two species."

Treat American Comb-Duck *Sarkidiornis sylvicola* as a separate species from *Sarkidiornis melanotos*

Note: This proposal is a modified version of SACC Proposal 825.

Background:

The American Comb-Duck *Sarkidiornis sylvicola* was treated as a species apart from the African Comb-Duck *S. melanotos* from the 19th century (including Hellmayr and Peters [as *S. carunculatus*]) until Delacour & Mayr (1945) treated it as subspecies of *melanotos*.

The reasons for this subordination were as follows (Delacour & Mayr 1945: 28):

"The Comb Duck (*Sarkidiornis melanotos*) includes two well-marked subspecies, one (*melanotos*) extending from Africa to south-east Asia…, the other (*carunculatus*) inhabiting South America. We have observed at Clères that the racial hybrids are not intermediate. In such hybrid broods some birds look like pure *melanotos* and others like pure *carunculatus*."

This subordination to the Old World taxon was adopted by Meyer de Schauensee (1966), Blake (1977), and the AOU (1998), but not by Wetmore (1965), Kear (2005), or del Hoyo & Collar (2014).

In his phylogenetic classification and a general listing of taxa, Livezey (1997) recognized *S. sylvicola* as an independent species, emphasizing the contrasting coloring of the sides and flanks, gray in *S. melanotos* and black in *S. sylvicola*.

The Delacour hybrids were obtained (artificially?) in his private zoo, in Clères, Normandy, France. Generally, the resulting hybrids have intermediate parental characteristics. I cannot comment on the meaning of non-intermediate hybrids in BSC. However, this curious resilience of characters seems to favor the independence of these phenotypes. Regardless, hybridization in captivity is not a valid basis for considering two taxa to be conspecific under any modern version of the BSC.

There may be other diagnostic differences between *sylvicola* and *melanotos*. Apparently, *sylvicola* has smaller dimensions in both sexes (at least, on average) than *melanotos*. The calls (the species is basically mute) appear to be lower-pitched, with more bass, in *melanotos*; however, the sampling (Xeno-canto) is very small.

Recommendation:

I recommend splitting these two taxa, considering the well-marked differences between them (see illustration below) and adopting the English name American Comb-Duck (the name used for the *sylvicola* group in AOU 1998) for *S. sylvicola*.

Literature Cited:

American Ornithologists' Union. 1998. Check-list of North American birds. 7th edition. American Ornithologists' Union, Washington, D.C.

Blake, E. R. 1977. Manual of Neotropical Birds, Vol. 1. University of Chicago Press, Chicago.

del Hoyo, J., and N. Collar. 2014. HBW and BirdLife International Illustrated Checklist of the Birds of the World, Vol. 1: Non-passerines. Lynx Edicions, Barcelona.

Delacour, J. T., and E. Mayr. 1945. The family Anatidae. Wilson Bull, 57: 3-55

Kear, J. 2005. Ducks, Geese and Swans. Oxford Univ. Press, Oxford.

Livezey, B. 1997. A phylogenetic classification of waterfowl (Aves: Anseriformes), including selected fossil species. Annals Carnegie Museum 66: 457–496.

Meyer de Schauensee, R. 1966. The species of birds of South America and their distribution. Livingston Publishing Co., Narberth, Pennsylvania.

Wetmore, A. 1965. The birds of the Republic of Panamá, Part 1. Smithsonian Miscellaneous Collections 150.

Submitted by: Fernando Pacheco

Date of Proposal: May 2019 (SACC proposal), modified for NACC on 28 October 2019

Votes and comments from SACC:

Comments from Claramunt: "YES. Tough call. However, these birds are much more similar than what those illustrations suggest. Check the illustrations in the HBW instead (see below). Basically, the main difference is black versus grayish flanks. However, *sylvicola* is also smaller, and del Hoyo & Collar (2014) mentioned the shape of the comb, which seems slightly different, but a more detailed analysis would be desirable.

"That they hybridize in captivity is not evidence of potential free interbreeding in the wild. The statement about hybrids being similar to one or the other parent suggests that the main

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distinguishing character, the color of the flanks, is produced by a single Mendelian gene. However, the differences between the two taxa are not restricted to a single gene, as there are size differences. In addition, flank color (and maybe comb shape) may be involved in sexual selection and potentially species recognition. Taken together, I think that elevating *sylvicola* to species is reasonable, pending some falsifying evidence of reproductive compatibility or genomic homogeneity."

sylvicola:

melanotos:

Comments from Stiles: "YES; as noted by Santiago, the original reason for lumping them was ill-founded."

Comments from Robbins: "YES, for recognizing *Sarkidiornis sylvicola* as a species based on the rather dramatic morphological differences. As others have noted, captive hybridity is meaningless for assessing species limits, especially with regard to waterfowl."

Comments from Zimmer: "YES". As noted in the Proposal, and by the comments from others on the committee, hybridization in captivity, particularly with a notoriously promiscuous group like waterfowl, is meaningless in establishing species limits. The plumage differences are fairly dramatic, and there are accompanying mensural differences as well as likely differences in comb size and shape, all of which trumps the flimsy basis for lumping these taxa in the first place, in my opinion."

Comments from Jaramillo: "YES – Particularly as waterfowl are abnormally uniform, not tending to show much geographic variation, other than in species that have culturally mitigated migration routes (geese)."

Comments from Remsen: "YES, but largely because the initial rationale for the lump was based on nearly irrelevant captive breeding. By the way, this one is screaming out for a genetic analysis not for classification but for estimating the age of the split. These two really do not seem to differ very much, phenotypically, thus suggesting a relatively recent split, i.e. transoceanic dispersal. I wish we had comparative information on displays and voice on which to evaluate this one in terms of species rank."

Transfer White-shouldered Tanager *Tachyphonus luctuosus* to the genus *Loriotus*

Note: This proposal is a modified version of SACC Proposal 825.

Background:

NACC recently revised the taxonomy of several groups of tanagers based on Burns et al. (2016). However, their proposed transfer of three species of *Tachyphonus*, one of which (*T. luctuosus*) occurs in the NACC area, to the new genus *Islerothraupis* was not considered at that time due to discovery of an older name, as discussed in Piacentini et al. (2019) and below.

New Information:

To summarize and explain the whole case, I'm copying here the first three paragraphs of our paper:

"In a revision of the generic classification of the tanagers, Burns et al. (2016) proposed the name *Islerothraupis* with type species *Tanagra cristata* Linnaeus, 1766 (long known as *Tachyphonus cristatus*); however, they overlooked a previous designation of that species as the type of a genus. In 1821, Feliks Pawel Jarocki, in the second volume of *Zoologiia czyli Zwiérzętopismo Ogólne podług Naynowszego Systematu ułożone* ("Zoology, or general natural history account according to the newest arranged system"), page 133, specified *Tanagra cristata* as the type of a proposed subgenus *Loriotus.* The original text in Polish is available at the website www.rcin.org.pl, the Digital Repository of Scientific Institutes, which has made a wide diversity of scholarship in Polish available over the Internet. The original description of *Loriotus*, in parallel with other names Jarocki introduced in his Zoologiia, is minimal: "*Dziób ostro kończysty, cokolwiek zgięty. Żuchwy sczęki spodniey przy nasadzie bardzo mało zgrubiałe.*" (Bill ending in a point, somewhat curved. Lower mandible slightly thickened at base.)

"Nevertheless, it complies with the rules for a new genus-group name proposed before 1931 and is therefore available (ICZN 1999: articles 11 and 12). In fact, several other genera and subgenera introduced by Jarocki in the same book, such as *Remiz*, *Phoeniculus*, *Crinifer*, and *Vestiaria*, have been in continuous use as genera since Mathews & Iredale (1918) called attention to Jarocki's long-overlooked work, advanced for its time. The ICZN (1966) has suppressed one of Jarocki's names, *Cardinalis* (type species *Tanagra rubra* "GL" = *Fringilla rubra* Linnaeus, 1758, long known as *Piranga rubra*), but this action was not based on any nomenclatural problem in Jarocki's work; rather it allowed for reinstatement of the younger name *Cardinalis* Bonaparte, 1838 as the genus for *Loxia cardinalis* Linnaeus, 1758, the Northern Cardinal.

"Unlike the long-accustomed name *Cardinalis* for the cardinals, *Islerothraupis* has no history of wide usage, and so we recommend that it be treated as a junior objective synonym of *Loriotus* Jarocki, 1821. Accordingly, the three species we had included in *Islerothraupis*, *Tanagra cristata* Linnaeus, *Tachyphonus luctuosus* d'Orbigny & Lafresnaye, and *Tanagra rufiventer* Spix,

should be known as *Loriotus cristatus, Loriotus luctuosus*, and *Loriotus rufiventer*, respectively. *Loriotus* should be regarded as masculine in gender, in agreement with its Latinized form."

Recommendation:

Based on the ICZN, I don't see any option other than adopting the name *Loriotus*, which has clear priority, so I recommend a Yes vote to transfer *T. luctuosus* to *Loriotus*.

Literature Cited:

Bonaparte, C. L. (1838) A geographical and comparative list of the birds of Europe and North America. J. van Voorst, London.

Burns, K. J., Unitt, P., & Mason, N. A. (2016) A genus-level classification of the family Thraupidae (Class Aves: Order Passeriformes). Zootaxa 4088: 329–354.

ICZN [International Commission on Zoological Nomenclature] (1966) Opinion 784. Cardinalis Bonaparte, 1838 (Aves): Validated under the plenary power. Bulletin of the International Commission on Zoological Nomenclature 23: 201–203.

ICZN [International Commission on Zoological Nomenclature] (1999) International Code of Zoological Nomenclature, fourth edition. International Trust for Zoological Nomenclature, London.

Jarocki, F. P. (1821) Zoologiia czyli Zwiérzętopismo Ogólne Podług Naynowszego Systematu Ułożone. Łątkiewicz, Warsaw.

Mathews, G. M, & Iredale, T. (1918) A forgotten ornithologist. Austral Avian Record 3: 142–150.

Piacentini, V.Q.; Unitt, P. & Burns, K.J. (2019) Two overlooked generic synonyms in the Thraupidae (Aves: Passeriformes). Zootaxa 4608: 593-594.

Submitted by: Vitor de Q. Piacentini

Date of Proposal: May 2019 (SACC proposal), modified for NACC on 28 October 2019

Votes and comments from SACC:

Comments from Stiles: "YES, the priority is indisputable, especially because various of Jarocki's names have been widely accepted. (For curiosity, what was the case with the "other generic synonym"?)."

Comments from Claramunt: "YES. Since the issue has been raised, the Code does not give room for alternatives. *Islerothraupis* is too young to take precedence over *Loriotus*."

Comments from Zimmer: "YES", due to clear priority."

Comments from Areta: "YES, based on the principle of priority. It remains to be seen what SACC will do with *Rauenia* (for *"Pipraeidea" bonariensis*). I would certainly endorse *Rauenia* for it."

Comments from Bonaccorso: "YES, priority rules. However, it would be interesting if people that describe new supra-specific taxa (many of whom are not taxonomists, but evolutionary biologists) had the chance to consult SACC (through their taxonomy experts) before naming those taxa. Many people were probably already getting used to *Islerothraupis,* which generates a lot of instability."

Comments from Stotz: "YES. This appears to be a straightforward switch to an overlooked generic name with priority."

Comments from Pacheco: "YES. A perfectly justified exchange concerning ICZN rules."

Revise the taxonomy of species currently placed in *Locustella*: (a) transfer *L. ochotensis* to *Helopsaltes*, and (b) revise the linear sequence of species

Description of the problem:

The Locustellidae has only recently been recognized as a separate family from the "Old World Warblers" Sylviidae (Alström et al. 2006). The morphological similarity and skulking behavior of many species had led to its species-level diversity being severely underestimated prior to the advent of availability of extensive sound recordings and DNA analyses. One major result of a fairly recent phylogenetic study (Alström et al. 2011) was the recognition that *Bradypterus sensu lato* was highly paraphyletic, which led to adoption of a generic division between African *Bradypterus sensu stricto* and Eurasian taxa now united in *Locustella*. The NACC area has accepted records for just three vagrant species of Locustellidae, which are currently listed in this order: Middendorff's Grasshopper-Warbler *Locustella ochotensis*; River Warbler *L. fluviatilis*; and Lanceolated Warbler *L. lanceolata*.

New information:

The most recent family-level molecular phylogeny of the Locustellidae (Alström et al. 2018) included analyses of cyt*b* and four nuclear regions of all genera and 59 species. Toepad samples were used for 17 of the species (for many of these, fresh tissue would have been impossible to obtain). The phylogeny showed a deep divergence (dated to ca. 14 mya) within the Eurasian *Locustella* clade (Clades J and K in the tree below). Although no diagnostic morphological characters for Clade J are known, vocal analyses in Alström et al. (2018) show that the songs of species in Clade J differ from those of species in Clade K in being more complex, with more different note types and in thus sounding less reeling and insectile. The divergence estimate for Clades J and K is almost as old as that between Clades A and B, so for greater consistency in divergence time with other generic-level rankings in the group, Alström et al. (2018) advocated generic separation of Clades J and K. *Locustella naevia* of Clade J is the type species of *Locustella* Kaup, and as no generic name was believed to be available, Alström et al. (2018) named Clade K as the new genus *Helopsaltes* ("marsh musician").

Subsequent treatments:

The IOC list (Gill and Donsker 2019) already recognizes Clade K of Alström et al. (2018) as *Helopsaltes*.

Effect on AOU-CLC area:

Two of the vagrant species to NACC are in Clade J (*fluviatilis* and *lanceolata*), so if *Locustella* is split into two genera, these would remain in *Locustella*, while the third, *ochotensis*, is in Clade K and thus would be moved to *Helopsaltes*. There would also be some minor linear resequencing: following our conventions, *Helopsaltes ochotensis* should continue to be listed first, as a

member of the less species-rich genus, while *L. lanceolata* should precede *L. fluviatilis* as per the branching pattern.
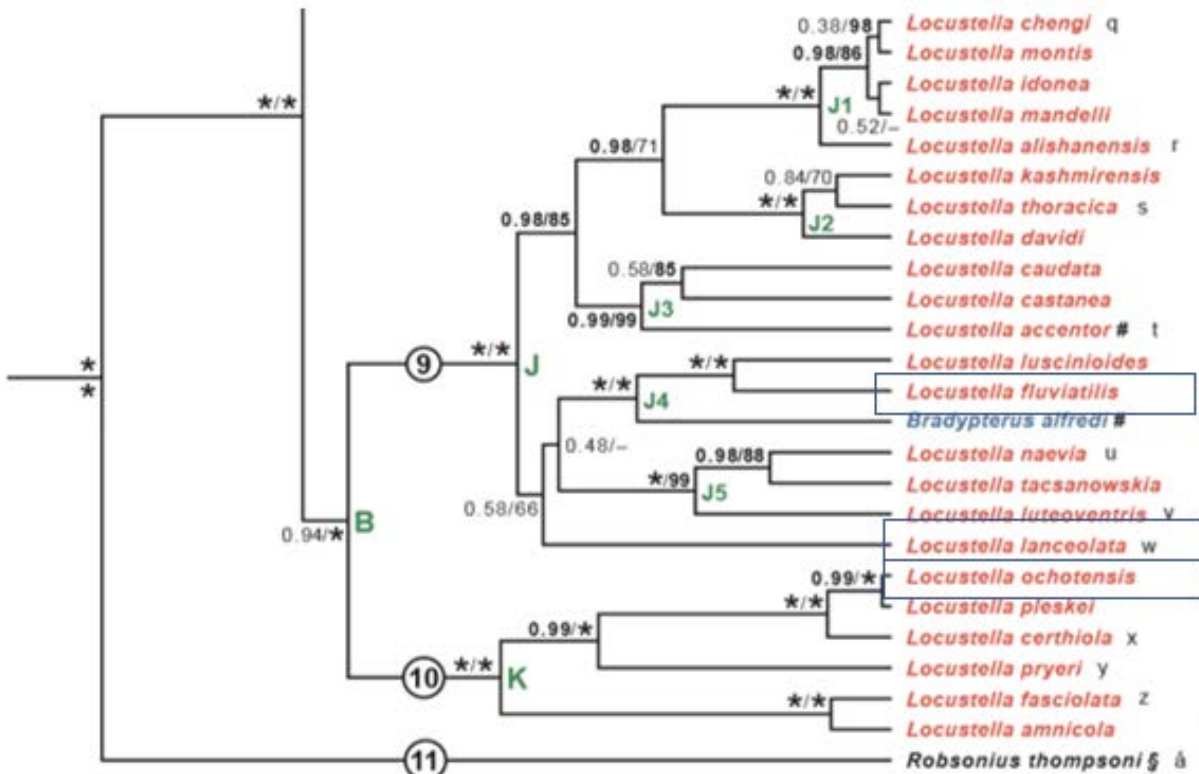
Relevant portion of Fig. 1 (Alström et al. 2018), with boxes added around NACC-relevant taxa.

Recommendation: I recommend (a) that we recognize the new genus *Helopsaltes* for Clade K, with *Locustella ochotensis* thus becoming *Helopsaltes ochotensis*; and (b) that we list *L. lanceolata* before *L. fluviatilis*. Please vote separately for each of these two recommendations.

Literature cited:

Alström, P., P.G.P. Ericson, U. Olsson, and P. Sundberg. 2006. Phylogeny and classification of the avian superfamily Sylvioidea. Molecular Phylogenetics and Evolution 38: 381-397.

Alström, P., S. Fregin, J.A. Norman, P.G.P. Ericson, L. Christidis, and U. Olsson. 2011. Multilocus analysis of a taxonomically densely sampled dataset reveal extensive non-monophyly in the avian family Locustellidae. Molecular Phylogenetics and Evolution 58: 513-526.

Alström, P., A. Cibois, M. Irestedt, D. Zuccon, M. Gelang, J. Fjeldså, M.J. Andersen, R.G. Moyle, E. Pasquet, and U. Olsson. 2018. Comprehensive molecular phylogeny of the grassbirds and allies (Locustellidae) reveals extensive non-monophyly of traditional genera, and a proposal for a new classification. Molecular Phylogenetics and Evolution 127: 367-375.

Gill, F. and D. Donsker. (Eds). 2019. IOC World Bird List (v9.2). http://www.worldbirdnames.org/
doi : 10.14344/IOC.ML.9.2

Submitted by: Pamela C. Rasmussen, Michigan State University

Date of proposal: 21 November 2019

Change the taxonomy of the Phasianidae: (a) eliminate subfamilies and (b) revise the linear sequence of species

Background:

Our current arrangement of the Phasianidae divides the species in our area into three subfamilies: Phasianinae, Tetraoninae, and Meleagridinae. The 11 species of Phasianinae on the checklist are all introduced, whereas the 14 species of Tetraoninae and Meleagridinae are native to the AOS area. Our current linear sequence is as follows:

Phasianinae (partridges and pheasants)
Alectoris chukar Chukar
Francolinus pondicerianus Gray Francolin
Francolinus francolinus Black Francolin
Pternistis erckelii Erckel's Francolin
Tetraogallus himalayensis Himalayan Snowcock
Perdix perdix Gray Partridge
Coturnix japonica Japanese Quail
Gallus gallus Red Junglefowl
Lophura leucomelanos Kalij Pheasant
Phasianus colchicus Ring-necked Pheasant
Pavo cristatus Indian Peafowl
Tetraoninae (grouse)
Bonasa umbellus Ruffed Grouse
Centrocercus urophasianus Greater Sage-Grouse
Centrocercus minimus Gunnison Sage-Grouse
Falcipennis canadensis Spruce Grouse
Lagopus lagopus Willow Ptarmigan
Lagopus muta Rock Ptarmigan
Lagopus leucura White-tailed Ptarmigan
Dendragapus obscurus Dusky Grouse
Dendragapus fuliginosus Sooty Grouse
Tympanuchus phasianellus Sharp-tailed Grouse
Tympanuchus cupido Greater Prairie-Chicken
Tympanuchus pallidicinctus Lesser Prairie-Chicken
Meleagridinae (turkeys)
Meleagris gallopavo Wild Turkey
Meleagris ocellata Ocellated Turkey

This subfamily arrangement was our treatment as far back as the 7th edition of the checklist (1998) and, in modified form, as far back as the 6th edition (1983), in which Odontophorinae (New World quail) and Numidinae (guineafowl), now recognized as separate families, were also included in the Phasianidae. The current linear sequence is presumably based on traditional ideas concerning relationships.

New Information:

Recent publications on Galliformes, which include the morphological-molecular study of Crowe et al. (2006) and the UCE studies of Wang et al. (2013) and Hosner et al. (2016), have consistently indicated that our classification is at odds with evolutionary relationships among phasianid species in several key ways:

1. The francolins are not monophyletic. Some species (those in *Francolinus* and *Scleroptila*) are closely related to *Gallus* (junglefowl) and *Bambusicola* (bamboo-partridges), whereas others (those now placed in *Pternistis*) are closely related to Old World partridges, quail, and spurfowl (e.g., *Alectoris*, *Coturnix*, *Tetraogallus*). We addressed this to some extent in Proposal 2019-A-15, which resulted in our transferring *Francolinus erckelii* to the genus *Pternistis.* However, *Francolinus* and *Pternistis* remain together in our linear sequence.

2. The typical pheasants (those in *Phasianus* and *Lophura*, among other genera) are not closely related to the peafowl and argus pheasants of the genera *Pavo*, *Afropavo*, and *Argusianus* (and presumably *Rheinardia*).

3. The turkeys (currently subfamily Meleagridinae) and grouse (subfamily Tetraoninae) are sister groups nested deep within the Phasianidae, such that recognition of these as subfamilies appears dubious.

The genomic studies of Wang et al. (2013) and Hosner et al. (2013) provided the best sampled trees of Phasianidae to date. The simplified tree of Wang et al. (their Fig. 3 below) nicely illustrates the paraphyly of the francolins, the polyphyly of the pheasants, and the nested position of the grouse + turkeys. Hosner et al. (2016) sampled the most species in our area and their tree (their Fig. 2 below) forms the basis for the proposed new linear sequence.

Most global references do not recognize subfamilies within the Phasianidae. The one that does, Howard and Moore, recognizes two subfamilies: the Rollulinae (consisting only of the genera *Xenoperdix, Rollulus, Arborophila, Rhizothera, Melanoperdix*, and *Caloperdix*, none of which occur in our area) and the Phasianinae. To maintain the Tetraoninae and Meleagridinae as separate subfamilies, or even as a single combined subfamily, would require recognition of numerous subfamilies consisting entirely of Old World species, which is probably inadvisable generally and moreover is well beyond our mandate.

Recommendation:

I recommend that we (a) eliminate subfamilies from our taxonomic treatment of this group, and (b) revise the linear sequence of species as below. The only reasonable alternative to eliminating subfamilies would be to recognize the subfamily Phasianinae and to place all AOS species in this subfamily, which is certainly a valid option but seems unnecessary. The recommended linear sequence is as follows:

Meleagris gallopavo Wild Turkey
Meleagris ocellata Ocellated Turkey
Bonasa umbellus Ruffed Grouse

Falcipennis canadensis Spruce Grouse
Lagopus lagopus Willow Ptarmigan
Lagopus muta Rock Ptarmigan
Lagopus leucura White-tailed Ptarmigan
Centrocercus urophasianus Greater Sage-Grouse
Centrocercus minimus Gunnison Sage-Grouse
Dendragapus obscurus Dusky Grouse
Dendragapus fuliginosus Sooty Grouse
Tympanuchus phasianellus Sharp-tailed Grouse
Tympanuchus cupido Greater Prairie-Chicken
Tympanuchus pallidicinctus Lesser Prairie-Chicken
Perdix perdix Gray Partridge
Phasianus colchicus Ring-necked Pheasant
Lophura leucomelanos Kalij Pheasant
Pavo cristatus Indian Peafowl
Francolinus pondicerianus Gray Francolin
Francolinus francolinus Black Francolin
Gallus gallus Red Junglefowl
Tetraogallus himalayensis Himalayan Snowcock
Alectoris chukar Chukar
Coturnix japonica Japanese Quail
*Pternistis erckelii* Erckel's Francolin

Neither species currently placed in *Dendragapus* was included in Wang et al. (Spruce Grouse, which they refer to as *D. canadensis*, is now placed in *Falcipennis*) or Hosner et al.; the position of these two species in the linear sequence is based on the sister relationship with *Tympanuchus* in Crowe et al. (2006). This also maintains the current relative positions of these two genera in the linear sequence. I note in passing that the Indian Peafowl follows the other pheasants in our linear sequence even though they are not closely related – it just works out that way.

References

Crowe, T., R. Bowie, P. Bloomer, T. Mandiwana, T. Hedderson, E. Randi, S. Pereira, and J. Wakeling. 2006. Phylogenetics, biogeography and classification of, and character evolution in, gamebirds (Aves: Galliformes): effects of character exclusion, data partitioning and missing data. Cladistics 22:495–532.

Hosner, P. A., B. C. Faircloth, T. C. Glenn, E. L. Braun, and R. T. Kimball. 2016. Avoiding missing data biases in phylogenomic inference: an empirical study in the landfowl (Aves: Galliformes). Mol. Biol. Evol. 33:1110–1125.

Wang, N., R. T. Kimball, E. L. Braun, B. Liang, and Z. Zhang. 2013. Assessing phylogenetic relationships among Galliformes: a multigene phylogeny with expanded taxon sampling in Phasianidae. PLoS One 8:e64312.

Submitted by: Terry Chesser
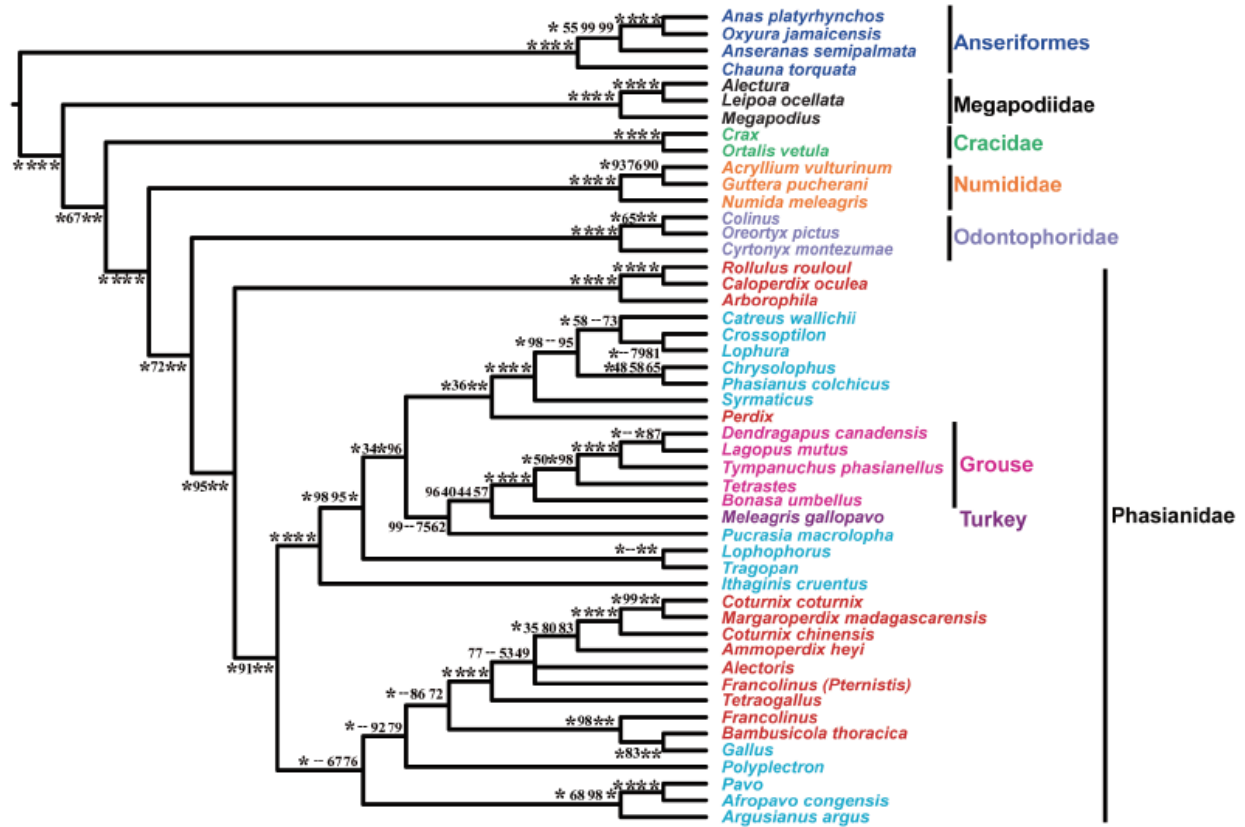
Figure 3. Consensus tree with support from concatenated analyses. Monophyletic genera with more than one species are collapsed into a single branch. Groups of taxa are indicated using the same color coding as Figure 1.
doi:10.1371/journal.pone.0064312.g003

Figure 3 from Wang et al. (2013).
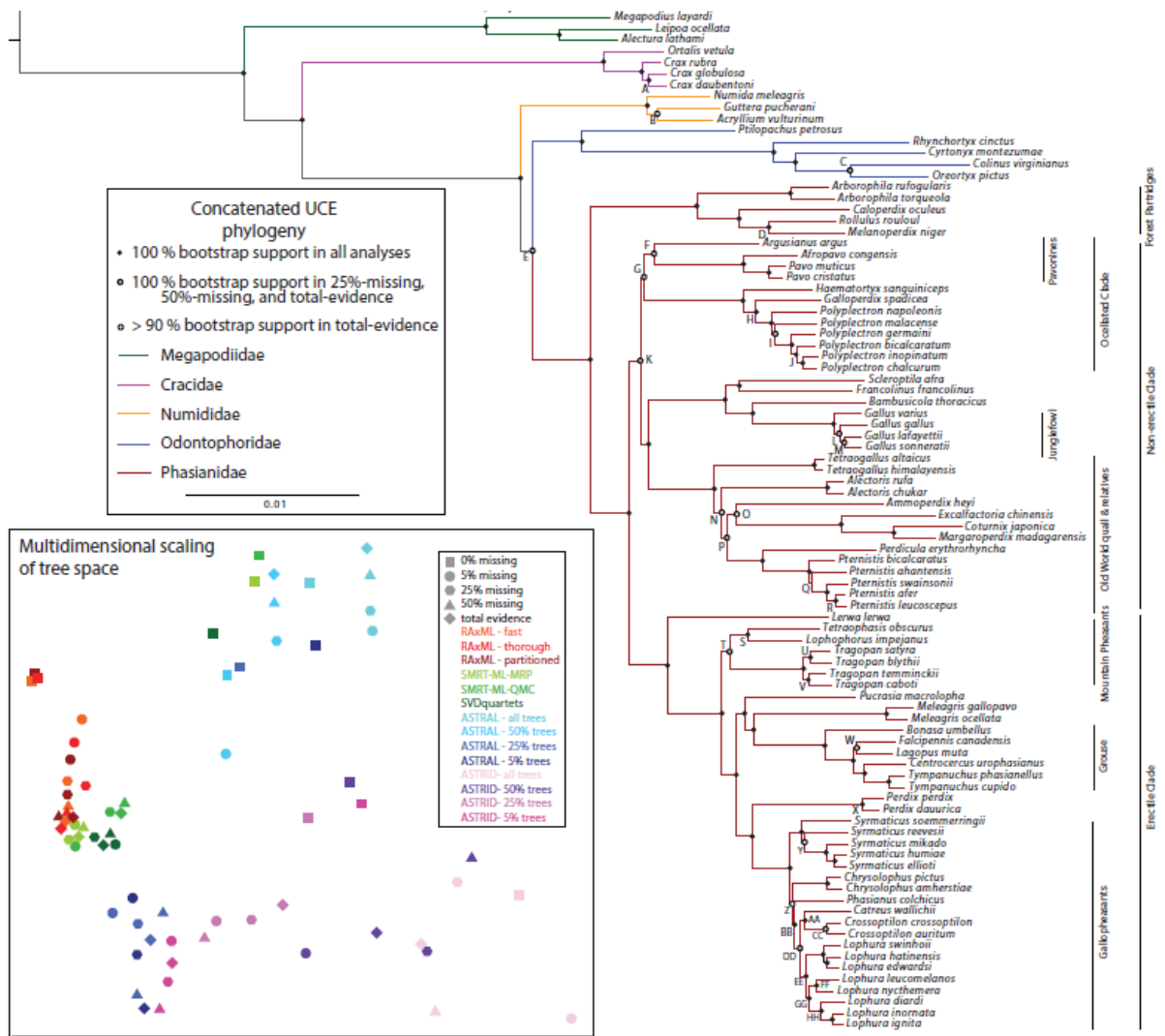
Fig. 2. Phylogeny of 90 galliform taxa inferred with ML analysis of 2,208,355 bp from 4,817 concatenated UCE loci. Inset shows multidimensional-scaled visualization of tree space, with each point representing a consensus tree produced with different inferential procedures and different thresholds of missing data (70 iterations, total). Concatenated ML, SMRT-ML, and SVDquartets trees (with the exception of those inferred from the small 0% missing data set) and ASTRAL/ASTRID trees with the most resolved gene trees converge on the same area of multidimensional tree space (lower right); RF distances between these analyses were generally <5.

Figure 2 from Hosner et al. (2016).

Revise the linear sequence of the macaws (*Ara* spp.)

Description of the problem:

Although the Cuban Macaw *Ara tricolor* has been extinct since the mid-19th century, it is the best-known of the several putative Antillean endemic macaws, all extinct and several of dubious validity (Wiley and Kirwan 2013). Based on plumage, *Ara tricolor* has been suggested to be closely related to the other but much larger (Forshaw and Cooper 1973) red macaws, *A. macao* and *A. chloropterus*. Unlike other Antillean macaws, there are several extant specimens of *A. tricolor*, 19 skins and fragments from three fossil sites (Olson and Suárez 2008). The skins have not previously been sampled for genetic analysis.

New information:

Two *A. tricolor* specimens are held at the Swedish Museum of Natural History, and toepads of both were sampled (Johansson et al. 2018). Complete mtDNA genomes were sequenced for five of the seven species of macaws that occur in the NACC area, all except *A. ambiguus* and *A. chloropterus*, for which partial mitochondrial sequence (16S and CO1) was obtained. Contrary to expectations that it would prove most closely related to the two extant red macaws, in this phylogeny *A. tricolor* is sister to the clade that includes both large red and large green macaws (*A. militaris* and *A. macao*).
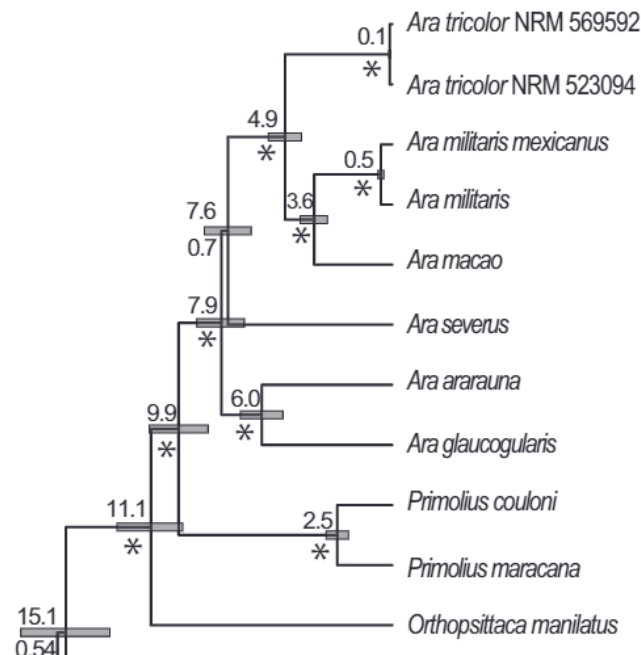
Relevant portion of Figure 1 in Johansson et al. (2018), a phylogeny based on complete mitochondrial sequences. Estimated divergence dates are above the nodes and posterior probabilities below (* = 1.0 pp).

Johansson et al. (2018) also produced a phylogeny based on the partial mitochondrial data; this included all species in our area. The top half of this phylogeny is poorly supported, but the clade containing *tricolor* is relatively robust and supports the position of *tricolor* as sister to a clade containing *militaris* and *macao*, as well as the two species not sampled in the mt-genome phylogeny, *ambiguus* and *chloropterus*. This phylogeny indicates that *ambiguus* is sister to and very closely related to *militaris*, and that *chloropterus* is also part of this clade, but that its placement is unresolved relative to *macao* and *militaris/ambiguus*.
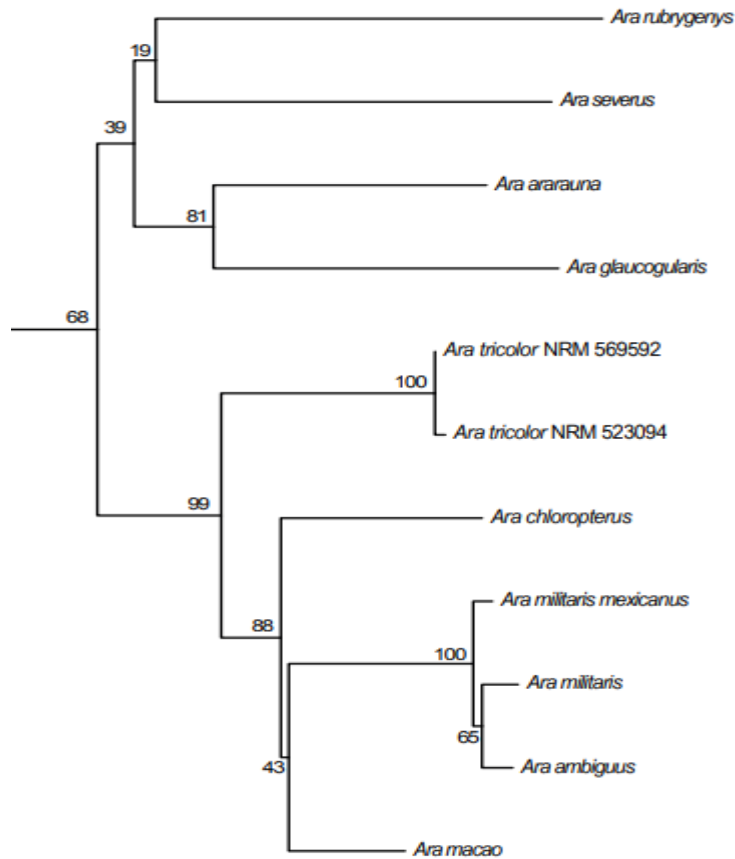
Relevant portion of Figure S1 of Johansson et al. (2018), a phylogeny based on sequences of the mitochondrial genes 16S and CO1.

Our current sequence of macaws recorded for the NACC area is:

Ara severus
Ara militaris
Ara ambiguus
Ara chloropterus
Ara macao
Ara tricolor
Ara ararauna

Acceptance of this proposal would resequence these macaws as follows:

Ara ararauna
Ara severus
Ara tricolor
Ara macao
Ara chloropterus
Ara militaris
Ara ambiguus

In generating this linear sequence, we considered *macao* + *chloropterus* + *militaris/ambiguus* to form a 3-way polytomy, and placed *militaris/ambiguus* last because it consists of more species, and *macao* first because of its more northerly distribution than *chloropterus*.

Given that the remainder of the Johansson et al. (2018) phylogeny is not densely sampled, we focused only on the macaws for this proposal.

Recommendation:

We recommend adopting this minor sequence change.

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Submitted by: Pamela C. Rasmussen and Terry Chesser

Date of proposal: 4 December 2019

Revise the taxonomy of hummingbird genera *Atthis* and *Selasphorus*: (a) Merge *Atthis* into *Selasphorus*, and (b) change the linear sequence of species in these genera

Aim:

This proposal recommends merging the hummingbird genus *Atthis* into *Selasphorus*, because *Selasphorus* is paraphyletic if *Atthis* is recognized. *Selasphorus* Swainson, 1832, has priority over *Atthis* Reichenbach, 1854. If the committee votes to merge *Atthis* into *Selasphorus*, then the linear classification should also be updated. Thus, this proposal consists of two subproposals: (a) merger of genera *Atthis* and *Selasphorus*, and (b) modification of the linear classification of *Selasphorus* and allies.

Background:

Current AOS taxonomy (AOU 1998) — after the 53rd supplement (Chesser et al. 2012), which merged *Stellula* into *Selasphorus* — recognizes two species in the genus *Atthis* and seven in the genus *Selasphorus*. The Howard and Moore (Dickinson and Remsen 2013) and Clements (Clements et al. 2018) checklists are congruent with AOS.

Atthis
    A. heloisa (Bumblebee Hummingbird)
    A. ellioti (Wine-throated Hummingbird)
Selasphorus
    S. platycercus (Broad-tailed Hummingbird)
    S. rufus (Rufous Hummingbird)
    S. sasin (Allen's Hummingbird)
    S. flammula (Volcano Hummingbird)
    S. ardens (Glow-throated Hummingbird)
    S. scintilla (Scintillant Hummingbird)
    S. calliope (Calliope Hummingbird)

The genus *Atthis* has historically been considered to be closely related to *Selasphorus* (Ridgway 1911), yet the two genera have been maintained as separate by most authors (Salvin and Godman 1896; Cory 1918; Peters 1945; Friedman et al. 1950; Eisenmann 1955; Schuchmann 1999). However, Howell and Webb (1995) merged *Atthis* with *Selasphorus*, although without any particular justification. Additionally, *Atthis* was considered synonymous with *Selasphorus* by Johnsgard (1983), which, according to Zyskowski et al. (1998), was done in spite of a potentially closer relationship between *Atthis* and *Stellula*.

According to Ridgway (1911), *Atthis* differs from *Selasphorus* "in form and coloration of the tail in the adult male, which is slightly rounded, with rectrices broadly rounded at tip, the lateral rectrices with basal half (more or less) cinnamon-rufous, succeeded by a black band and white terminal spot; gorget with feathers rather more strongly individualized and relatively longer, especially the lateral ones."

New Information:

McGuire et al. (2014) published a molecular phylogeny of the hummingbirds, which included 284 species and 436 samples. The genetic data consisted of six loci: four nuclear loci and two mitochondrial gene regions plus flanking tRNAs. The nuclear loci were intron 7 of beta fibrinogen (FGB), intron 5 of the adenylate kinase gene (AK1), a segment of the ornithine decarboxylase gene (ODC), and a segment of the Z-linked muscle skeletal receptor tyrosine gene (MUSK). The mitochondrial sequences included the complete NADH dehydrogenase subunit 2 (ND2) and half of the NADH dehydrogenase subunit 4 (ND4), and flanking tRNAs. This study included samples of the genus *Calypte*, which was previously hypothesized to be the sister clade of *Selasphorus* (McGuire et al. 2007). Within *Selasphorus*, McGuire et al. (2014) included one sample of three species (*S. platycercus*, *S. rufus*, and *S. scintilla*) and more than one sample of the four remaining species (*S. sasin*, *S. flammula*, *S. ardens*, and *S. calliope*). New to this study was the inclusion of samples of one of the two species in the genus *Atthis*, *A. heloisa*. The phylogeny showed *Atthis* embedded within *Selasphorus*, as the sister clade of the group *S. ardens*/*scintilla* and *S. flammula* (Figure 1). The nodes that support *Atthis* as embedded within *Selasphorus* were strongly supported, and the overall node depth of the crown group for the newly proposed *Selasphorus* would be similar to that of *Calypte*.
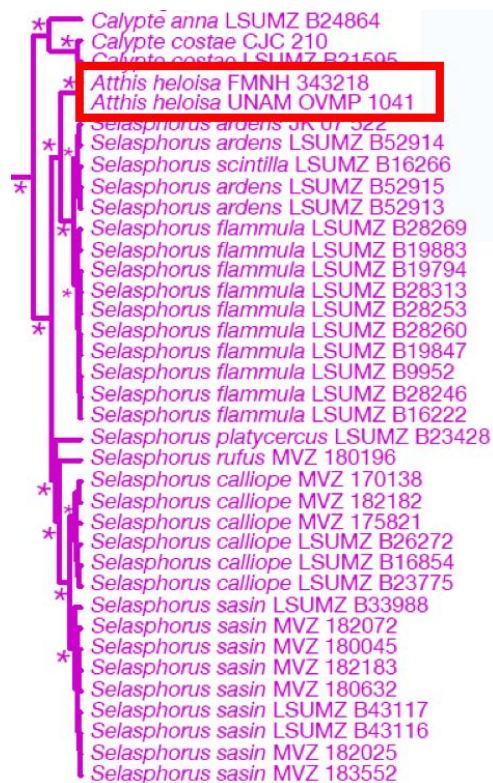
Figure 1. Time-calibrated phylogenetic estimate for hummingbirds and outgroup species, from McGuire et al. (2014). The tree is a BEAST MCMC analysis of six concatenated genes (two mtDNA, four nuclear); asterisks at the nodes represent 100% posterior probability support. Here, the complete phylogeny was trimmed to show the relationships of *Atthis* and *Selasphorus*. *Atthis* is highlighted with a red rectangle to illustrate paraphyly of *Selasphorus* if *Atthis* is recognized.

Subsequently, Licona-Vera and Ornelas (2017) studied the evolution of migratory behavior in bee hummingbirds through phylogenetic and biogeographic analyses. Their dataset included 132 samples of the bee hummingbirds, which represented all 16 genera. The phylogenetic reconstruction was based on sequences of six gene regions, the same as those used by McGuire et al. (2014), two mitochondrial protein coding genes (1041 bp of ND2 and 807 bp of ND4) and four nuclear loci (1085 bp of FGB, 551 bp of AK1, 577 bp of ODC, and 635 bp of MUSK).
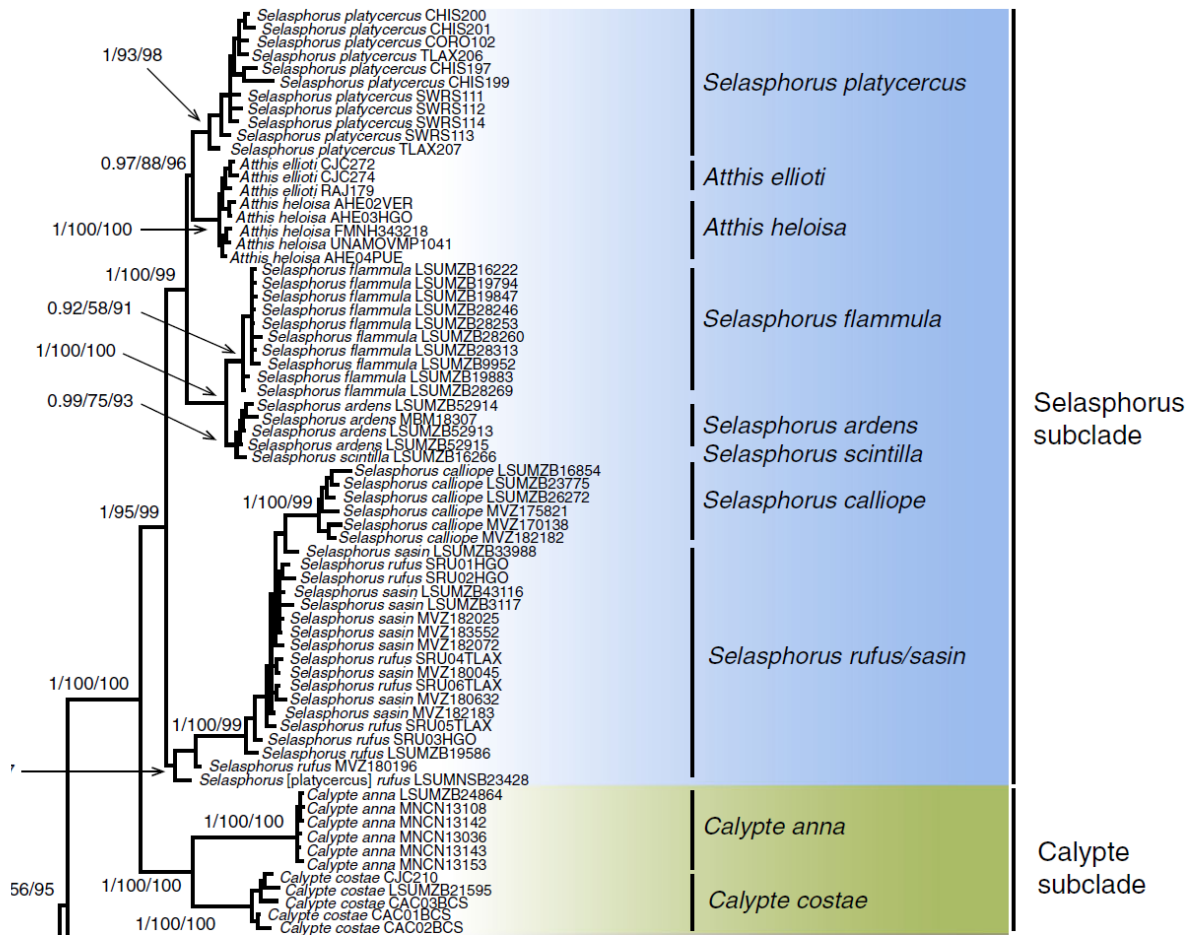
Figure 2. Phylogenetic 50% majority-rule consensus tree of the Mellisugini, from Licona-Vera and Ornelas (2017), based on Bayesian analysis of the combined mitochondrial and nuclear loci. Numbers at the nodes represent Bayesian posterior probabilities / Maximum Likelihood bootstrap support / Maximum Parsimony bootstrap support. Here, the complete phylogeny was trimmed to show the relationships of *Atthis* and *Selasphorus*.

In addition to the *Selasphorus/Atthis* species included in McGuire et al. (2014), Licona-Vera and Ornelas (2017) incorporated samples from *A. ellioti* for the first time in a phylogeny, and sequenced several individuals of *S. platycercus* and *S. rufus*. Again, the phylogeny recovered *Atthis* as embedded within *Selasphorus*, although this time *Atthis* was inferred as the sister clade of *S. platycercus*, perhaps as a result of the dense population-level sampling of species, which allowed a more accurate understanding of how genetic diversity is partitioned within the clade (Figure 2). The authors noted that the sample of *S. platycercus* (LSUMNS B23428)

included in McGuire et al. (2014) grouped with the *rufous/sasin* group rather than with the other 11 samples of *platycercus*, calling into question the identification of this individual.

In addition to recent studies that have increased our knowledge of phylogenetic relationships, there have also been improvements of our understanding of behavioral evolution within the bee hummingbirds. Clark et al. (2018) reported that diving behavior is present in 31 species of the bee clade and absent only in the two species of *Atthis*, which are also two of the four species that do not produce any sound with the tail.

Despite phenotypic differences in the diving behavior and bioacoustics of the genus *Atthis*, reconciling phylogenetic relationships and maintaining *Atthis* as a separate genus would require the formation of three new genera, including a monotypic genus for *S. platycercus*. Thus, we view lumping *Atthis* into *Selasphorus* as the most straightforward solution to reconcile phylogeny and taxonomy in the bee hummingbirds.

Recommendation:

(a) We recommend merging the genus *Atthis* into *Selasphorus*. The phylogenetic trees clearly show that *Atthis* is nested within *Selasphorus*. Although the two species of *Atthis* share morphological and behavioral synapomorphies within the bee hummingbird clade, the current taxonomy does not reflect our best understanding of phylogenetic relationships within this clade.

(b) If subproposal (a) passes, then the linear sequence of the species within *Selasphorus* (including *Atthis*) requires reorganization. Using standard guidelines for linear sequencing (e.g., sister clade with the fewest species placed first, and clade with more northwesterly distribution placed first if numbers of species are equal), we propose arranging the species as follows:

Current sequence	Proposed sequence
Atthis heloisa	*Selasphorus calliope*
Atthis ellioti	*Selasphorus rufus*
Selasphorus platycercus	*Selasphorus sasin*
Selasphorus rufus	*Selasphorus platycercus*
Selasphorus sasin	*Selasphorus heloisa*
Selasphorus flammula	*Selasphorus ellioti*
Selasphorus ardens	*Selasphorus flammula*
Selasphorus scintilla	*Selasphorus scintilla*
Selasphorus calliope	*Selasphorus ardens*

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Submitted by: Rosa Alicia Jiménez & Nicholas A. Mason, Museum of Vertebrate Zoology, University of California, Berkeley

Date of Proposal: 13 December 2019

Split *Aegolius acadicus brooksi* from Northern Saw-Whet Owl *A. acadicus acadicus*

Effect on the North American Checklist:

This would elevate to species rank the sole recognized subspecies of Northern Saw-whet Owl (*Aegolius acadicus brooksi*, "Haida Gwaii Saw-whet Owl").

Background:

The nominate form of the Northern Saw-whet Owl **(***Aegolius acadicus acadicus*) is largely migratory, breeds from southern Alaska to Nova Scotia south to California and Maryland, and is largely invariable in size or color across its range (Rasmussen et al. 2008). It is at least partly nomadic, appears to shows little philopatry, and will stay on to breed in wintering areas if conditions are favorable (Marks and Doremus 2000, Bowman et al. 2010, Marks et al. 2015). The subspecies *A. a. brooksi* is a resident (nonmigratory) population endemic to Haida Gwaii (Queen Charlotte Islands), British Columbia, that has distinctly darker, diagnostically different plumage. The nominate form occurs on Haida Gwaii as a migrant and winter visitant. Seven of 120+ specimens from Haida Gwaii are *A. a. acadicus* (Sealy 1998, Withrow et al. 2014), but it has never been recorded breeding there, although they breed in the Alexander Archipelago of Alaska (with nests from as close as Forrester Island; Willet 1915) and coastal British Columbia (Prince Rupert [Cannings et al. 2015], Bella Coola [Campbell et al. 1990]), just 50 - 100 km away. Additionally, there is no phenotypic evidence of hybridization and no records of *A. a. brooksi* off of Haida Gwaii.

A. a. brooksi shows adaptations to a marine food source, one that nonbreeding, nominate *acadicus* apparently do not take advantage of (Hobson and Sealy 1991, Sealy 1999). The Haida Gwaii form is completely sedentary (e.g., Sealy 1998) and probably has a smaller home range size than the mainland form (Waterhouse et al. 2017).

A rigorous comparative investigation of the advertising calls of *brooksi* and *acadicu*s has not been undertaken, but based on published pitch and frequency information they do not appear to be appreciably different (see Rasmussen et al. 2008). Individual variation is present (Holschuh and Otter 2005). The pitch and frequency of *A. ridgway*i (e.g., XC 355039, 166217, 381313) are very similar to these two as well (Marshall 1943), suggesting that vocal differences are not very useful for species delimitation in this group (or that *ridgwayi* is perhaps not a separate species).

Haida Gwaii birds are 100% diagnosable by plumage (Fig. 1), with much reduced white streaking around the face, reduced spotting on the back and wings, and overall darker/buffier coloration of parts that are generally white in mainland birds. The reduced spotting is reminiscent of the Unspotted Saw-whet Owl (*A. ridgwayi*). *A. a. brooksi* was described by Fleming (1916) as a subspecies of *Aegolius acadicus*, and has all but universally been treated at that level since (e.g., Cory 1918, AOU 1931, Peters 1940, AOU 1957, Cannings 1993, König et al. 2008, Dickinson and Remsen 2013). However, Brooks and Swarth (1925), both close observers of variation in birds of British Columbia, treated it as a distinct species (note,

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Figure 1. Dorsal and ventral views of *Aegolius acadicus acadicus* (top pair) and *A. a. brooksi* (bottom pair). Top-to-bottom: male, female, male, female. All specimens at UAM.

however, that the taxon was named for Brooks). Taverner (1953) echoed the sentiment of Brooks and Swarth (ibid), but ultimately treated it as a subspecies.

Mitochondrial DNA and AFLP data showed that *brooksi* differed consistently from *acadicus* and that gene flow estimates from mtDNA peaked at zero, driven largely by a single fixed difference between populations in ND2 (Topp and Winker 2008, Pruett et al. 2013, Withrow and Winker 2014). These datasets, with limited genomic sampling, did not produce estimates of gene flow rates robust enough to warrant a change in status. There have been no field studies directly examining how the two forms interact.

New information:

Recent genomic work using 2,517 UCE loci from six *brooksi* and seven *acadicus* (with both alleles called and thus ≥12 haplotypes each for coalescent analyses) demonstrated that levels of gene flow between these two taxa are low enough to theoretically put them on independent genetic trajectories, particularly given evidence of divergent selection (see below), with an estimated 0.7 (0.3-1.2; 95% CI) individual *acadicus* moving into *brooksi* per generation and 4.4 (2.0-6.7) *brooksi* moving into *acadicus* (Winker et al. 2019).

Important context: Under neutral conditions, levels of gene flow below one individual per generation result in populations continuing to diverge (Wright 1943, Cabe and Alstad 1994). The

presence of divergent selection can accommodate somewhat higher levels of gene flow than this and still enable divergence to proceed (Rice and Hostert 1993, Hostert 1997; but see Postma and van Noordwijk 2005). When sampling thousands of loci across the genome, small numbers of individuals effectively represent populations under a coalescent analytical framework (Felsenstein 2005). The higher rates of gene flow from *brooksi* into *acadicus* probably reflect a phenomenon that is no longer occurring (e.g., postglacial expansion), not surprising given that these estimates are a long-term average. These results show that despite opportunity for gene flow, it is occurring at remarkably low rates. In this case the specimen evidence has shown the same pattern, i.e., no evidence of intergradation. This is occurring despite the fact that migratory *acadicus* occurs frequently as a migrant and wintering bird on Haida Gwaii, with plenty of opportunities to stop and breed on Haida Gwaii as it does elsewhere when breeding conditions are suitable.

Recommendation:

The gene flow estimates from programs like δaδi are estimating the long-term effective rate of gene exchange, and in a dataset encompassing thousands of loci they are a dependable reflection of levels of reproductive isolation. While we are in the infancy of using population genomics to accurately assess levels of gene flow, adding this complementary approach to other available evidence for species delimitation is potentially very powerful. In this case, the evidence strongly suggests that *brooksi* is effectively reproductively isolated from nominate *acadicus* despite opportunities for gene flow. We thus recommend a vote to split them.

English name:

Haida Gwaii Saw-whet Owl, although a bit of a mouthful, is an appropriate English name. It is (1) the term most often used by those dealing intimately with the birds (e.g., COSEWIC 2006); (2) it maintains, with minor modification, historic English formulations for this taxon (see below); and (3) it keeps the "saw-whet" (as in Unspotted Saw-whet Owl) that will convey its close relationship to Northern Saw-whet Owl (which would not require a name change, due in part to the large asymmetry in range size).

The first English formulation for a putative Queen Charlotte Island/Pacific Northwest owl taxon was "Northwest Saw-whet Owl" (Osgood 1901, AOU 1910), but this name applied to "*A. a. scotaea*," now recognized to be synonymous with *A. a. acadicus* (although it was described from Haida Gwaii; see Sealy 2013). Fleming (1916) did not propose an English name in his description of *brooksi*, but "Queen Charlotte Saw-whet Owl" (e.g., Cory 1918, Brooks and Swarth 1925, Gabrielson and Lincoln 1959) or "Queen Charlotte Owl" (e.g., AOU 1931, Taverner 1953, Bent 1961, Johnsgard 1988, Holt et al. 1999) were common formulations. After British Columbia agreed in 2009 to adopt the name Haida Gwaii for what were previously called the Queen Charlotte Islands, the English name(s) of *brooksi* followed suit.

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Submitted by: Jack Withrow and Kevin Winker

Date of Proposal: 27 November 2019

Change the generic taxonomy of Puerto Rican Screech-Owl *Megascops nudipes*: (a) remove it from the genus *Megascops*, and (b) place it in a monospecific *Gymnasio*

Background:

The Puerto Rican Screech-Owl *Megascops nudipes* was described as *Strix nudipes* by Daudin in 1800. Bonaparte erected the genus *Gymnasio* for the species in 1854. Unaware of this, Cabanis proposed the genus *Gymnoglaux* for *nudipes* the following year. Confusingly, the species now known as *Margarobyas lawrencii* (Cuban Bare-legged Owl) has sometimes been considered the type species of *Gymnoglaux* (e.g., AOU 1983), but *Gymnoglaux* is now recognized as an objective junior synonym of *Gymnasio* (for a summary of the considerable historical nomenclatural confusion between these two species, including use of the name *Strix nudipes* Daudin, 1800, for Cuban Bare-legged Owl, see Olson & Suárez 2008). Over the decades following description of the two genera, most authors placed Puerto Rican Screech-Owl and Cuban Bare-legged Owl together in either *Gymnasio* or *Gymnoglaux* (e.g., Sclater & Salvin 1868, Sharpe 1875, Lawrence 1878, Ridgway 1914).

Peters (1940) moved Puerto Rican Screech-Owl to the genus *Otus*, stating that "[*Otus nudipes*] has been for many years placed in the genus *Gymnasio* Bonaparte 1854, of which it is the type. It does not however possess any characters sufficient to warrant its separation from *Otus*, and is merely a strongly marked insular species of that genus." The species has since been nearly universally treated as congeneric with the screech-owls (in *Otus* and later in *Megascops*; e.g. Bond 1978), including by the AOU following expansion of the Checklist's geographic coverage to include the Caribbean in the 6th edition (AOU 1983).

New Information:

Dantas et al. (2016) published a phylogeny including 30 taxa in the genus *Megascops* (see their Fig. 1 on the next page). They sequenced 20 of the 21 species recognized at the time by the AOU-NACC and SACC, including *M. nudipes*—the first time this species was included in a molecular phylogeny—and members of a few other owl genera, including *Psiloscops* but not *Margarobyas*. They sequenced three mitochondrial genes and three nuclear introns (one autosomal and two Z-linked). In their tree, *M. nudipes* is sister to Flammulated Owl *Psiloscops flammeolus*, and together these two species are sister to the rest of *Megascops*. Dantas et al. estimated the split between these two clades to have occurred around 20 mya, and the split between *P. flammeolus* and *M. nudipes* around 12-13 mya (see Fig. 2 from their paper).

Salter et al. (2020) recovered the same relationships among the four species of screech-owls and relatives included in their analyses (including *P. flammeolus* and *M. nudipes*) as Dantas et al. (see Fig. 2 from their paper). In addition, they were able to sequence nuclear UCEs and a partial mitochondrial genome from toepad samples of *M. lawrencii*, including this species in a molecular phylogeny for the first time. Although its precise relationships remain uncertain due to the poor quality of the available sequences, it's clear that *M. lawrencii* is only distantly related to screech-owls, contrary to previous suggestions that it might be closely related to *M. nudipes*.
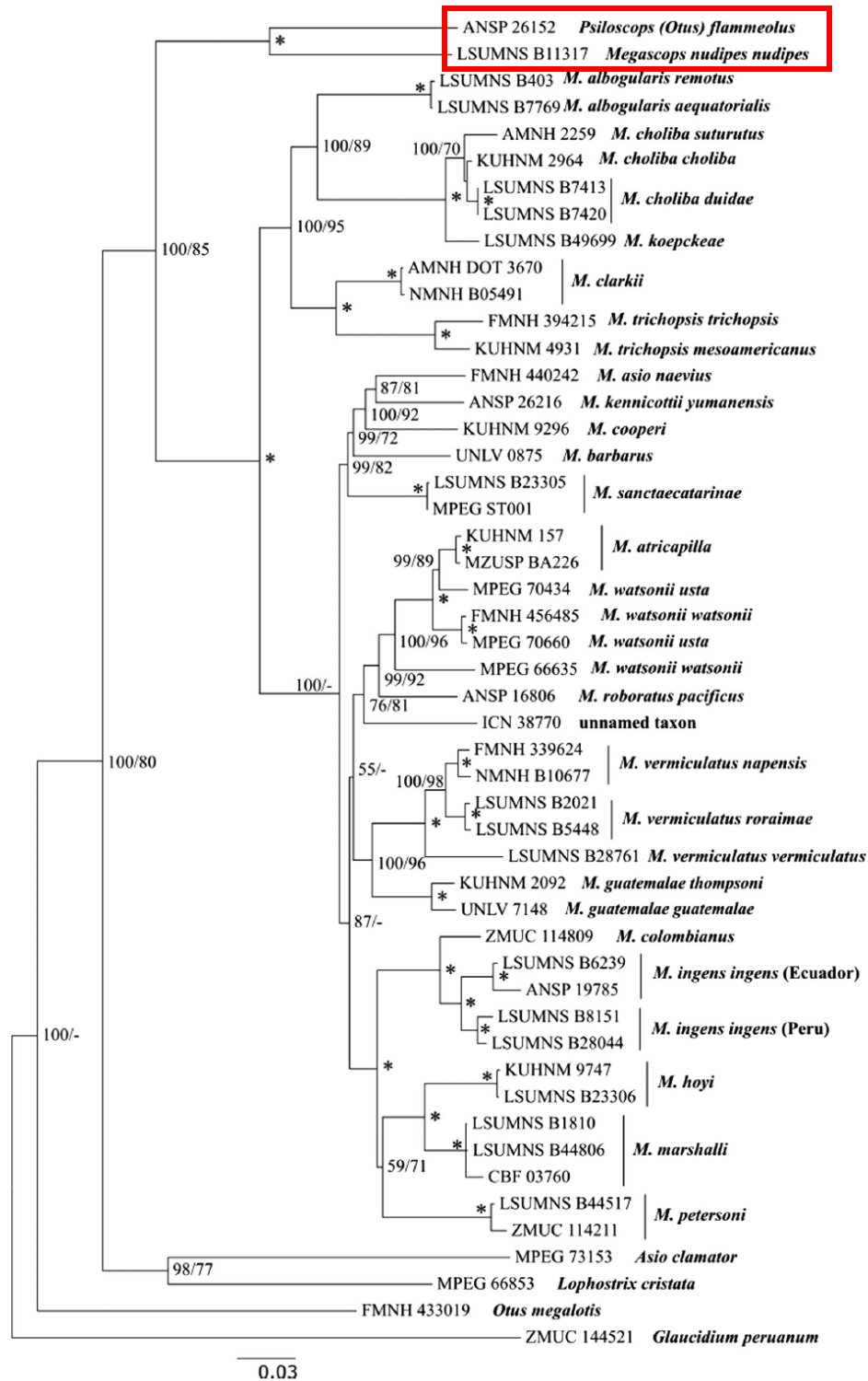
Fig. 1. Bayesian Inference phylogeny estimate based on a concatenation of all sequenced genes (Cytb, ND2, COI, BF5, CHD and MUSK). Node labels are BI/ML posterior probability and bootstrap support values, respectively. Asterisks associated with nodes indicate that both BI and ML support values are equal to or above 95%. Nodes denoted with a "−" indicate that they were not recovered by the ML analysis.

Fig. 1 from Dantas et al. (2016). *Megascops nudipes* and *Psiloscops flammeolus* are highlighted in the red box.

Fig. 2. Bayesian chronogram inferred from the mitochondrial genes sequenced (see text for details). Horizontal bars denote 95% posterior probability age intervals. *M. = Megascops.*
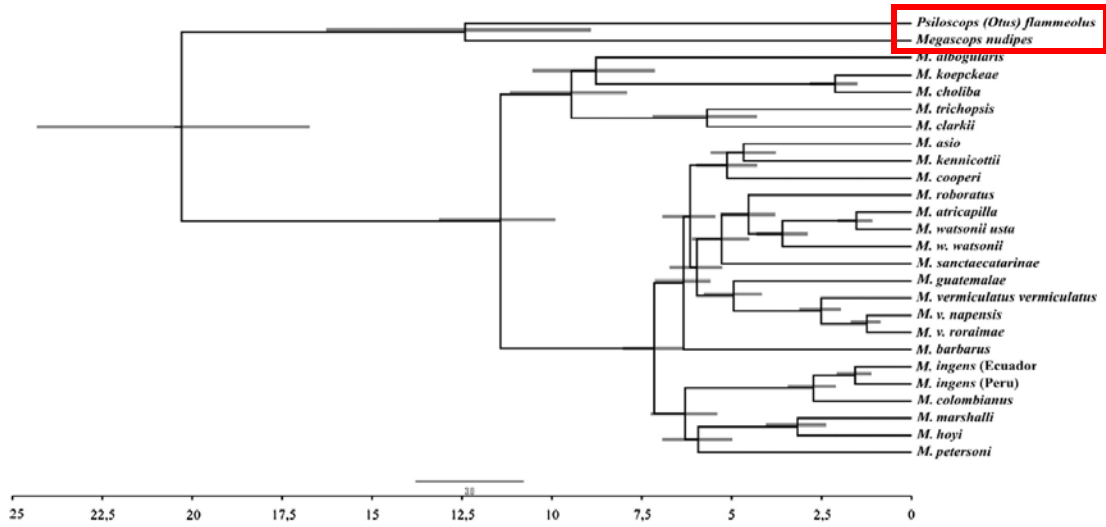
Fig. 2 from Dantas et al. (2016). *Megascops nudipes* and *Psiloscops flammeolus* are highlighted in the red box.

FIGURE 2. Cladogram of 46 owls (44 typical owls, 2 barn owls) inferred with (**A**) maximum likelihood (ML) and Bayesian inference (BI) analyses and (**B**) SVDquartets analysis of 4,235 nuclear ultraconserved element loci. ML and BI analyses produced identical topologies. Taxa in bold represent monotypic genera. Rounded gray boxes bracketing species names denote typical owl tribes: Ninox. = Ninoxini, Aeg. = Aegolini, Puls. = Pulsatrigini. All nodes received 100% bootstrap support / Bayesian posterior probability (BPP) unless otherwise labeled (ML bootstrap support/BPP). Nodes with <70% support have been collapsed, and pink branches and dotted lines indicate conflicting relationships. See Supplemental Material Figure S1 for a phylogram of the same relationships.

Fig. 2 from Salter et al. (2020). *Megascops nudipes*, *Psiloscops flammeolus*, and *Margarobyas lawrencii* are highlighted in red boxes.

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Recommendation:

Megascops as currently constituted is paraphyletic. Options to fix this are as follows:

1. Merge *Psiloscops* into *Megascops*, or
2. Remove Puerto Rican Screech-Owl *M. nudipes* from *Megascops*:
      2a. Merge Puerto Rican Screech-Owl *M. nudipes* and Flammulated Owl *P. flammeolus* into the same genus (for which *Gymnasio* Bonaparte, 1854, has priority over *Psiloscops* Coues, 1899), or
      2b. Place Puerto Rican Screech-Owl *M. nudipes* in a monospecific *Gymnasio*.

I strongly recommend option 2b. Option 1 would result in the loss of a separate genus for Flammulated Owl, which is different enough from all screech-owls in vocalizations and morphology that it was long thought to be more closely related to scops-owls. Furthermore, this option would add heterogeneity to *Megascops* and would obscure the distant relationship of Flammulated Owl and Puerto Rican Screech-Owl to the other members of this clade. Option 2a would obscure the major morphological and vocal differences between Flammulated Owl and Puerto Rican Screech-Owl, as well as the relatively deep genetic divergence between the two species. Additionally, all else being equal, it introduces a nomenclatural change for two species rather than one. Option 2b seems the most reasonable, because it doesn't create a morphologically and behaviorally undiagnosable *Gymnasio* and doesn't create an unnecessary nomenclatural change for Flammulated Owl.

Regardless of which option is approved, the committee will also need to consider a change to the English name of *nudipes* (or to that of *flammeolus*), because the group name "screech-owl" would no longer be restricted to a monophyletic group. Options will be considered in a separate proposal in the next set.

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Submitted by: Max T. Kirsch

Date of Proposal: 9 January 2020

Revise the linear sequence of *Megascops* and related genera

Background:

The linear sequence of *Megascops* and related genera in the current AOS Check-list of North and Middle American Birds is as follows:

- *Psiloscops*
    - *Psiloscops flammeolus*
- *Megascops*
    - *Megascops kennicottii*
    - *Megascops asio*
    - *Megascops seductus*
    - *Megascops cooperi*
    - *Megascops trichopsis*
    - *Megascops choliba*
    - *Megascops barbarus*
    - *Megascops guatemalae*
    - *Megascops centralis*
    - *Megascops clarkii*
    - *Megascops nudipes*

New Information:

Dantas et al. (2016) sampled the majority of screech-owls and close relatives, including all North and Middle American species except for *M. seductus* (see their tree in Proposal 2020-B-9). Their phylogeny conflicts with the current linear sequence on the checklist.

Recommendations:

A proposed revised linear sequence, following Dantas et al. (2016) and following conventions of least to most species-rich clades (including South American taxa not on the checklist) and northwest to southeast for sister taxa, is as follows:

- *Psiloscops*
    - *Psiloscops flammeolus*
- *Gymnasio*
    - *Gymnasio nudipes*
- *Megascops*
    - *Megascops trichopsis*
    - *Megascops clarkii*
    - *Megascops choliba*
    - *Megascops barbarus*
    - *Megascops kennicottii*
    - *Megascops asio*

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- *Megascops seductus**
- *Megascops cooperi*
- *Megascops guatemalae*
- *Megascops centralis*

This taxonomy is predicated on the transfer of *M. nudipes* to *Gymnasio*, as proposed in Proposal 2020-B-9 (if this does not pass as recommended, one or more changes will be made to the genus names above). *Megascops seductus*, noted above with an asterisk, was not sampled by Dantas et al. (2016), but is most likely a member of the *cooperi+kennicottii+asio* clade, based on similarities in vocalizations (Krabbe 2017). Because the current linear sequence of the three sampled species in this clade doesn't conflict with the phylogeny, it's probably best to leave this sequence unchanged for now in the absence of data on *seductus*.

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Submitted by: Max T. Kirsch

Date of Proposal: 9 January 2020

Split *Formicarius moniliger* from Black-faced Antthrush *F. analis*

Effect on the Checklist:

Approval of this proposal would split Black-faced Antthrush *Formicarius analis* into two species, both of which occur in the NACC area: (1) *F. moniliger* (SE Mexico to NW Honduras) and (2) *F. analis* (E Honduras to SE Amazonian Brazil). It would therefore add a species to the checklist. The recommended English name for new species *F. moniliger* is Mayan Antthrush. However, a split of *F. hoffmanni* of Central and South America from *F. analis sensu stricto* (i.e., restricted to South America) should also be considered. This is primarily an issue for SACC, which should consider it first, but it would affect the English and scientific names of the other species in our area (i.e., *F. analis*, if not split from *hoffmanni*, or *F. hoffmanni*) so only a provisional English name is recommended for *F. analis* in this proposal, pending consideration of a *hoffmanni-analis* split by SACC.

Background:

Formicarius antthrushes are stout and long-legged birds that resemble small rails as they walk over the ground with short tail cocked. The AOS currently (AOU 1998) recognizes *Formicarius analis* (Black-faced Antthrush) as a single species that includes three groups:

- *moniliger* group: on the Gulf-Caribbean slope from southern Veracruz, northern Oaxaca, Tabasco, Chiapas, and eastern and southern Yucatan Peninsula south to northern Honduras.
- *hoffmanni* group: on the Caribbean slope of eastern Honduras and Nicaragua, on both slopes of Costa Rica and Panama, and Colombia, northern Venezuela, and Trinidad.
- *analis* group: in South America from southeastern Colombia, southern Venezuela, and the Guianas south, east of the Andes, to central Bolivia and Amazonian Brazil.

The species account in AOU (1998) also notes that the "*moniliger* and *hoffmanni* groups differ in voice, plumage, and elevational distribution, and probably deserve to be considered as distinct species (Howell 1994). The relationships among populations farther south, including those in South America, are complex (Howell 1994, Ridgely and Tudor 1994)."

Fourteen subspecies are typically recognized within this species or species complex (e.g., Krabbe and Schulenberg 2003), divided among the three groups recognized in AOU (1998) as follows:

1. *moniliger* group

moniliger P.L. Sclater, 1857	SE Mexico (from S Veracruz, N Oaxaca, Tabasco, Chiapas) to Guatemala (except Petén)
pallidus Lawrence, 1882	SE Mexico (E and S Yucatan Pen.), N Guatemala (N Petén)
intermedius Ridgway, 1908	E Guatemala, Belize, NW Honduras

2. *hoffmanni* group

umbrosus Ridgway, 1893	Caribbean slope of E Honduras (Olancho) to W Panama; Pacific slope of Costa Rica (to Gulf of Nicoya)
hoffmanni (Cabanis, 1861)	Pacific slope in SW Costa Rica (from Carara), W Panama (W Chiriqui)
panamensis Ridgway, 1908	Panama (Coclé to Darién), NW Colombia
virescens Todd, 1915	N Colombia (W base of Santa Marta Mts.)
griseoventris Aveledo & Ginés, 1950	NE Colombia, NW Venezuela (W Maracaibo Basin from Sierra de Perijá to N Táchira, N Mérida)
saturatus Ridgway, 1893	N Colombia, Venezuela (north of R. Apure, R. Orinoco from E Maracaibo Basin, S slope of Andes); Trinidad

3. *analis* group

connectens Chapman, 1914	E Colombia (from Meta and Vaupés)
crissalis (Cabanis, 1861)	E Venezuela (E Bolívar), the Guianas, NE Brazil (Amapá, Pará)
zamorae Chapman, 1923	E Ecuador, N and NE Peru, W Brazil (north of R. Amazon to Codajás)
analis (d'Orbigny & Lafresnaye, 1837)	E and SE Peru (south of R. Amazon from R. Ucayali), N Bolivia to S Amazonian Brazil (to R. Tapajós, Mato Grosso)
paraensis Novaes, 1957	SE Amazonian Brazil (R. Tapajós to Belém, W Maranhão)

In plumage, the *moniliger* group differs principally from the *hoffmanni* and *analis* groups by the golden-brown color of the nape extending around the front to form a collar, separating the black throat from the gray underparts, whereas the *hoffmanni* and *analis* groups differ in the color of the sides of the neck, which is typically rufous in *hoffmanni* and clay-colored in *analis* (Howell 1994).

Historical treatments of this species or species complex have varied considerably. Ridgway (1911) recognized two species within the group: *F. analis* and *F. moniliger*. *Formicarius analis* was mainly extralimital to his work on North and Central American birds, represented by a single subspecies in Costa Rica and western Panama. *Formicarius moniliger* was considered to include eight subspecies (*moniliger, intermedius, pallidus, umbrosus, hoffmanni, panamensis, saturatus,* and *crissalis*) distributed from Mexico to northern Colombia, many of which are now considered part of the *hoffmanni* group (or, in the case of *crissalis*, the *analis* group).

Cory and Hellmayr (1924) recognized a single species, *Formicarius analis*, with 12 subspecies: *analis, crissalis, connectens, zamorae, saturatus, virescens, panamensis, hoffmanni, umbrosus, intermedius, pallidus,* and *moniliger*. Peters (1951) included the same 12 subspecies with the addition of *F. a. olivaceus*, which is found in northern Peru and was later synonymized with *zamorae* (Krabbe and Schulenberg 2003). Eisenmann (1955) listed *Formicarius analis* as distributed in tropical Middle America (except El Salvador) and South America.

Davis (1972) appears to have been the first to recognize a species split in Honduras. He considered *F. moniliger* (Mexican Antthrush), distributed from Mexico to NE Honduras, to be distinct from *F. hoffmanni* (Hoffmann Antthrush), distributed from SE Honduras to W Venezuela and N Colombia (and both, by implication, to be distinct from *F. analis* of South America). He detailed differences in song between *moniliger* and *hoffmanni* and also mentioned the distinctive rufous collar below the black throat of *moniliger*.

Stiles and Skutch (1989) included the species *Formicarius analis* with a geographic range from SE Mexico to N Bolivia and E Brazil. The authors did not mention any controversy with species limits or taxonomic issues associated with this species.

Sibley and Monroe (1990) listed three groups within *Formicarius analis,* which they restricted by geographic distribution: *moniliger* (southern Veracruz to northern Honduras), *hoffmanni* (southern Honduras to Venezuela and Trinidad), and *analis* (Colombia to Brazil). These groups correspond to the species of Davis (1972) and to the groups of AOU (1998), but do not match the *moniliger-analis* split of Ridgway (1911), because Sibley and Monroe's *moniliger* is restricted to Mexico and northern Central America, whereas Ridgway's *moniliger* is found from Mexico to northern Colombia.

Howell (1994) suggested recognizing Sibley and Monroe's *moniliger* group as a different species from the *hoffmanni* and *analis* groups, on the basis of consistent differences in song and plumage in addition to the apparent altitudinal replacement of these *Formicarius* antthrushes in eastern Honduras. In addition to illustrating dramatic differences in song (compare A and B to C and D in Fig. 1 on the next page), Howell (1994) noted that the plumage differences between *moniliger* and *hoffmanni* in chest pattern are typical of those that separate other closely related species of *Formicarius*. This arrangement follows Davis (1972) as far as the split in Honduras between the *moniliger* and *hoffmanni* groups, but Howell (1994) did not advocate splitting *hoffmanni* and *analis* due to the lack of concordance of distributional breaks in plumage and song between these two groups. It is interesting to note that the songs of the more geographically distant groups, *moniliger* and *analis*, are more similar than those of the geographically intermediate *hoffmanni* group (compare A and B to G and H in Fig. 1).

The *moniliger-analis* split was incorporated into Howell and Webb (1995), and the geographic range of *Formicarius moniliger* (Mexican Antthrush) was drawn from south-eastern Mexico to northern Honduras.

Krabbe and Schulenberg (2003), following Howell (1994), considered the *moniliger* group to be a separate species from *Formicarius analis*. The subspecies included within each species (Krabbe and Schulenberg 2003) coincided with those in the Howard and Moore Checklist (Dickinson and Christidis 2014): *Formicarius moniliger* with three subspecies (*moniliger, pallidus, intermedius*), and *F. analis* with eleven subspecies (*umbrosus, hoffmanni, panamensis, virescens, griseoventris, saturatus, connectens, crissalis, zamorae, analis, paraensis*).

The Clements Checklist (2019) recognizes a single species, *Formicarius analis*, with three groups: *moniliger* with three subspecies (*moniliger, pallidus, intermedius*); *hoffmanni* with five subspecies (*umbrosus, hoffmanni, panamensis, virescens, griseoventris*); and *analis* with six

subspecies (*saturatus, connectens, crissalis, zamorae, analis, paraensis*). However, *saturatus* is alternatively considered part of the *hoffmanni* group (Patten 2015), as in AOU (1998).

A: *F. moniliger*, Palenque, Chiapas, Mexico (Coffey).
B: *F. moniliger*, Calakmul, Campeche, Mexico, 9 April 1992 (Howell).
C: *hoffmanni* group, S8H Road, Panama, Panama, 25 February 1983 (Behrstock).
D: *hoffmanni* group, Cerro Pirre, Darien, Panama, 7 March 1983 (Behrstock).
E: "*hoffmanni*" group, Parque Nacional Yacambú, Lara, Venezuela, 25 May 1992 (Behrstock).
F: "*hoffmanni*" group, Asa Wright Nature Centre, Trinidad, 16 October 1982 (Behrstock).
G: *analis* group, La Selva, Napo, Ecuador, 6 January 1991 (Behrstock).
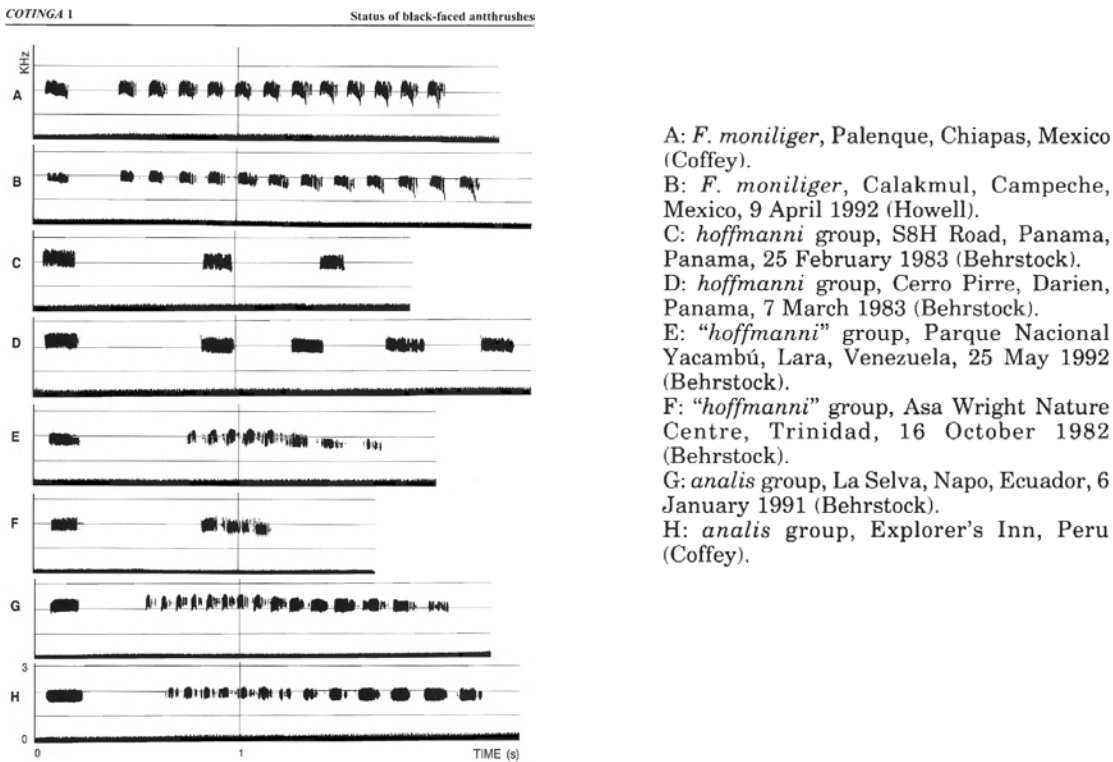H: *analis* group, Explorer's Inn, Peru (Coffey).

Figure 1. Songs of the *Formicarius analis* complex. From Howell 1994.

New Information:

There is new information on distribution, song, and genetics.

Gallardo (2014) reported that the *moniliger* and *analis* groups are not sympatric in Honduras but instead are separated by the Sierra de Agalta-Montañas de Malacate-Sierra Río Tinto mountain range. Gallardo also noted that *moniliger* occurs from sea level to 1800 m, while *analis* occurs from sea level to 850 m and in flatter terrain than *moniliger*. This information is consistent with what Monroe (1968) suggested based on color patterns of specimens (Fig. 2). We will add that the Olancho Valley area, which is located to the west of the Sierra de Agalta-Montañas de Malacate-Sierra Río Tinto mountain range, appears to be a strong barrier limiting the geographic ranges of many bird species (Howell and Webb 1995, Gallardo 2014), and might represent an interesting area for future biogeographic studies.

Patten (2015) conducted a qualitative analysis of XenoCanto song data, which greatly expanded the sampling in the figure of Howell (whose samples were from Mexico and Panama) to include sites very close to the gap in distribution (Fig. 3). Patten indicated that the vocal differences remain consistent as the two groups approach each other: "Almost no song recordings exist for Honduras, but recent ones by Carlos Funes suggest that birds south of the Olancho Valley (e.g., at Case de Tabla in the Reserva de la Biosfera Río Plátano, 04 July 2015; XC263471) utter songs similar to those of the *hoffmanni* Group, whereas birds north of this

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valley (e.g., at Montaña La Estrechura o Crudeza, Guata, 02 May 2013; XC184953) give songs like those of the *moniliger* Group".
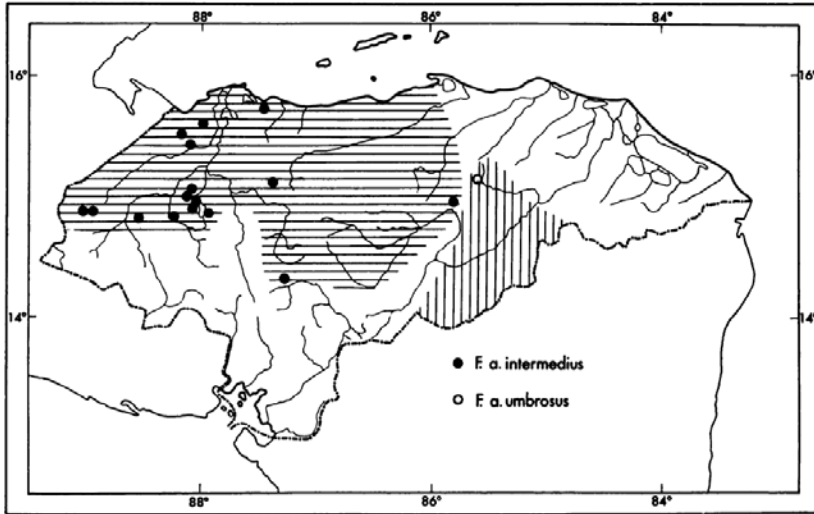
Figure 19. Range and specimen localities of the subspecies of *Formicarius analis* in Honduras.

Fig. 2. Map showing distributions of subspecies of *F. analis* in Guatemala (from Monroe 1968).

Figure 3. Localities where Carlos Funes recorded songs of *F. moniliger* and *F. analis*. Top map: north of Olancho Valley, XC184953 – *F. moniliger*. Bottom map: Olancho Valley, XC263471 – *F. analis*. Both maps were taken from xeno-canto.org.

In Miller's (2008) dissertation, he compared sequences of the complete mitochondrial gene ND2 (1041 bp) from 10 individuals of *moniliger* from Belize and 10 individuals of *hoffmanni* from Panama. He reported that the two groups did not share mitochondrial haplotypes (see his Figure 3.3 below, which has been trimmed to highlight the results for *F. analis*) and showed a net nucleotide difference (D_A) of 0.0853, which was the highest value found in the set of 60 species that he examined.
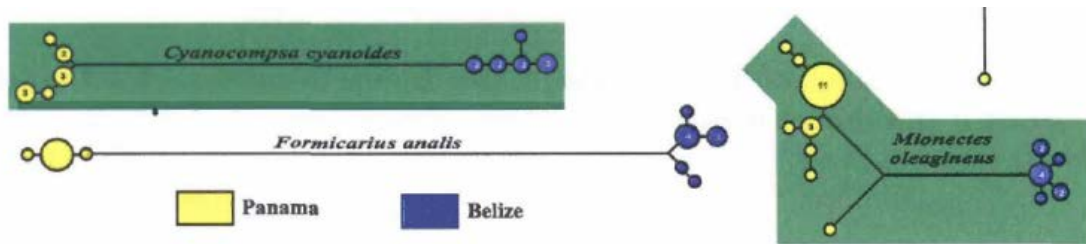
Figure 3.3. Minimum spanning trees for 19 species of resident Neotropical landbirds sampled in Belize and Panama. Among all 60 species studied, frugivores and nectivores (here framed in green) had lower levels of inter-population differentiation and were more likely to share haplotypes than insectivores; these tendencies are apparent among the 19 species shown here.

Recommendation:

We recommend splitting *Formicarius moniliger* from *Formicarius analis*. AOU (1998) indicated that these were probably good species but did not split them at that time. Additional data are now available, showing that the vocal differences between the groups noted by Howell (1994) are also present in the areas of close geographical approach in Honduras and that very large genetic differences separate individuals from Belize and Panama. Moreover, Gallardo has provided the best evidence to date that there is no contact zone to be studied. Although Patten (2015) suggested that playback experiments and genetic analyses in and near the contact zones, Honduras for *moniliger-hoffmanni* and Colombia for *hoffmanni-analis*, are a priority to understand reproductive isolation between the different groups, we consider that the plumage, song, and genetic data currently available make a good case for splitting *moniliger* from *hoffmanni*, which would continue to form part of *F. analis* pending further study of the South American forms.

For English names, Davis (1972) and Howell and Webb (1995) used Mexican Antthrush for *F. moniliger*. However, Marshall Iliff and Tom Schulenberg recommend using Mayan Antthrush instead, noting that

> the range of the *moniliger* group extends well beyond Mexico, but the heart of its range maps well onto the area formerly occupied by the Mayan civilization. Mayan Antthrush is already in use, e.g.

and in the Peterson field guide to Central America:

Fagan, J., and O. Komar. 2016. Field guide to the birds of northern Central America. Houghton Mifflin, Boston and New York. (where *moniliger* is not split, but Mayan still is invoked as a name for the northern group).

Finally, Steve Howell is at work on a new Mexico field guide, and he tells us (pers. comm.) that "I think Mayan Antthrush is a fine/better name and we are using it for Mexico."

Given this information, we recommend Mayan Antthrush, rather than Mexican Antthrush, as the English name for *moniliger*. For *analis sensu stricto*, we provisionally recommend following Howell and Webb (1995) in retaining Black-faced Antthrush for *F. analis*. Black-faced Antthrush is our current English name for *F. analis sensu lato*, but continued use of this name would appear to be justified because of the much larger distribution of *F. analis sensu stricto* relative to that of *F. moniliger* (under the "asymmetry of range size" exception to our guidelines for English names for newly split species).

However, a split of *F. hoffmanni* from *F. analis* should also be considered, and if this is adopted, then English names would need to be reconsidered. This is largely a SACC issue, so we propose that SACC consider this (soon) before we make a final decision on English names.

Please vote on the split of *Formicarius moniliger* from *F. analis*, and provide a provisional vote on adopting the English name Mayan Antthrush for *F. moniliger* while retaining Black-faced Antthrush for *F. analis* (pending a SACC vote and NACC consideration of a further split of *F. hoffmanni* from *F. analis*).

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