AOS Classification Committee – North and Middle America

Proposal Set 2020-A

4 September 2019

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Change the English name of Olive Warbler *Peucedramus taeniatus* to Ocotero

Background:

“Warbler” is perhaps the most widely used catch-all designation for passerines. Its use as a meaningful taxonomic indicator has been defunct for well over a century, as the “warblers” encompass hundreds of thin-billed, insectivorous passerines across more than a dozen families worldwide. This is not itself an issue, as many other passerine names (flycatcher, tanager, sparrow, etc.) share this common name “polyphyly”, and conventions or modifiers are widely used to designate and separate families that include multiple groups. In the Americas, native “warblers” are of course dominated by the parulids, but also include three small families: Phaenicophilidae and Teretistridae with two “warblers” apiece, and Peucedramidae, the Olive Warbler (*Peucedramus taeniatus*). These three families were historically all placed within Parulidae, but genetic evidence in the last 20 years has shown that their relationships to the Parulid warblers are far more distant. Although Phaenicophilidae and Teretistridae still cluster with the Parulidae in the New World nine-primaried oscine superfamily (Barker et al. 2015), *P. taeniatus* is far more distantly related, instead being closer to the Palearctic Prunellidae and other more basal passeroids (Ericson & Johansson 2003). The discovery that *P. taeniatus* constitutes a monotypic family and is phylogenetically distant from the New World nine-primaried oscines warrants a change to its English name that highlights its evolutionarily unique status and puts to rest its invalid former association with the Parulidae.

Precedent and Rationale:

As neither a parulid warbler, nor olive green on any significant portion of its body in any plumage (as its original description and early binomial names *Sylvia olivacea* and *Dendroica olivacea* would suggest), Olive Warbler has gained a reputation as one of the most impressively misnamed birds in North America. Being one of many New World species whose taxonomic status has changed dramatically in the past 20 years, *P. taeniatus* would certainly not be the first bird to get a new English name reflecting these discoveries. In 2000, the Stripe-headed Tanager *Spindalis zena* was split into four species and the genus name *Spindalis* was adopted as the English group name for these species (AOU 2000). More recently, the English group names of species in the passerellid genus *Chlorospingus* were changed from “Bush-Tanager” to Chlorospingus (Chesser et al. 2014) to “reduce the number of non-thraupid families that include species called ‘tanagers’” and to eliminate the use of a misleading common name, because “the *Chlorospingus* species… don’t really have anything to do with ‘bushes’ per se” (Proposal 2014-A-7).

Discarding the name “Olive Warbler” would be beneficial for several reasons. It would remove an inaccurate and misleading descriptor, not only since *P. taeniatus* is not related to any American warblers, but also because there are many parulid (and several vagrant phylloscopid) warblers in North America whose plumage can much more accurately be described as olive. It would restore some taxonomic credibility to the use of “warbler” in the Americas by reducing the number of native families with species called “warbler” on the checklist, and restricting its use to the New World nine-primaried oscines. Finally, it would highlight *P. taeniatus* as one of the most unique and interesting passerines in the Americas: the only representative of one of continental North America’s two endemic families, one whose evolutionary trajectory pushed it so far to convergence that its true affiliations remained undetected for over 150 years after its discovery.

A switch to a single-word name for *P. taeniatus* would be consistent with names of other species on the AOS check-list who are the sole representatives of their families, either worldwide (Sapayoa, Palmchat) or within the covered region (Verdin, Bushtit). Such a change would also fall in line with AOS guidelines for English names, as a single-word name reflects the taxonomic uniqueness of *P. taeniatus* (Rule 3, Checklist of North American Birds, 1983, pp. xxii-xxiii). Addition of plumage-accurate modifiers such as “Masked” or “Orange-headed” could also be used, but would not be necessary for such a distinct species, and could in fact wrongly imply the existence of related or similar taxa. Perhaps the most obvious place to start when considering alternative names for *P. taeniatus* is to simply adopt the genus name as the de facto English name, as done previously with the various species of Spindalis and Chlorospingus. However, Peucedramus is not used as a non-scientific name, and is somewhat clunky and difficult to pronounce. Most importantly, though, a one-word common name for *P. taeniatus* already exists, forgoing the non-ideal situation of replacing an existing common name with a directly-taken generic one.

I propose that the English name of *P. taeniatus* be changed to **Ocotero**, a name already commonly used throughout much of its range in Mexico and northern Central America. Ocotero is derived from *ocote*, a common Spanish term for various species of Latin American coniferous trees in the genus *Pinus*, which comprise a major and essential component of the habitat of *P. taeniatus*. Indeed, the name connects not only to its distribution, habitat and behavior, but also to its binomial name, with *Peucedramus* being a combination of the Greek *peuke* (pine) and *dromos* (to run). Ocotero presents a preferable alternative to the direct use of Peucedramus as a new English name, and fits with several other monotypic American families that have English names derived either from vernacular names or physical and behavioral traits (e.g. Sharpbill, Oilbird, and Limpkin). The use of Ocotero would fall in line with AOS naming conventions as an inoffensive and established non-English vernacular term for a species with no similar or closely related counterparts with established names (Rule 6, Checklist of North American Birds, 1983, pp. xxii-xxiii), and colloquial Spanish language terms are already found among the English names of many Latin American species, including doraditos (Tyrannidae), gallitos (Rhinocryptidae), and horneros, canasteros, and rayaditos (Furnariidae).

Recommendation:

The plumage and phylogenetic history of *P. taeniatus* make the common name of Olive Warbler uniquely ill-fitting and taxonomically misleading among American bird names. Ocotero (a) highlights *P. taeniatus*’s habitat and behavior, (b) reinforces *P. taeniatus*’s evolutionary uniqueness, (c) would be an easier adoption than the generic name Peucedramus, and (d) is a single-word name already used across much of the species' native range. It is in keeping with AOS naming conventions and, in emphasizing the species' unique monotypic status and habits, would be preferable.

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Submitted by: Alexander Lin-Moore, Yale University

Date of proposal: 4 April 2019

Change the generic classification of the Trochilini (part 1)

Background:

The phylogeny of McGuire et al. (2014) has forced major changes in the classification of the Trochilini. This is the first of two proposals that deal with changes already adopted by SACC, which voted to approve the options recommended by us in the proposal in each case. Some of these were with respect to taxa that were extralimital to SACC, and thus were advisory votes only; they were included in the SACC proposal because they are necessary components in the structure of evaluating subsequent changes. Comments by SACC members are available at: http://www.museum.lsu.edu/~Remsen/SACCprop780.htm. Part 2 deals mostly with cases that are entirely extralimital to NACC but are necessary to include in the NACC proposal for it to make sense.

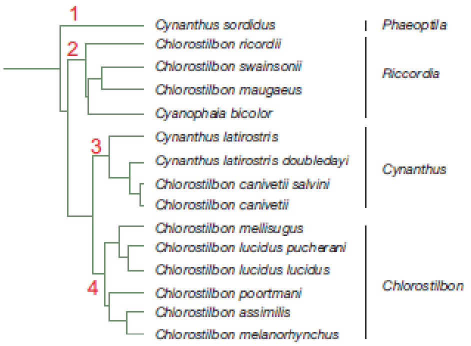
New Information:

Two recent studies of the generic classification of the Trochilini or “Emeralds” detected numerous instances of polyphyly and other incongruences with respect to the DNA-based phylogeny of this group (Stiles et al. 2017a, 2017b), the largest major clade of hummingbirds, with over 100 species. The first study addressed problems of generic nomenclature in the Trochilidae, with particular reference to two of the largest and most problematic genera, *Amazilia* and *Leucippus*. The second paper proposed a new generic classification of the Trochilini to bring it into the best possible accord with the phylogeny of McGuire et al. (2014), which treated 275+ species, including most or all species in all of the ca. 30-35 currently recognized genera. Our overall objective was to produce a classification taking as its base the branching pattern of the phylogeny, while preserving stability of existing nomenclature wherever possible. We tried to produce cohesive, diagnosable genera while avoiding producing large, undiagnosable genera on the one hand, and an excessive number of small or monotypic genera on the other; this necessitated a rather more flexible treatment of branch lengths. In the process, we found numerous instances of homoplasy in plumage color and pattern as well as discordance of plumages in other monophyletic groupings. We have all been weaned on a classification based to a very large extent on plumage, so the new classification resulted in many drastic reallocations of generic circumscriptions: this required the resurrection of nine generic names currently considered synonyms, the synonymizing of seven currently recognized genera, and the creation of one new genus. We here present the new generic classification for review by the NACC. This classification is presented in Figure 1 of Stiles et al. (2017b) below, and as we work through this, we present our reasoning for each change in brief; for further details regarding nomenclatural issues, see Stiles et al. (2017b).

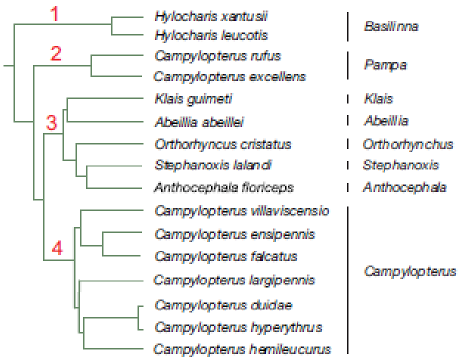
We began by dividing the Trochilini into four large groups (A, B, C and D), within each of which we recognized from two to seven subgroups, and further divided these to produce new generic groupings. We found that many of these new groupings showed strong geographical coherence, sometimes at odds with similarities in plumage. In this proposal we treat groups A, B and C; a subsequent proposal will deal with group D, by far the most difficult, including untangling the chaos associated with the generic names *Amazilia* and *Leucippus*.

Trochilini (Emeralds)

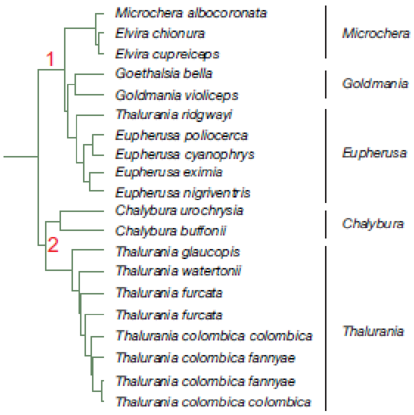
Group A



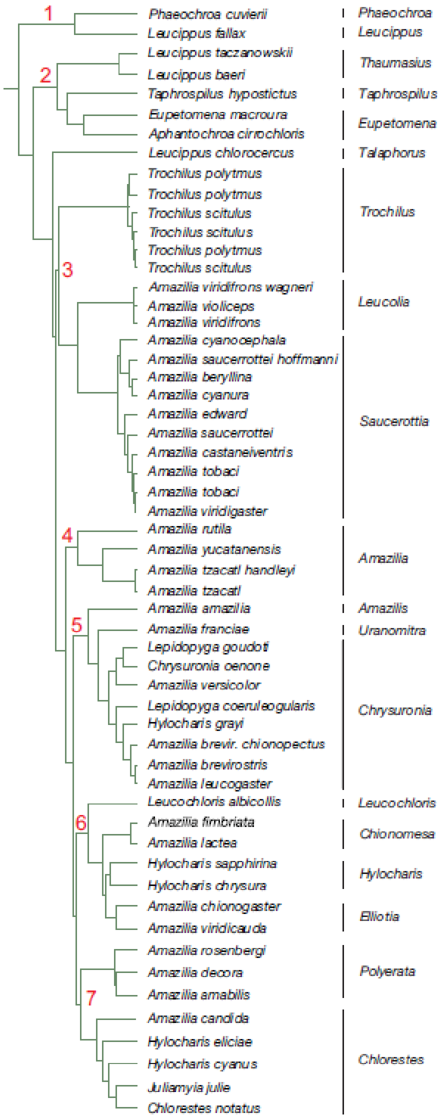
Group B



Group C



Group D



Group A includes the currently recognized genera *Chlorostilbon, Cyanophaia*, and *Cynanthus*. One alternative would be to lump all the other genera into *Cynanthus*, which has priority*.* We rejected this option because it would mask considerable genetic and phenotypic diversity. Because "*Cynanthus*" *sordidus* is clearly an outlier (subgroup A1, sister to the rest of group A), we advocate returning it to its status as the monotypic genus *Phaeoptila* (it had been lumped into *Cynanthus* without explanation by Peters). Examining the remaining groupings, a broad *Cynanthus* includes two coherent subgroups of *Chlorostilbon* (subgroups A2 and A4), separated by *Cynanthus* itself (subgroup A3): in effect, *Chlorostilbon* as a genus is polyphyletic. Subgroup A2 includes three species of the Greater Antilles and *Cyanophaia bicolor* of the Lesser Antilles*,* the most divergent in plumage; Subgroup A4 includes the *Chlorostilbon* species of southern Middle America and South America including the type species, *mellisugus.* We therefore advocate resurrecting the genus *Riccordia* for subgroup A2, and including within it *Cyanophaia*. We ascribe the greater divergence in plumage of *bicolor* to rapid evolution on isolated small islands: a similar case in the Polytminae involves the Lesser Antillean genera *Eulampis* and *Sericotes*, which the phylogeny found to be nested within *Anthracothorax.*

Cynanthus forms a compact generic group A3, the surprise being that nested within it are three to five (depending upon how finely one splits these taxa) species nearly always included in *Chlorostilbon* because of their plumages. Recognizing these as a separate genus *Chloanges* is not acceptable, as this would make *Cynanthus* itself paraphyletic; we therefore include these species in *Cynanthus.* One conclusion is that the "typical" plumage of *Chlorostilbon* shows homoplasy; however, another conclusion is that *Cynanthus* represents a coherent biogeographical radiation in northern Middle America.

Group B includes species in several genera. Subgroup B1 comprises two Mexican species often included in *Hylocharis* in the past, *leucotis* and *xantusii*. This is clearly untenable because the type species of *Hylocharis* (*sapphirina*) is in Group D in the phylogeny. We therefore follow several recent authors in placing these species in the genus *Basilinna.* Subgroup B2 includes two Mexican species of *Campylopterus,* separated from the rest of this genus by subgroup B3. We therefore advocate resurrecting the generic name *Pampa*, as used and diagnosed by Ridgway, for these species including as well its type species, *curvipennis,* not included in the phylogeny but close to (and sometimes lumped with) *excellens,* thus resolving the apparent polyphyly of *Campylopterus.*

Subgroup B3 includes five small genera (*Klais, Abeillia*, *Orthorhynchus, Anthocephala* and *Stephanoxis*, all on long branches. One alternative would be to lump all five into *Orthorhynchus,* the oldest name. A second would be to lump *Klais* into *Abeillia*, and the remaining three into *Orthorhynchus*. However, the lack of morphological or biogeographic coherence among this group leads us to continue recognizing all five genera, which also promotes stability. Subgroup B4 includes the bulk of the genus *Campylopterus* including its type species *largipennis*, with species ranging from Middle America through much of South America. Although some of the branch lengths are rather long, we see nothing to be gained by splitting a well-diagnosable genus like *Campylopterus* into three or four small genera, at least one of which would require a new genus name; we therefore recommend continued recognition of a broad *Campylopterus*, again preserving stability.

Group C includes only two subgroups. Subgroup C1 comprises two clades. The first is a tight group of three species in two genera, *Microchera* and *Elvira*, all of which inhabit lower middle elevations of the mountains of Costa Rica and western Panamá. Given the short branch lengths joining them, we consider that all are best considered congeneric; *Microchera* has priority. *Microchera* has long been considered monotypic due to the very distinctive male plumage of *albocoronata*; however, the female plumage is quite similar to those of *Elvira.*

The second clade breaks into two groups: the first comprises the monotypic genera *Goldmania* and *Goethalsia* of the Darien highlands of eastern Panama and adjacent Colombia; the second includes *Thalurania ridgwayi* and the several species of the genus *Eupherusa.* We see no reason for maintaining two monotypic genera in the former group, and lump *Goethalsia* into *Goldmania,* which has priority. The two species are similar in morphology, share an unusual type of undertail coverts, and differ only in color patterns; they show a somewhat leapfrog-like pattern of distribution on isolated mountaintops in the Darien. These two species are adjacent in all recent classifications.

The surprise in the second group is *Thalurania ridgwayi*, which has been included in this genus since its description, based on its green throat and chest, dark abdomen, and bright blue-violet crown. However, the genetic data preclude inclusion of *ridgwayi* in *Thalurania*, and a close examination of its plumage reveals previously overlooked similarities in plumage with *Eupherusa.* Furthermore, its Pacific slope distribution accords much better with that of *Eupherusa* than that of *Thalurania*, which extends northward in the Caribbean lowlands to Guatemala and only occupies the Pacific slope from southwestern Costa Rica southwards into South America. Hence, we advocate inclusion of *ridgwayi* in the genus *Eupherusa.* The only other option would require naming a new genus for *ridgwayi*, which we deem unnecessary given its close genetic relationship to *Eupherusa.*

Recommendations:

We now present the following proposals for consideration by NACC. Although several of these are mostly or strictly in the domain of the SACC, we present them here because they affect the classification of some genera of North America as well.

1: A. Expand the genus *Cynanthus* to include *Chlorostilbon sensu lato.*
   B. Separate the species *sordida* in the genus *Phaeoptila*; doing so then permits further consideration of the circumscription of *Chlorostilbon*. ***We strongly favor this option.***

2: A. Restrict *Cynanthus* to exclude the *canivetii* group of species of *Chlorostilbon,* segregating these in the genus *Chloanges.*
   B. Include the aforementioned species in *Cynanthus.* ***We favor this option because option A would render Cynanthus paraphyletic.***

3: A. Retain the Antillean species in *Chlorostilbon.*
   B. Split *Chlorostilbon* into two genera, reviving the generic name *Riccordia* for the Antillean species including *Cyanophaia*, with the second genus including the majority of the species of *Chlorostilbon* including its type species; nearly all of these species are South

American. ***We strongly favor this option, because option A would produce a polyphyletic Chlorostilbon.***

4: A. Retain the species *excellens* and its close relatives in the genus *Campylopterus.*
B. Split *Campylopterus* into two genera, reviving *Pampa* for *excellens*, *curvipennis* (not sampled but believed to be closely related to *excellens*), and *rufus*. ***We strongly favor this option because option A would render Campylopterus polyphyletic.***

5: A. Retain the non-*Pampa* species of *Campylopterus* in this genus, which includes its type species. ***We favor this option, especially as at least one new generic name might be required for option B, and Campylopterus as restricted is well diagnosable.***
B. Split the restricted *Campylopterus* into three or four small genera.

6: A. Retain generic rank for *Orthorhynchus, Abeillia, Klais, Anthocephala* and *Stephanoxis.* ***We favor this option because all of these genera are separated on long branches, and because of the lack of morphological or biogeographical concordance between them.***
B. Lump all of these genera into *Orthorhynchus.*
C. Lump the first two genera into *Abeillia* and the last three into *Orthorhynchus.*

7: A. Continue to recognize *Microchera* and *Elvira* as separate genera.
B. Lump *Elvira* into *Microchera.* ***We favor this option because of biogeographical concordance, short branch lengths, and previously overlooked similarities in female plumages.***

8: A. Continue to recognize *Goethalsia* and *Goldmania* as separate genera.
B. Lump *Goethalsia* into *Goldmania.* ***We favor this option as the two species are similar morphologically and biogeographically, the difference between them being only coloration, especially of the males.***

9: A. Name a new genus for "*Thalurania*" *ridgwayi*, because the genetic data preclude its inclusion in *Thalurania.*
B. Include *ridgwayi* in the genus *Eupherusa* reflecting hitherto overlooked similarities in plumage, biogeographical concordance and genetic proximity. ***We favor this option.***

10: A. Continue to recognize the genera *Thalurania* and *Chalybura.* ***We favor this option: although sharing a few similarities in plumage, these genera are separated on long branches and are readily diagnosable from each other.***
B. Lump *Chalybura* into *Thalurania*, which is its sister genus in the phylogeny.

Note that a new linear sequence will also be required for the Trochilini. This will be the subject of a future proposal, once the new generic assignments have been implemented.

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Submitted by: Gary Stiles and Van Remsen

Date of Proposal: 20 May 2019

Change the generic classification of the Trochilini (part 2)

Background:

This is the second set of proposals on changes to generic limits in the Trochilini based on the phylogeny of McGuire et al. (2014). These changes were already adopted by SACC, which voted to approve the options recommended by us in the proposal in each case. Some of these were with respect to taxa that were extralimital to SACC, and thus were advisory votes only; they were included in the SACC proposal because they are necessary components in the structure of evaluating subsequent changes. Comments by SACC members are available at: http://www.museum.lsu.edu/~Remsen/SACCprop781.htm. Part 2 deals mostly with cases that are extralimital to NACC but are necessary to include in the NACC proposal for it to make sense.

New Information:

The genetic tree of the Trochilidae (McGuire et al. 2014) showed that the generic taxonomy of the hummingbirds was incongruent with phylogeny at many points, and that the tribe Trochilini, popularly known as the Emeralds, epitomized this conflict. The bewildering array of problems to be resolved was summarized briefly by Stiles et al. (2017a), and a resolution of these in a new generic taxonomy was presented by Stiles et al. (2017b). Based on the genetic tree, we divided the Trochilini into four groups. In part 1 of this proposal, we treated Groups A, B and C; this proposal deals with the largest and most difficult group of genera, Group D. We divided this group into seven subgroups, within each of which we recognize from one to four genera. The nomenclatural issues are more complicated in this group, and for more detail and explanation of our resolution of these, see Stiles et al. (2017a, b). As in part 1, we work through the groups in the order in which they appear in the figure, reproduced in Proposal 2020-A-2.

Subgroup D1 includes only two genera, *Leucippus* (extralimital) and *Phaeochroa,* separated on long branches*.* Recent classifications of *Leucippus* have included several other species, but the phylogeny places all of these in different subgroups, leaving *fallax,* its type species, alone in what becomes a monotypic genus. Both occur in dry habitats, *Phaeochroa* mainly on the Pacific slope of Middle America and northern Caribbean Colombia, *L. fallax* in dry to desertic habitats in extreme northern Colombia and Venezuela. *Phaeochroa* is also monotypic in most classifications, with *cuvierii* as its type, although some would recognize *roberti* of the Caribbean slope of Middle America as a separate species. Both *fallax* and *cuvierii* are rather dull-colored but they differ in pattern: *fallax* is uniform buff below, whereas *cuvierii* is mostly green below, speckled or scaled with buffy-whitish; *cuvierii* is much larger, and the outer primaries are flattened and thickened much like those of *Campylopterus* in group B; indeed, Schuchmann (1999) included *cuvierii* in *Campylopterus* for this reason. However, this placement is refuted by the phylogeny: the “sabre” wings of each were derived independently. We advocate recognizing both of these as monotypic genera.

Subgroup D2 includes two well-separated clades. The first consists of two extralimital species included in *Leucippus* in recent taxonomies, *taczanowskii* and *baeri.* The phylogeny precludes their inclusion in *Leucippus*, but the generic name *Thaumasius* is applicable, its type species being *taczanowskii.* These two species share a rather dull, brownish plumage, differing in pattern and size, but both occupy relatively dry habitats of the Pacific slope of extreme southern Ecuador and northern Peru. The second clade includes three species on long branches, currently segregated in three extralimital monotypic genera: *Taphrospilus hypostictus, Eupetomena macroura* and *Aphantochroa cirrochloris.* In plumage, *hypostictus* and *cirrochloris* are dull in coloration although differing in pattern; *macroura* is very different in plumage, dark blue with a longer, forked tail. However, *cirrochloris* and *macroura* are sister species sharing a similar pattern of distribution in lowland southeastern South America as well as “saber” wings resembling those of *Campylopterus* in the males, whereas *hypostictus* occupies mainly subtropical elevations along eastern Andean slopes from southern Colombia to northern Bolivia, and lacks the modified primaries of the other two. This species has been included in *Leucippus* by some authors, but the phylogeny precludes this treatment. Here, three options are available: (a) lump all three in a single genus, for which *Eupetomena* takes priority; (b) lump *Aphantochroa* and *Eupetomena* because of their sister status, shared distribution and modified primaries in males, while maintaining a monospecific *Taphrospilus* or (c) maintain three monospecific genera. We consider (a) the worst option because it gives no information regarding relationships and would subsume considerable genetic differences; option (c), while preserving stability, also ignores relationships among these species. We therefore prefer option (b), which is most informative in this respect as well as in distribution and morphology, although its two species are widely divergent in plumage color. However, such “color clashes” also occur in several other subgroups in group D, as detailed below.

Subgroup D3 first includes a clear outlier with no close relatives, extralimital “*Leucippus*” *chlorocercus* (it could even be considered a subgroup by itself), which therefore requires its separation in the monotypic genus *Talaphorus*, which was originally described for it. Its distribution, along the upper reaches of large Amazonian rivers, is also unique. Its inclusion in *Leucippus* in the past was due to its dull colors and conservative plumage evolution having masked its genetic distinctiveness. Next in this subgroup is a distinct clade including only the genus *Trochilus*. Unique in morphology and distribution, *Trochilus* clearly merits generic rank.

Next in subgroup D3 are two well-separated clades formerly included in *Amazilia* (but such inclusion is refuted by the phylogeny; see below). The first clade comprises three Mexican species: *violiceps, wagneri* and *viridicauda*, for which the generic name *Leucolia* is applicable. We note here that we had accepted *viridicauda* as its type following the recommendation of Elliot, but this was incorrect because it was described after *Leucolia* was named; we have submitted a manuscript (Stiles et all, submitted) substituting *violiceps* as the type species to correct this error. The final clade in D3 includes ten species in two compact clusters separated by a very short branch, such that they all should be considered as a single genus *Saucerottia.* The four species of the first cluster are Middle American, the six of the second cluster occur from southern Middle America into northern South America; all share certain morphological features and glittering green over the chest or the entire underparts. In the past, *Saucerottia* had often been considered a subgenus within *Amazilia,* but generic status is supported by the phylogeny.

Subgroup D4 includes only three species: *rutila, yucatanensis*, and *tzacatl*; because the first is the type species of *Amazilia*, these three constitute the necessarily much-restricted genus

Amazilia. The genetic distinctness of this subgroup was not recognized heretofore due to numerous convergences in plumage with species of several other subgroups.

Subgroup D5 includes two successive outliers on relatively long branches, then two much more closely related clusters of three and five species. The first outlier is the species *amazilia*, often considered the type species of the genus *Amazilia* in the past, but the genetic tree does not support its inclusion therein. We have proposed that the earliest generic name for this species is *Amazilis*; see Stiles et al. (2017a) regarding the nomenclatural complexities involved. This species appears to be an old isolate at the southwestern extreme of the distribution of what we dubbed the "amazilian complex", and it also has a unique plumage pattern. The second outlier, on a slightly shorter branch, is extralimital "*Amazilia*" *franciae*, which we also consider to constitute a separate genus, for which the name *Uranomitra* is applicable. It is the only member of the complex with a montane distribution and marked sexual dichromatism, as well as several morphological differences from others in this complex.

The third group of species in subgroup D5 provides the most extreme mismatch between the genetic data and plumage features. The first cluster includes three extralimital species currently placed in three genera: *Chrysuronia oenone, Leucippus goudoti* and *Amazilia versicolor*; the second, four extralimital species in three genera: *Leucippus coeruleogularis, Hylocharis grayi, Amazilia brevirostris* (usually including *chionopectus*) and *A. leucogaster.* The white-bellied species *versicolor, brevirostris* and *leucogaster* were included in *Agyrtria* by Schuchmann (1999), but the spelling *Agyrtrina* is correct. Two options exist here: a) give each cluster a separate generic name; or b) combine both clusters in a single genus. For the first option, the generic name *Chrysuronia* has priority; for the second, *Eucephala* (the original genus name of *grayi*). For the second option, *Chrysuronia* takes priority over *Eucephala.* We favor the second option because of the short branch connecting the two clusters, and the enlarged genus *Chrysuronia* is scarcely more heterogeneous in plumage than either cluster produced by the first; in addition, option b combines in the same genus members of two genera that must disappear in the interest of priority, *Agyrtrina* and *Lepidopyga.* The two most divergent species in male plumage, "*Lepidopyga*" *goudoti* and *coeruleogularis*, are not even sisters in the phylogeny, and the "*Agyrtrina*" species also appear in both clusters. The females of all of these species are more or less "white-bellied", as are the males in the monomorphic species.

In subgroup D6, the extralimital species *albicollis* is an outlier on a long branch, and we favor continuing to recognize its distinctness by maintaining it in the monospecific genus *Leucochloris*; its plumage is also unique. The second cluster in this subgroup, on a fairly long branch, includes two extralimital species: "*Amazilia*" *lactea* and *fimbriata*, which share a similar plumage pattern, differing merely in colors. The phylogeny precludes their inclusion in *Amazilia*, and for them, the generic name *Chionomesa* is available and applicable. Both species are widely distributed in lowland cis-Andean South America, *fimbriata* more northern, *lactea* more southeastern in ranges. We favor placing both in *Chionomesa.* The third and similarly distinct cluster in subgroup D6 includes the extralimital species *sapphirina* and *chrysura*, which we consider should constitute the restricted genus *Hylocharis*, of which *sapphirina* is the type species. These share a unique plumage feature and both occur in southeastern South America, although *sapphirina* has a broad but disjunct range in South America north of the Amazonian watershed.

The fourth cluster in subgroup D6 includes two extralimital species previously placed in either *Leucippus* or *Amazilia*: *chionopectus* and *viridicauda*. These species are less distinct genetically from the preceding cluster, such that they could be included in *Hylocharis*, but they are widely discordant in distribution and ecology, being found at middle and upper elevations in the Andes of Peru and Bolivia, such that we consider them to best represent a distinct genus. Their distinctiveness had previously been suggested by Peters, but neither he nor we found a generic name applicable to them. We therefore proposed a new genus *Elliotia* for them. Unfortunately, this name was found to be preoccupied, and we have submitted a manuscript substituting another name. We therefore suggested to SACC members that they evaluate the evidence for generic status of these two species under the generic name yet to be published.

Subgroup D7 includes two genetically distinct clusters. The first contains the species "*Amazilia*" *amabilis, decora*, and *rosenbergi* (extralimital). For these, the generic name *Polyerata* is applicable, with *amabilis* as its type species. The circumscription of this genus by some recent authors included several other species that the phylogeny placed in other subgroups, but *Polyerata* as here restricted is clearly valid, and we advocate its recognition. The second subgroup includes five species arranged in a stepwise cascade with short branches separating them: "*Amazilia*" *candida*, "*Hylocharis*" *eliciae*, "*Hylocharis*" *cyanus* (extralimital), *Juliamyia julie*, and *Chlorestes notatus* (extralimital). Inclusion of any of these species in *Amazilia* or *Hylocharis* is not supported by the phylogeny. Because all of the branch lengths are short, we consider that any further subdivision of this group would be arbitrary and could require the resurrection of at least one generic name and the probable erection of one new genus, we prefer considering all of these species congeners; the generic name *Chlorestes* takes priority. Thus, the generic name *Juliamyia* is placed in synonymy: in fact, the two most closely related species are *notatus* and *julie,* which differ considerably in male plumages but share one unique feature, their strongly rounded tails. Once again, in this group as a whole, female plumages are much more similar than those of the males, and that of the one monomorphic species, *candida*, also fits the situation in the enlarged *Chrysuronia* above.

Finally, we leave two Middle American species unclassified (*incertae sedis*) because we lack genetic information for them and are reluctant to place them on the basis of plumage characters that have been repeatedly shown to exhibit homoplasy: "*Amazilia" luciae* and "*Amazilia*" *boucardi*. We are open to solutions as far as what to do with these two in the NACC classification. To us, the best option would be to leave them in *Amazilia* with an asterisk before the genus name and a note to indicate the uncertainty of placement. Unfortunately, they are almost certainly unrelated to true *Amazilia*. Another option would be to make our best guess based on plumage and biogeography, but phenotype has proven to be unreliable and placement in a genus based on biogeography would be guesswork. Leaving these species in *Amazilia* would also preserve stability until they can be confidently placed based on new data.

Recommendations:

We now present the results of this generic rearrangement for evaluation by NACC in the following series of proposals.

1. A. Consider subgroup D1 as a single genus, for which *Leucippus* takes priority.

B. Recognize *Leucippus* and *Phaeochroa* as distinct monospecific genera. ***Given the long branches and morphological distinctiveness, we strongly favor this alternative.***

2. (Extralimital)
   A. Maintain *baeri and taczanowskii* in *Leucippus.*
   B. Recognize the genus *Thaumasius* for these two species. ***We strongly favor this option, because option A would produce a polyphyletic Leucippus****.*

3. (Extralimital)
   A. Continue to recognize three monospecific genera *Aphantochroa*, *Eupetomena* and *Taphrospilus*.
   B. Lump *Aphantochroa* into *Eupetomena* while maintaining a monospecific *Taphrospilus.* ***We favor option B as being most concordant regarding relationships, morphology and distributions, although* cirrochloris *and* macroura *differ strongly in plumage; we consider option C as the worst alternative.***
   C. Lump all three into a single genus *Eupetomena.*

4. (Extralimital)
   A. Recognize the monospecific genus *Talaphorus* for *chlorocercus.* ***Given its great genetic distinctness, there really is no other sensible option here.***

5. A. Recognize the genus *Leucolia* for the extralimital species *viridifrons*, *violiceps*, and *wagneri.* ***Again, there is no real alternative: they cannot remain in* Amazilia*, no other generic name previously applied for them accords with the genetic tree, and they share a characteristic distribution.***

6. A. Split the genus *Saucerottia* into two genera, one Middle American and the other found from southern Middle America into South America.
   B. Maintain a single genus *Saucerottia* including both groups above. ***We strongly favor this option given the close relationships and morphological congruence of these two groups.***

7. A. Restrict the genus *Amazilia* to the species in subgroup D4. ***We strongly favor option A.***
   B. Continue to recognize a broader *Amazilia*, although its limits would be difficult to define and would subsume too much genetic divergence.

8. (Extralimital)
   A. Recognize the genus *Amazilis* as a monospecific genus for the species *amazilia* based upon its distinctness genetically and in plumage and distribution. ***We favor option A.***
   B. Include more of subgroup D5 in *Amazilis.*

9. (Extralimital)

A. Recognize the monospecific genus *Uranomitra* for the species *franciae*, given that it is so distinct genetically, morphologically and in its highland distribution from the following species cluster. ***We favor option A.***

B. Include *franciae* and the following group in *Amazilis.* This option would produce a very heterogeneous group subsuming a great deal of genetic, morphological, and distributional diversity.

10. (Extralimital)

A. Divide the remaining ten species of group D5 into two genera, *Chrysuronia* and *Eucephala.*

B. Include all eight species in the genus *Chrysuronia*. Although decidedly heterogeneous in male plumages, the combined group is little more so than each of them separately, the groups are closely related, and this option would include members of two genera that must be sunk due to phylogeny but are not sisters in the phylogeny. ***We favor option B.***

11. (Extralimital)

A. Continue to separate *albicollis* in a monospecific genus, recognizing its genetic distinctiveness and unique plumage. ***We favor this option, because option B would subsume much genetic and distributional divergence.***

B. Combine *Leucochloris* with one or more clusters of subgroup D6.

12. (Extralimital)

A. Recognize *Chionomesa* for the species *fimbriata and lactea.* ***We favor this option, because the other subgroups are approximately equal in genetic distinctiveness and differ greatly in distribution.***

B. Combine these with one or more clusters in subgroup B6.

13. (Extralimital)

A. Recognize a restricted *Hylocharis* for the species *sapphirina* and *chrysura.* All other species previously included in this genus are placed in different parts of the phylogeny, and the genus as here restricted shows a unique plumage feature and a largely congruent distribution. ***We favor this option, for the reasons given more fully below.***

B. Include at least the following group in *Hylocharis* to reflect genetic similarity.

14. (Extralimital)

A. Recognize a new genus for the species *chionogaster* and *viridicauda* (here called *Elliotia,* but this is preoccupied; its name to be supplied in a submitted manuscript). ***We favor this option, because option B would produce a morphologically, ecologically and biogeographically incoherent grouping.***

B. Include these species in *Hylocharis.*

15. A. Recognize the restricted genus *Polyerata* for the species *amabilis, decora*, and extralimital *rosenbergi.* This proposal is novel only in its restriction; the inclusion of several other species in some classifications is precluded by the genetic data,

although we also do not include two species for lack of genetic data (see below). ***There is no really feasible alternative here.***

16. A. Divide the remaining cluster in subgroup D7 into two to four genera.
    B. Consider the five species in this cluster congeneric under the name *Chlorestes.* ***We favor this option because these species occur in a stepwise cascade with very short branches between them, such that any subdivision would be arbitrary and would require at least one new generic name.***

17. A. Retain *A. luciae* and *A. boucardi* in *Amazilia* but insert an asterisk before the genus name and include a note to indicate that these species, not included in the phylogeny of McGuire et al. (2014), are almost certainly not true *Amazilia*. ***There is no reasonable alternative to this other than making an educated guess based on phenotypic characters, which have been shown to be unreliable indicators in this group. Retention of these species in*** **Amazilia** ***would also preserve stability until new data allow them to be placed.***

Note that a new linear sequence will also be required for the Trochilini. This will be the subject of a future proposal, once the new generic assignments have been implemented.

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Submitted by: Gary Stiles and Van Remsen

Date of Proposal: 20 May 2019

Split Garnet-throated Hummingbird *Lamprolaima rhami*

Effect on the NA Checklist:

This proposal would split the Garnet-throated Hummingbird (*Lamprolaima rhami*) into two allopatric species on either side of the Isthmus of Tehuantepec.

Background:

The Garnet-throated Hummingbird (*Lamprolaima rhami*) consists of various disjunct populations from southern Mexico east to central Honduras (Fig. 1), including the Sierra Madre Oriental (Puebla to Veracruz), northern highlands of Oaxaca, highlands of Guerrero and Sierra Madre del Sur, southern highlands of Oaxaca and Sierra de Miahuatlan, highlands of Chiapas and Guatemala, and highlands of Honduras and El Salvador. *Lamprolaima rhami* predominantly occupies cloud forests, but also inhabits upland forests, pine-oak forests, and pine-oak scrub in different parts of its range, with an elevational distribution of 1200–3000 m. It is a mostly sedentary species with small-scale elevational movements between breeding and non-breeding months.

Most authorities recognize three subspecies (*rhami*, *occidentalis*, and *saturatior*), but the status of these is contentious, with some claiming that the subspecies are either clinal, age-dependent, or both (Schuchmann and Boesman 2019). Until recently, patterns of intraspecific genetic and phenotypic variation were unknown, precluding validation or refutation of the current taxonomic treatment. A new study presents data that sheds light on genetic and phenotypic variation among populations within the *L. rhami* complex, in which the authors suggest the presence of two species.

New information:

Zamudio-Beltrán and Hernández-Baños (2018) conducted a phylogeographic study that also examined morphometric differences within the *L. rhami* species complex. This study sampled 54 individuals of two subspecies from 14 localities; *saturatior* was not sampled (Fig. 1). Zamudio-Beltrán and Hernández-Baños (2018) produced two data sets, including a 1402 bp mitochondrial data set (Control Region *CR*; and subunits 6 and 8 of ATPase) for all 54 *L. rhami* individuals. They also sequenced additional mtDNA (ND2 and ND4) and nuclear sequences (*BFib7*, *MUSK* introns 4 & 5, *ODC 6 & 8,* and *AK1*) for 31 of these individuals for a total alignment of 5069 bp.

The haplotype network constructed from mtDNA identified two groups separated by the Isthmus of Tehuantepec (Fig. 1). The group west of the Isthmus of Tehuantepec includes *L. r. occidentalis* and *L. r. rhami* from the Sierra Madre Oriental and Sierra Madre del Sur, whereas the group to the east includes *L. r. rhami* from Chiapas and the Guatemala Highlands. Interestingly, individuals of *L. r. rhami* are present in both haplogroups. However, the mtDNA haplogroups were not reciprocally monophyletic, although all populations west of the Isthmus of Tehuantepec did form a clade (Fig. 2).

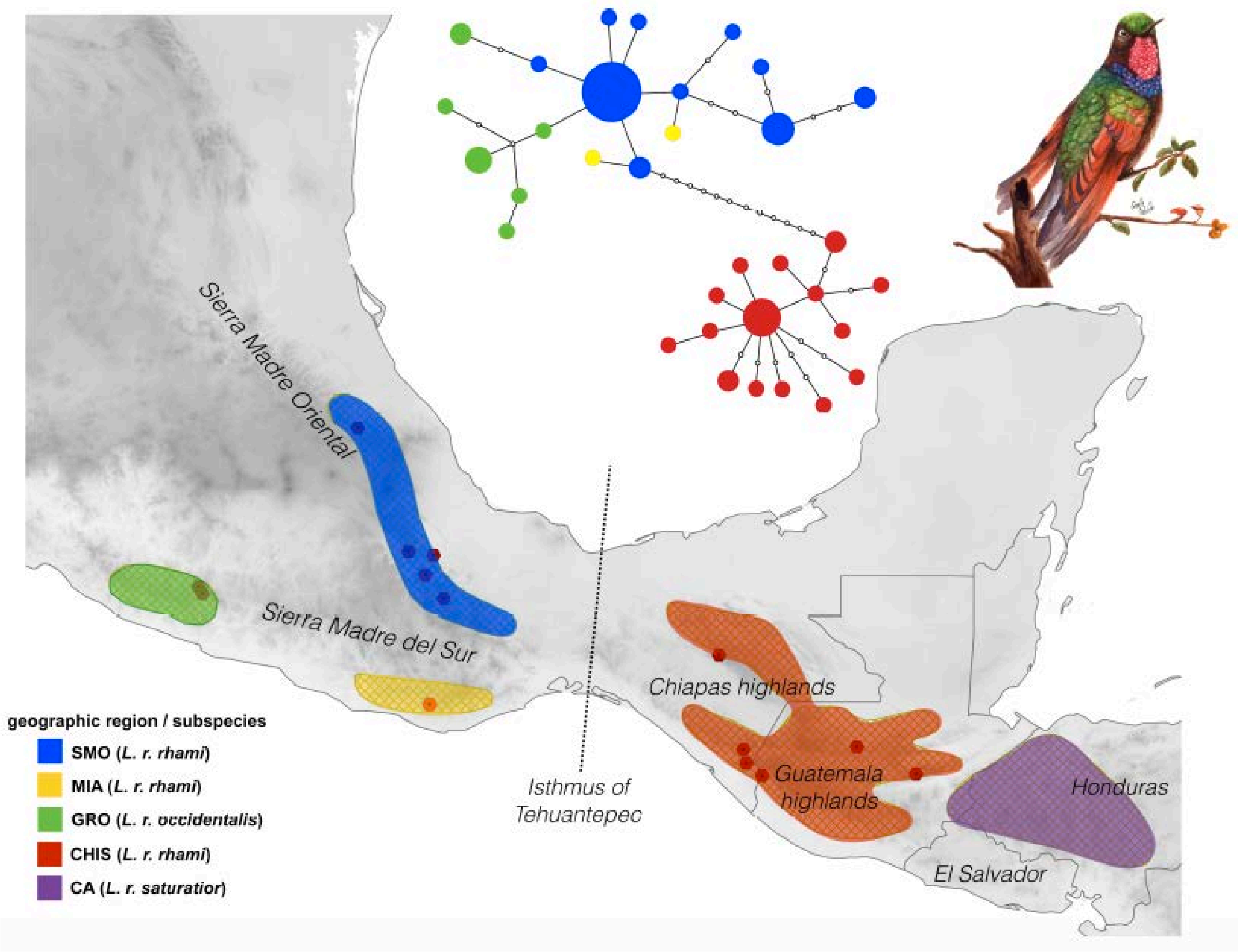

Figure 1: Distribution of Garnet-throated Hummingbird (*Lamprolaima rhami*) and sampling localities from Zamudio-Beltrán and Hernandez-Baños (2018). Mitochondrial haplotype network shown above.

Based on a Bayesian Phylogenetics and Phylogeography (BP&P) analysis of their multilocus dataset, the authors found support for a two-species delimitation scenario (Fig. 3) in which samples from the CHIS population (Chiapas and Guatemala highlands, orange in Fig. 1) was split from the remaining populations to the west of the Isthmus of Tehuantepec (Sierra Madre Oriental in blue; Guerrero Highlands in green; Sierra Made del Sur, Sierra of Miahuatlan in Oaxaca in yellow). Populations on either side of the Isthmus of Tehuantepec that form the putative species split approximately 200 kya (95% HPD: 90–317 kya).

The authors also found significant differences in morphology between populations east and west of the Isthmus of Tehuantepec. Specifically, males differed in bill width and wing chord while females differed in bill length. However, it is unclear whether these characters are diagnostic. The remaining phenotypic measurements did not differ significantly between populations east and west of the Isthmus of Tehuantepec.

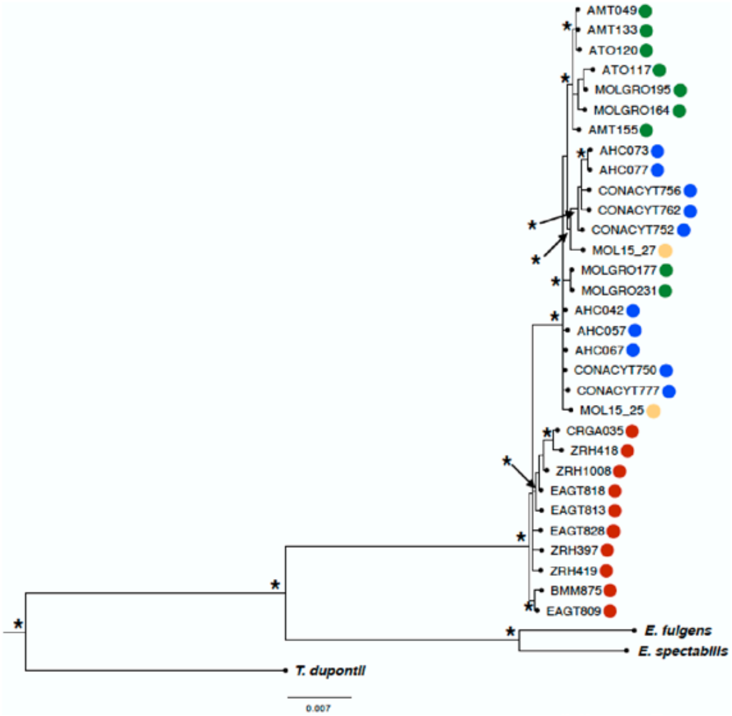

Figure 2: Concatenated phylogeny based on mtDNA and nuclear DNA. Posterior probabilities greater than 0.95 shown with an asterisk. Colors correspond to those used in Figure 1. Note lack of reciprocal monophyly and well supported nodes between populations east and west of the Isthmus of Tehuantepec.

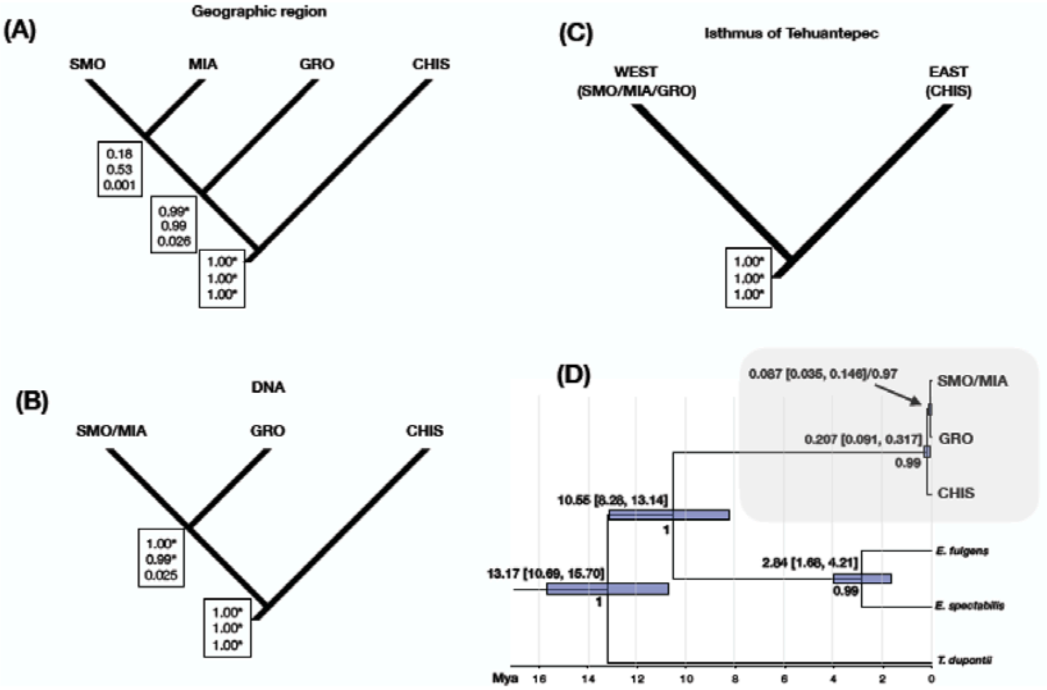

Figure 3: Results from BP&P species delimitation analysis. Panel D includes estimates of the timing of splits between subspecies or putative species.

Recommendation:

I recommend a "NO" vote on splitting *L. rhami* based on the data at hand. Differences in mtDNA and nuDNA alone are insufficient to support a taxonomic split under the BSC. The putative species are allopatric and are distributed on either side of the Isthmus of Tehuantepec, a well-studied biogeographic barrier in many groups of birds. However, the recent divergence of the putative species (~200 kya) and the slight phenotypic differences between them suggest that they would likely be able to interbreed should they come into secondary contact. The two phylogroups here are likely better considered as subspecies within the *L. rhami* complex.

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

Date of proposal: 15 August 2019

Recognize *Amazilia alfaroana* as a species not of hybrid origin, thus moving it from Appendix 2 to the main list

Effect on the NA Checklist:

A 'YES' vote on this proposal would transfer Guanacaste Hummingbird (*Amazilia alfaroana*) from Appendix 2 of the AOS Checklist, which includes 'forms of doubtful status or hybrid origin', to the main list. In doing so, the AOS would recognize *Amazilia alfaroana*, which is known solely from the holotype, as a valid taxon.

Background:

The Guanacaste Hummingbird (*Amazilia alfaroana*) is known from a single vouchered specimen (NHMUK 1898.3.12.13), collected on the Volcán de Miravalles of northwestern Costa Rica on 10 September 1895 (Underwood 1896: 441–442). Although described as a species, most authorities have recognized *A. alfaroana* as a form of *A. cyanifrons* (Carriker 1910, Ridgway 1911, Simon 1921, Peters 1945, Slud 1964, AOU 1983, Stiles and Skutch 1989), which is otherwise endemic to Colombia. The note on *alfaroana* in AOU (1998) reads as follows: "[known] only from the single specimen taken in Costa Rica and described as a new species, *A. alfaroana* Underwood, 1896. The type closely resembles *A. cyanifrons* and does not appear to be a hybrid between any Middle American species of *Amazilia*. The unique specimen of *alfaroana* is tentatively considered to represent a subspecies of *A. cyanifrons* (Stiles and Skutch 1989); its status can be clarified only by additional data."

More recently, Weller (1999) suggested that the species status of *A. alfaroana* could not be rejected and that its hybrid origin was unlikely. Weller (2001) subsequently argued for the recognition of *A. alfaroana* as a species separate from both *A. cyanifrons* and *A. saucerottei*. Weller (2001) noted that *A. alfaroana* possesses a distinctive iridescent turquoise-bluish cap, which is less well-defined than in *A. cyanifrons* and absent in *A. saucerottei*; and a bluish-green back, which lacks any of the strong bronze to copper tones seen in *A. cyanifrons* and *A. saucerottei*.

Shortly thereafter, the NACC moved *A. alfaroana* from the main list to Appendix 2 (forms of hybrid origin or doubtful status), accepting its removal from *A. cyanifrons* but stating that "its status as a species rather than a hybrid individual has not been adequately demonstrated" (Banks 2002).

Kirwan and Collar (2016) recently revisited the *A. alfaroana* holotype and collected mensural data, which they use as further support for the recognition of *A. alfaroana* as a distinct species.

New Information:

Kirwan and Collar (2016) measured the sole *A. alfaroana* specimen (originally recorded as a female, but now thought to be a male according to Weller 2001) in addition to two series of individuals from potential parental species, including *A. cyanifrons* (n = 11) and *A. saucerottei* (n

= 11). Kirwan and Collar (2016) found that the *A. alfaroana* holotype has a distinctly longer bill and tail than either of the putative parental taxa (Table 1).

TABLE 1. Comparative mensural data (in mm) for the holotype of *Amazilia alfaroana* (NHMUK 1898.3.12.13), Steely-vented Hummingbird *A. saucerottei hoffmanni* (*n* = 11, six males, five unsexed, Costa Rica and Nicaragua) and Indigo-capped Hummingbird *A. cyanifrons* (*n* = 11, all unsexed, Colombia). All specimens held at NHMUK and measured by GMK using a metal wing rule with perpendicular stop at zero and dial callipers: wing from carpal joint to tip, flattened against the ruler (to 0.5 mm); tail from pygostyle to tip (to 0.5 mm); and bill from tip of maxilla to skull (to 0.1 mm). Mean plus standard deviation (and range).

Taxon	bill	wing	tail
A. alfaroana	24.4	55.5	34
A. saucerottei hoffmanni	21.2 ± 0.89 (19.6–22.5)	54.8 ± 1.23 (53–57)	29.4 ± 1.48 (27–31)
A. cyanifrons	20.4 ± 0.82 (19.2–21.5)	55.5 ± 1.46 (53.5–57.0)	29.9 ± 1.98 (27–32)

Kirwan and Collar (2016) also noted qualitative differences in *A. alfaroana* compared to *A. cyanifrons* and *A. saucerottei* (Figure 1). Specifically, *A. alfaroana* has a paler blue and more restricted crown patch compared to a more saturated blue and extensive crown patch in *A. cyanifrons* and no crown patch in *A. saucerotti*. Furthermore, *A. alfaroana* has a more continuous gradient of green to white as the chin transitions to the belly, while *A. cyanifrons* has narrow whitish edges that form more of a scaled pattern. Finally, *A. alfaroana* has bluish-black (dark-blue steel *sensu* Underwood 1986) undertail-coverts with narrow whitish feather edges compared to mid-gray with broad whitish edges in both *A. cyanifrons* and *A. saucerottei*.

Importantly, *A. saucerottei hoffmanni* occurs at the locality from which *A. alfaroana* was collected, which led Kirwan and Collar (2016) to consider other potential parental types from the area, including Long-billed Starthroat (*Heliomaster longirostris*), Crowned Woodnymph (*Thalurania colombica*), Purple-throated Mountain-gem (*Lampornis calolaemus*), Fiery-throated Hummingbird (*Panterpe insignis*), and Violet-headed Hummingbird (*Klais guimeti*). Kirwan and Collar (2016) noted that none of these putative parentals have the same shade of blue in their crown as *A. alfaroana* and that many are much larger or have different bill shapes. Furthermore, *A. alfaroana* lacks the distinctive plumage characters of the aforementioned putative parental species, such as the throat coloration of *P. insignis* or the purple gorget of *H. longirostris*.

Based on the distinctive mensural and qualitative plumage characters of *A. alfaroana* and the lack of clear candidates for parental taxa, Kirwan and Collar (2016) argued that the current evidence best supports species status for *A. alfaroana*. Notably, however, searches for other individuals that bear resemblance to *A. alfaroana* have been unsuccessful, albeit limited (e.g., Stiles and Skutch 1989). Although tracts of suitable habitat appear to remain intact in the Pacific slope of the Tilarán Highlands where it was first collected (Kirwan and Collar 2016), *A. alfaroana* may have simply gone extinct since its initial description. Nonetheless, Kirwan and Collar (2016) call into question the NACC's decision to list *A. alfaroana* as a taxon of hybrid origin based on their analyses and recommend its treatment as a distinct species.

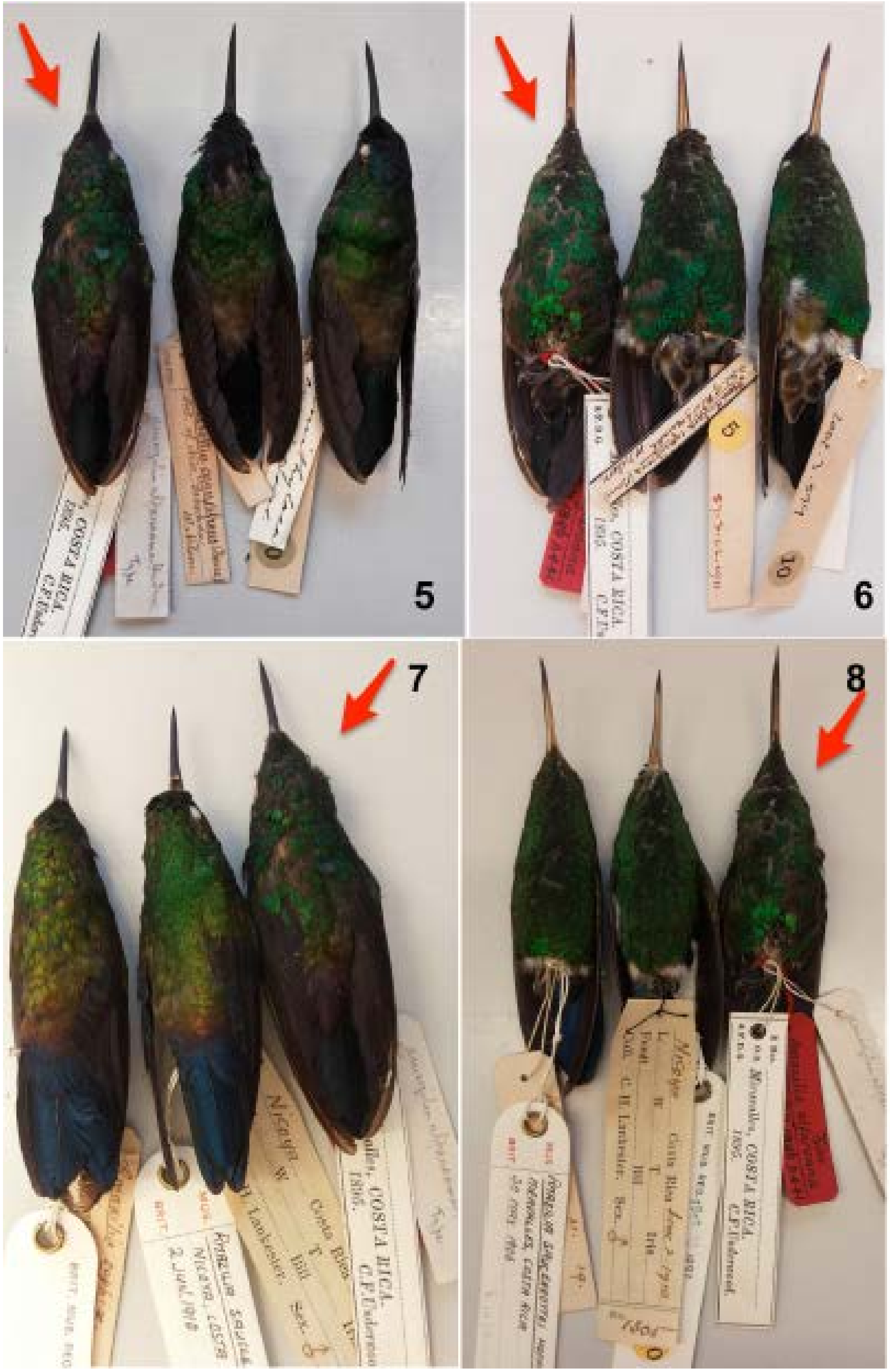

Figure 1. Photographs from Kirwan and Collar (2016) illustrating qualitative plumage differences between A. *alfaroana* and putative parental taxa *A. cyanifrons* and *A. saucerottei*. Red arrows indicate *A. alfaroana* in each frame.

Recommendation:

Although the data presented by Kirwan and Collar (2016) suggest that *A. alfaroana* is phenotypically distinctive and not a hybrid between *A. cyanifrons* and *A. saucerottei*, its status remains unclear. Genetic data would go a long way to resolve whether the holotype is some strange, uncommon hybrid or variant or alternatively the sole representative of a relictual or extinct lineage. Until surveys discover additional individuals or genetic data confirming its evolutionary distinctiveness is reported, I personally feel it should retain its status as a dubious taxon in Appendix 2 of the NACC and recommend a "NO" vote on this proposal.

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

Date of proposal: 15 August 2019

2020-A-6 N&MA Classification Committee pp. 123-124

Change the linear sequence of species in the genus *Dendrortyx*

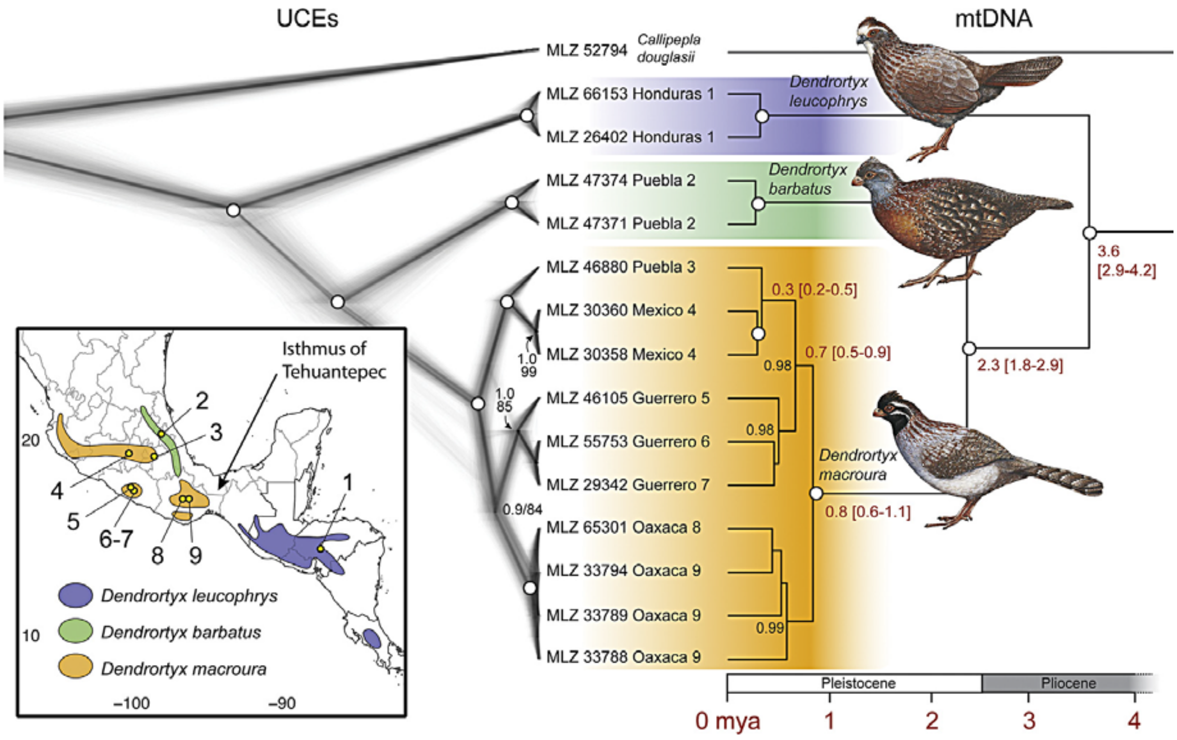
Background:

The genus *Dendrortyx* (wood partridges) consists of three species endemic to the highlands of Mexico and Central America. The current linear sequence of these species is:

Dendrortyx barbatus (Bearded Wood-Partridge, Colin barbu)
Dendrortyx macroura (Long-tailed Wood-Partridge, Colin à longue queue)
Dendrortyx leucophrys (Buffy-crowned Wood-Partridge, Colin à sourcils blancs)

New Information:

Tsai et al. (2019) published a phylogenetic study of *Dendrortyx*, sampling 14 individuals for genomic nuclear (UCEs) and mitochondrial DNA. Separate analyses of their nuclear and mitochondrial data resulted in trees with virtually identical topologies:



Both nuclear and mitochondrial trees show that *barbatus* and *macroura* are sister species, and that *leucophrys* is sister to *barbatus*/*macroura*. Because *leucophrys* is sister to the rest of the genus, and because the distribution of *macroura* extends further northwest than that of *barbatus*, our linear sequencing guidelines require a reversal of our current linear sequence to:

Dendrortyx leucophrys (Buffy-crowned Wood-Partridge, Colin à sourcils blancs)
Dendrortyx macroura (Long-tailed Wood-Partridge, Colin à longue queue)
Dendrortyx barbatus (Bearded Wood-Partridge, Colin barbu)

Recommendation:

I recommend that we make this minor change.

Literature Cited:

Tsai, W. L. E., C. Mota-Vargas, O. Rojas-Soto, R. Bhowmik, E. Y. Liang, J. M. Maley, E. Zarza, and J. E. McCormack. 2019. Museum genomics reveals the speciation history of *Dendrortyx* wood-partridges in the Mesoamerican highlands. Molecular Phylogenetics and Evolution 136: 29-34.

Submitted by: Terry Chesser

Date of Proposal: 23 August 2019

Make two changes concerning *Starnoenas cyanocephala*: (a) assign it to the new monotypic subfamily Starnoenadinae, and (b) change the English name to Blue-headed Partridge-Dove

Background:

The Blue-headed Quail-Dove, *Starnoenas cyanocephala* (Columbiformes), is endemic to Cuba, with records from Jamaica and Florida most likely resulting from human introduction (Olson and Wiley 2016). Once common and widespread across the island, its populations have declined significantly due to habitat destruction and excessive hunting and trapping for food, and its current conservation status is 'Endangered' (BirdLife International 2016).

Described as *Columba cyanocephala* by Linnaeus in 1758, the species was placed in its own genus by Bonaparte in 1838. Subsequent authors have recognized a series of anatomical traits that distinguish *S. cyanocephala* from most New World doves and pigeons, including:

- absence of uropygial gland and of ambiens muscle, and presence of intestinal caeca (Garrod 1874, Coues 1884);
- reticulate tarsus, in which the tarsus is covered by small hexagonal scales instead of a series of plate-like scutes as in the rest of the genera in the Columbidae, except for *Goura* (Coues 1884);
- the size and shape of sternum (Shufeldt 1891, Verheyen 1957);
- eutaxic wing, in which the fifth secondary feather in the wing is present, contrary to the diastataxic wing, in which absence of this feather creates a space or diastema[1] (Verheyen 1957);
- notarium (fusion of thoracic vertebrae) consisting of four fused vertebrae (Verheyen 1957).

Curiously, these characteristics are shared with several Australasian and Old World species, to the point that *S. cyanocephala* has been grouped with some Australasian genera (Salvadori 1893, Beddard 1898, Peters 1937). Verheyen (1957) maintained *Starnoenas* in a separate subfamily, 'Starnoenaninae', based on the traits previously mentioned and other morphological characters.

Other authors considered these traits to be enough to keep *S. cyanocephala* in its own genus but not to question its affinities to New World columbids (Goodwin 1958, Bond 1982). Its English name reflects the fact that several authors considered it closely related to species in the genera *Geotrygon, Zentrygon* and *Leptotrygon* (the latter two formerly considered part of *Geotrygon*; Banks et al. 2013). However, the AOU Checklist Committee recognized that the "phylogenetic relationships of this species within the Columbidae are uncertain" (Chesser et al. 2014:CSv).

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[1] The eutaxic or diastataxic condition of the wings usually characterizes entire families or orders, and the Columbidae is one example of family polymorphic for this trait (Bostwick and Brady 2002).

New information:

Olson and Wiley (2016) performed an extensive description of the plumage coloration, anatomy, and behavior of *S. cyanocephala* based on previous literature, examination of collection material, and personal observations. They revisited and expanded the information summarized before, and added new information highlighting how anomalous *S. cyanocephala* is compared to other New World columbids. Unfortunately, they had no information on genetic relationships to other columbids, because no genetic study of Columbidae had included *Starnoenas*, and this has not changed since publication of their paper three years ago.

Olson and Wiley (2016) first focused on *S. cyanocephala* due to the distinctive configuration of its carpometacarpus, which according to the authors is similar to that of species in the order Galliformes (the minor metacarpal is distinctively bowed, creating a broad intermetacarpal space; see Figure 6 in Olson and Wiley 2016). The authors considered that the galliform-like configuration of the carpometacarpus may also be related to the rapid, noisy take-off that characterizes escape locomotion in *S. cyanocephala* (see below).

Starnoenas cyanocephala is almost strictly terrestrial, and only takes a short, low flight when frightened, with a noisy take-off that resembles that of partridges and distinguishes it from other quail-doves (Garrido 2005). This rapid take-off is another characteristic shared with Australian species (Boles 1999), a behavior that previous authors have related to the morphology of the sternum. Australian columbids in the genera *Petrophassa* and *Geophaps* show a sternal morphology similar to that of some partridges (see Figure 1 in Boles 1999). Once again, the sternum of *S. cyanocephala* is much more similar to that of an Australian species, *Petrophassa smithi*, than to those of other New World columbids, with a narrower and much longer corpus; longer, slender lateral margin of the anterior notches; and small, narrow posterior notches (see Figure 4 in Olson and Wiley).

Olson and Wiley (2016) also described the courtship behavior of *S. cyanocephala*, concluding that it shares more components with the mating behavior of columbids in the ‘bronzewing’ group and allies, in the genera *Geopelia, Phaps, Ocyphaps,* and *Geophaps*. Particularly interesting is the bowing movement of the male, during which his neck is withdrawn into his shoulders, and his head and neck colors are fully presented to the female (Olson and Wiley 2016). The most distinctive plumage markings in *S. cyanocephala* are concentrated in the head, neck and chest. The front of the head and the crown are bright blue, surrounded by a black band continuous from the bill across the eyes and around the back of the head. Below the black band, a white stripe extends from the bill to the neck but not continuously around the back of the head; below the white stripe another thin black line runs from the throat to the side of the head. A black patch surrounded by a white stripe extends from the throat onto the upper breast. The imbricated furrows of feathers of the neck around the margin of the black patch are also blue. Goodwin (1958) considered the head coloration of *S. cyanocephala* to be very similar to that of *Geotrygon frenata* and *G. linearis*, “except for the blue (instead of bluish grey) on the head and the rather different shade of brown on the upperparts” (Goodwin 1959: 333). However, no other New World columbids show similar patterning, except for some species of *Geotrygon* and *Zentrygon*, in which a distinctly colored crown or a distinct subocular white stripe and underlying black line is present (Olson and Wiley 2016). In this sense, the Australian species *Geophaps plumifera* and *G. smithii* are much more similar to *S. cyanocephala* than are New World species.

Recommendation:

In my view, the evidence gathered by Olson and Wiley (2016), although intriguing, is not conclusive regarding the systematic affinities of *S. cyanocephala*. As they recognized, it would be challenging to explain a close relationship to the Australian or other Old World species. Considering this difficulty, a genetic assessment of the affinities of *S. cyanocephala* would be fundamental before considering any taxonomic change. The NACC currently recognizes no subfamilies in the Columbidae, so recognizing Starnoenadinae would imply also recognizing one or more subfamilies to include the rest of the species in the family. I consider the data presented by Olson and Wiley (2016) insufficient to make such a major change and I recommend voting NO on part (a), the proposal to assign *S. cyanocephala* to a new subfamily.

Olson and Wiley (2016) also proposed to change the English name of *S. cyanocephala* because ‘‘quail-dove’’ is currently used for species in the genera *Geotrygon, Zentrygon* and *Leptotrygon,* and they consider all New World columbids more similar to one another than any one of them is to *S. cyanocephala*. Again, I think a genetic assessment of the affinities of *S. cyanocephala* should be made before making this change. Therefore, I also recommend voting NO on part (b), the proposal to change the English name of *S. cyanocephala* to Blue-headed Partridge-Dove.

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Submitted by: Natalia C. García, Fuller Evolutionary Biology Program - Cornell Lab of Ornithology, Cornell University.

Date of Proposal: 25 August 2019

Recognize Mexican Duck *Anas diazi* as a species

Background:

The NACC considered this issue recently via the notably comprehensive proposal 2018-C-10 submitted by Tom Schulenberg. That proposal resulted in substantial debate and ultimately received three votes of YES and seven votes of NO by the members of the NACC.

This proposal is intended as an addendum to the material presented in 2018-C-10 to reflect new genomic results not available at that time. For full background on this topic please see 2018-C-10 and its associated comments.

Much of the ongoing uncertainty about this potential split results from contrasting interpretations of the degree of differentiation among *diazi* and its very close relatives in the mallard complex, and particularly the extent of past and present hybridization and introgression between *diazi* (Mexican Duck) and *platyrhynchos* (Mallard) in their zone of contact in the southwestern USA and in northern Mexico.

At the time of proposal 2018-C-10, the available genomic data were generally uninformative; as outlined in that proposal: "Lavretsky et al. (2014a) considered variation across *platyrhynchos*, *diazi*, *A. fulvigula* (Mottled Duck), and *A. rubripes* [American Black Duck] in 17 nuclear introns, and Lavretsky et al. (2015) conducted genomic scans of 3532 autosomal loci. The general pattern was for nuNDA to show little resolution, not only between *diazi* and *platyrhynchos*, but also between these two taxa and nominate *fulvigula*, *A. fulvigula maculosa*, and *rubripes* (but see also Lavretsky et al. 2014b)."

New Information:

A new paper by Lavretsky et al. (2019) examines differentiation among members of the North American mallard complex using a ddRAD-seq dataset of 3200 loci. Figure 1 summarizes the results that are most germane to the taxonomic status of *diazi*.

Some of the main take-aways from this figure include the clear separation of *diazi* (MEDU in Fig. 1) in both the PCA and the ADMIXTURE analyses. In panel b, the ADMIXTURE plot for different values of K (in this type of analysis, K is a pre-set value of how many populations to which individuals can potentially be assigned; K=2 means that all variation is partitioned into two populations, K=3 assumes three populations, etc.) *diazi* stands out as very cleanly separated at K=4 and K=5, which are the most biologically realistic K values for this situation. This panel can also be interpreted to show that *diazi* (MEDU) is more diagnosably differentiated from *platyrhynchos* (MALL) than is *rubripes* (ABDU) from *platyrhynchos.*

In addition to the ADMIXTURE analysis, which separated the five taxa genetically, Lavretsky et al. (2019) analyzed their data using fineRADstructure, which emphasizes recent coancestry. In that analysis, the five taxa were again separated, as in the ADMIXTURE analysis, with no individual *diazi* having higher coancestry with individuals from *platyrhynchos*, *rubripes*, or *fulvigula* as compared to other *diazi* individuals in the dataset. In the dendrogram depicting relationships among the samples, *diazi* appeared to be sister to a clade that included *rubripes* and *platyrhynchos*. Further, fineRADstructure did not detect any *diazi* samples that showed evidence of recent admixture.

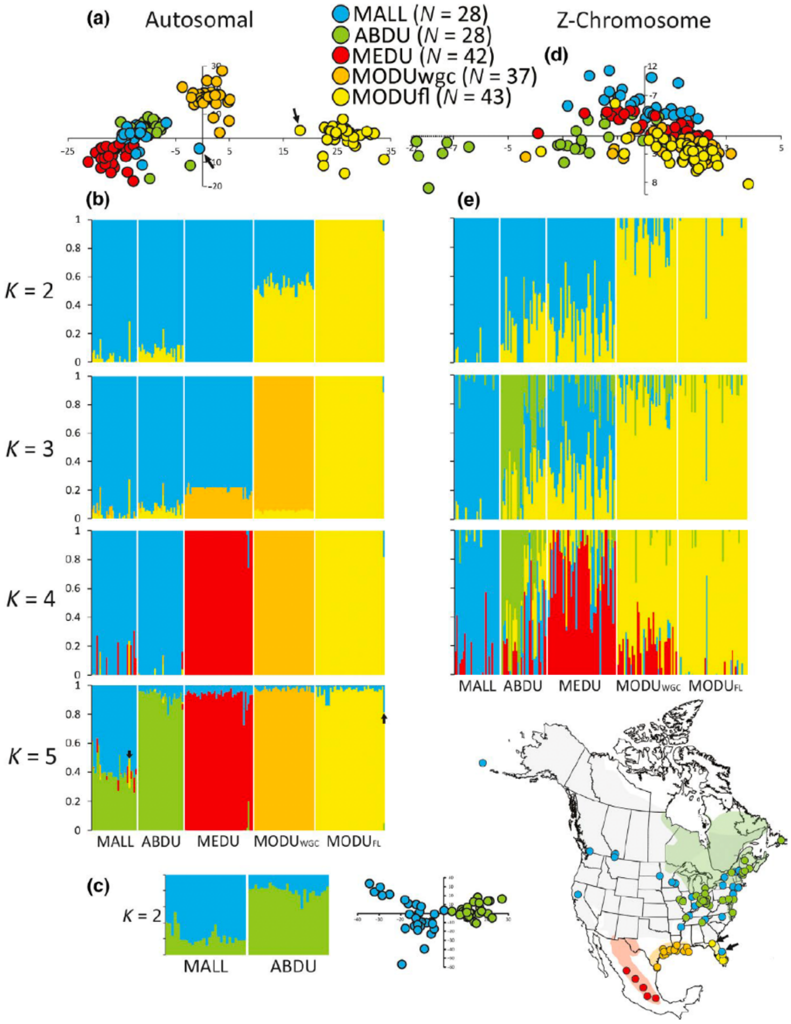

FIGURE 1 Lower right: breeding distributions (adapted from Baldassarre, 2014) and sampling localities are colour coded for mallards (blue), American black ducks (green), Mexican ducks (red), Florida mottled ducks (yellow), and West-Gulf Coast mottled ducks (orange) (Table S1). Principal component analyses (PCA, PC1 on the x-axis, PC2 on the y-axis; top, left) for (a) autosomal and (d) Z-linked loci (*N* = number of samples). ADMIXTURE results for (b) 3,017 autosomal loci and (e) 177 Z-linked loci. (c) PCA and ADMIXTURE analyses for mallards and black ducks only. Arrows highlight two samples consistently identified as admixed across PCA, ADMIXTURE, and fineRADstructure (see Figure 3) analyses

Finally, Lavretsky et al. (2019) investigated signatures of selection and patterns of differentiation across the genome. They detected outlier loci on the Z-chromosome between *diazi* and *platyrhynchos*, as a well as a significant outlier locus on chromosome 14 between *diazi* and all other members of the Mallard complex in North America, suggesting directional selection in *diazi* relative to all other taxa at this or a linked locus. This particular region contained an allele that was fixed, or nearly fixed, in *diazi*, and rare or absent in all other taxa.

As an aside, there is also highly diagnosable differentiation between the two disjunct *fulvigula* (Mottled Duck) populations in all analyses, but that topic is outside the scope of this proposal.

In general, these results substantially bolster the argument that *diazi* is distinct from *platyrhynchos.* As summarized by Lavretsky et al. (2019):

> In general, our results are at odds with expectations for a group of birds known for high rates of hybridization (Baldassarre, 2014; Ottenburghs, Ydenberg, Van Hooft, Van Wieren, & Prins, 2015). Secondary contact between various monochromatic taxa and the dichromatic mallard has long been assumed to result in high rates of hybridization (Champagnon et al., 2013; Guay & Tracey, 2009; Lavretsky, Hernández Baños, et al., 2014a; US Fish & Wildlife Service, 2013), and in some cases, concern about the possibility of genetic extinction (Rhymer, 2006; Rhymer & Simberloff, 1996). Moreover, high rates of gene flow have been invoked to explain similar levels of molecular variation despite substantial differences in known census sizes (Table 1; Avise et al., 1990; Lavretsky et al., 2015; Lavretsky, McCracken, et al., 2014b; McCracken et al., 2001; Peters et al., 2014). Our results, however, suggest that none of the sampled groups are extensively admixed based on f3-statistics (Table S4), let alone being at risk for merging into a hybrid swarm. Whereas TreeMix identified gene flow from mallards into either Mexican ducks or black ducks in two different data partitions (Figure 7; Table S3), f4-statistics were equivocal with respect to rejecting a null hypothesis of no gene flow involving mallards (Table S4). In addition, other recent studies have detected a relatively low frequency of hybrids and/or recent backcrosses—for example, between mallards and either mottled ducks (~5%; Peters et al., 2016; Ford et al., 2017) or Mexican ducks (~2%; Lavretsky et al., 2015). Thus, although hybridization is known to occur between mallards and each of the monochromatic species, our results suggest that contemporary gene flow and introgression may be lower than assumed.

However, there remain at least two caveats in Lavretsky et al. (2019) that keep this from being a clear-cut case for recognizing *diazi*. One is that several types of analyses suggested evidence of some gene flow between *diazi* and *fulvigula* (but note that this is between Mexican and Mottled ducks, not Mexican Ducks and Mallards). Another is that Lavretsky et al. (2019) noted specifically that "*we intentionally avoided sampling in geographic regions where mallards and Mexican ducks come into contact…*", which makes great sense given the main goals of their study, but which leaves open the question of how much genetic interchange is happening within that contact zone. However, it is notable that their more southerly (= sampled) *diazi* populations show little genomic evidence for past hybridization with *platyrhynchos*. A reasonable interpretation is that if there is substantial ongoing hybridization within the contact zone, it is quite recent and/or subject to some form of postzygotic fitness cost. Otherwise, mallard genetic variants should be diffusing into these more southerly Mexican Duck populations.

Recommendation: We recommend that the committee revisit this proposed split in light of the new genomic data. This remains a grey-zone situation in which both outcomes are taxonomically reasonable given the modest overall differentiation and the presence of at least some ongoing hybridization, but the case for splitting is now arguably a bit stronger than previously. Given that the NACC has chosen to split other forms within this complex that show similar or lesser levels of differentiation and greater levels of genetic interchange, we recommend that the NACC recognize *diazi* at the species level.

Literature Cited:

Lavretsky, P., J. M. DaCosta, M. D. Sorenson, K. G. McCracken, and J. L. Peters. 2019. ddRAD-seq data reveal significant genome-wide population structure and divergent genomic regions that distinguish the Mallard and close relatives in North America. Molecular Ecology DOI: 10.1111/mec.15091

Submitted by: Irby Lovette and Shawn M. Billerman

Date of Proposal: 28 August 2019

Split Royal Tern *Thalasseus maximus* into two species

Background:

Royal Tern (*Thalasseus maximus*) is comprised of two subspecies, one in the Americas and one in Africa. The nominate subspecies breeds from the Atlantic Coast in North America south to the Gulf of Mexico and the Caribbean, to northern South America, and locally on the Pacific Coast in southern California and Sinaloa, Mexico. A disjunct austral population breeds from southern Brazil south to Chubut, Argentina. The other subspecies, *T. m. albididorsalis*, breeds locally in western Africa, being most concentrated in coastal Mauritania, but also around Senegal and Gambia, and likely extending east to Nigeria. The two taxa are similar, and the validity of the subspecies has sometimes been questioned (Gochfeld et al. 2019). However, they differ in some key traits. First, *albididorsalis* has a shallower and paler bill than *maximus*; in particular, *albididorsalis* lacks a strong gonydeal angle, and the bill color tends to be more yellow-orange as opposed to red-orange (Buckley and Buckley 2002). In addition, *albididorsalis* averages smaller in mass, but with longer wings, resulting in a smaller wing/bill ratio (Buckley and Buckley 2002; Gochfeld et al. 2019), and the tail fork is shallower in *albididorsalis* (Olsen and Larsson 1995). West African *albididorsalis* is also paler than nominate *maximus* (Gochfeld et al. 2019). Buckley and Buckley (2002) noted that *albididorsalis* is morphologically more similar to austral populations of *maximus*, both having longer, thinner bills that are more yellow-orange, compared to the heavier, red-orange bills of northern populations of *maximus*.

New Information:

Collinson et al. (2017) sequenced mtDNA and nuclear DNA to clarify the relationships of the Royal Tern with respect to the other species in the genus *Thalasseus*, a group that has been notoriously challenging to classify. In a concatenated phylogeny of three mtDNA genes (*COI, ND2,* and *cytb*), well-resolved relationships were recovered within *Thalasseus*: West African *albididorsalis* was sister to the Lesser Crested Tern (*T. bengalensis*) with strong support (posterior probability of 0.99; Fig. 1a), whereas nominate *maximus* was sister to the clade containing both *albididorsalis* and *bengalensis*, also with strong support (posterior probability of 0.99; Fig. 1a). Divergence between *albididorsalis* and *maximus* based on the three mtDNA genes varied between 1.1% and 1.5%, corresponding to 400-500,000 years of divergence (Collinson et al. 2017). A concatenated phylogeny based on 7 nuclear genes recovered very similar relationships within *Thalasseus*. Specifically, West African *albididorsalis* was found to be sister to *bengalensis* with very strong support (99/100 bootstrap support; Fig. 1b), with nominate *maximus* in turn sister to them (albeit with lower support, 83/100 bootstrap support; Fig. 1b).

Note that *Thalasseus* and terns in general include various species-level taxa which are notoriously similar morphologically (Sandwich Terns, Antarctic/Arctic terns, etc.). It is a group in which similar morphology does not always signify a close relationship (again see the “Sandwich” Terns). As such, it is a group in which molecular data is particularly helpful in unraveling taxonomic issues.

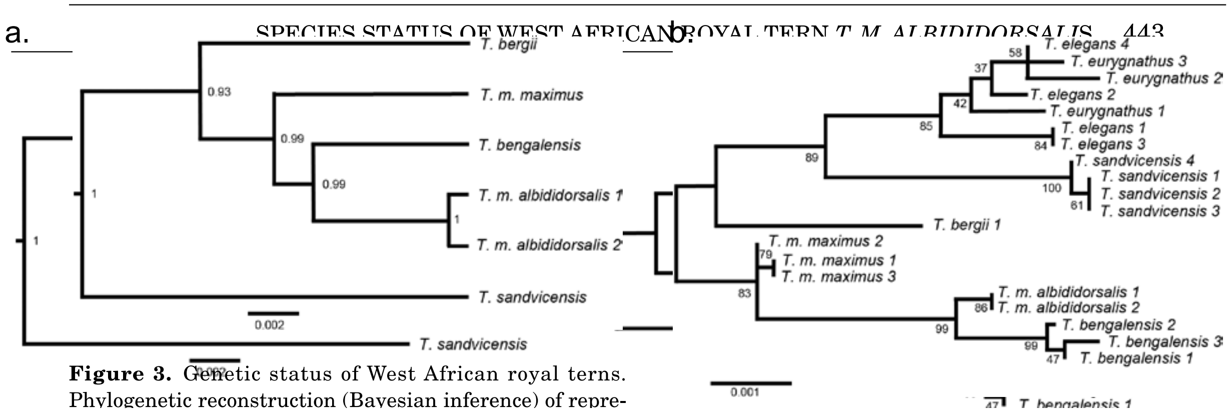

Figure 1. Adapted from Collinson et al (2017), Figs. 3 and 4. A) Concatenated mtDNA phylogeny (2448 bp of *cytb*, *COI*, and *ND2*), with statistical support for each node shown. Phylogeny based on Bayesian inference. B) Concatenated nuclear DNA phylogeny (4549 bp of 7 genes) using Maximum Likelihood, with bootstrap support shown for each node.

Recommendation:

We recommend that the committee vote to split the two subspecies of Royal Tern based on the results in Collinson et al. (2017) that suggest that African *albididorsalis* is more closely related to Lesser Crested Tern than to nominate *maximus*, in addition to known morphological and biogeographical differences. Although they are morphologically similar, they do differ in subtle traits. Collinson et al. (2017) further argued that the results they obtained are likely not the result of introgression between *albididorsalis* and *bengalensis*, given the concordance of the mtDNA and nuclear DNA datasets.

Perhaps owing to their extreme similarity, no common names have previously been proposed for either of the two daughter taxa. The African form is restricted in range and is found where few birders interact with them. The American form, on the other hand, is widespread and common and is also the nominate subspecies. We suggest keeping the current English name for the American form (Royal Tern) and creating a new name for the African species. Given that *albididorsalis* is sister to Lesser Crested Tern and that “crested tern” is associated with the genus *Thalasseus* (although admittedly “crested tern” does not designate a monophyletic group), we think African Crested Tern or West African Crested Tern (the name suggested at https://www.worldbirdnames.org/updates/proposed-splits/) would be appropriate English names, but we should leave this to others to decide. We do not believe that the two species should be called American Royal Tern and African (or West African) Royal Tern, in part because this would imply a sister relationship that does not exist. Not changing the familiar name Royal Tern, widely used for the common American form, is another key here, as it will minimize confusion and maximize name stability.

There are no records of *albididorsalis* for North or South America. Vagrants in western Europe, mostly in Spain, are thought to represent *albididorsalis*, while others, especially those from Ireland, Britain, Norway, and Portugal may represent nominate *maximus*. At least two birds banded in North America have been recovered in Wales (Buckley and Buckley 2002).

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Collinson, J. M., P. Dufour, A. A. Hamza, Y. Lawrie, M. Elliott, C. Barlow, and P-A. Crochet. 2017. When morphology is not reflected by molecular phylogeny: the case of three 'orange-billed terns' *Thalasseus maximus*, *Thalasseus bergii*, and *Thalasseus bengalensis* (Charadriiformes: Laridae). Biological Journal of the Linnean Society, 121: 439-445

Gochfeld, M., J. Burger, and E. F. J. Garcia. 2019. Royal Tern (*Thalasseus maximus*). In: del Hoyo, J., A. Elliott, J. Sargatal, D. A. Christie, and E. de Juana (eds). Handbook of the Birds of the World Alive. Lynx Edicions, Barcelona

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Submitted by: Shawn M. Billerman and Alvaro Jaramillo

Date of Proposal: 29 August 2019

Recognize Great White Heron *Ardea occidentalis* as a species

Effect on the NA Checklist:

This would elevate to species rank a taxon formerly treated as a separate species (Great White Heron *Ardea occidentalis*).

Background:

The Great White Heron was treated as a species separate from Great Blue Heron (*Ardea herodias*) from its original description for more than a century through 1973, when AOU lumped it with Great Blue Heron based on evidence summarized in McGuire et al. (2019).

New information:

In the interest of streamlining proposals, I am not going to lay out all the details and will assume that committee members will read McGuire et al. (2019), where all the critical data are presented from the contact zone between the taxa.

The key points in my opinion are as follows:

1. The evidence for the 1973 lump was weak at best.

2. The notion that Great White Heron (GWHE) is a color morph of Great Blue Heron (GBHE) is convincingly dismantled.

3. The former recognition of the Würdemann's Heron (intermediate between GBHE and GWHE in plumage) as a valid subspecies has caused great confusion. It occurs entirely within the range of GWHE and represents gene flow between GBHE and GWHE. It continues to confound interpretation of the situation.

4. Mating between white birds and any individuals with blue plumage (a continuum of plumage phenotype from phenotypically pure GBH through the Würdemann's plumage type) was significantly non-random, i.e. assortative, e.g. 97 of 114 pairs (85%) were pure white-white or blue-blue.

Analysis and Recommendation:

As McGuire et al. emphasized, this is one of those inevitable borderline situations that create havoc for categorical classification schemes. McGuire et al. would be the first to point out that the situation is incompletely understood. However, here is what is known from the available evidence: when given the chance to pair, white birds pick white birds and blue birds pick blue birds to a much greater degree than expected by chance. In other words, these two taxa regard each other as "different" when it comes to mate choice. Thus, gene flow is reduced by assortative mating, and thus the two taxa should be ranked as separate species according to the most frequently applied operational definition of the BSC. I think the data are sufficient to place the burden-of-proof on treatment as the same species. Further, the data used to lump the two were woefully inadequate by modern standards, and the decision to lump them was a manifestation of the eagerness to do so in the Lumperama era.

In a comparative framework, the contact zone between these two resembles empirically that of Lazuli and Indigo buntings, Rose-breasted and Black-headed grosbeaks, White and Scarlet ibises, and others that we treat as separate species: gene flow is substantial but far from “free”; the contact zone is strongly dominated by phenotypically pure birds, and the frequency of mixed pairs is low. Free gene flow would produce a hybrid swarm at the contact zone; after 10 generations of free interbreeding, the chances of finding any pure birds in a closed system would be less than 1% (vs. at least 85% empirically in this system). Of course the real world contact zone is not a closed system, yet the level of immigration required to maintain 85% pure phenotypes seems unreasonably high.

English name:

Ardea occidentalis was known as Great White Heron throughout its history; it is an appropriate name, and I see no reason to change it. As for considerations for new names due to splitting daughter species from parent, there is no need to do so under C.3 in our draft English names guidelines.

Literature Cited:

McGuire, H. L., S. S. Taylor, and F. H. Sheldon. 2019. Evaluating the taxonomic status of the Great White Heron (*Ardea herodias occidentalis*) using morphological, behavioral and genetic evidence. Auk 136: uky010. https://doi.org/10.1093/auk/uky010

Submitted by: Van Remsen

Date of Proposal: 29 August 2019

Change the English name of Checker-throated Antwren *Epinecrophylla fulviventris* to Checker-throated Stipplethroat

The South American Classification Committee has changed the English names of all species in the genus *Epinecrophylla* from Something Antwren to the novel Something Stipplethroat. The rationale for this is complicated and derives largely from the problem created by multiple species splits in the genus that created severe English name problems, i.e., the desire to avoid cumbersome compound names or misleading non-compound names. See the SACC proposal (http://www.museum.lsu.edu/~Remsen/SACCprop696.htm) for details. This proposal went through three iterative modifications – a lot of work for something so trivial, but there was no easy way to avoid this, and our rationale was that as long as a change was needed, it was worth the effort to have the best outcome.

For the NACC area, only 1 of the 8 species in the genus is involved, and this species is shared with SACC: *Epinecrophylla fulviventris*, currently Checker-throated Antwren in NACC, Checker-throated Stipplethroat in SACC.

To resolve this conflict, I recommend following SACC on this, if only because this is overwhelmingly a SACC genus. Also, "antwrens" no longer form a monophyletic group, and thus Antwren is yet another English name that refers only to a morphotype. The novel English name Stipplethroat allows a 1-to-1 correspondence between a well-marked genus and an English name (increasingly difficult to do), one that also. highlights the main phenotypic difference between most species in *Epinecrophylla* from other species called Antwren. Thus, the new name carries phylogenetic and near-diagnostic plumage information

See the SACC proposal, especially the extensive comments, if interested in the details. This change would fall under C.4 of our draft English name guidelines.

Submitted by: Van Remsen

Date of Proposal: 3 September 2019

Modify the linear sequence of species in the Phalacrocoracidae

Background and New Information:

Our current classification of the Phalacrocoracidae is as follows:

Phalacrocorax penicillatus
Phalacrocorax brasilianus
Phalacrocorax auritus
Phalacrocorax carbo
Phalacrocorax urile
Phalacrocorax pelagicus

Kennedy and Spencer (2014) produced a new hypothesis for relationships in the family based on DNA sequence data. Nodes in their tree (see below) were generally strongly supported:

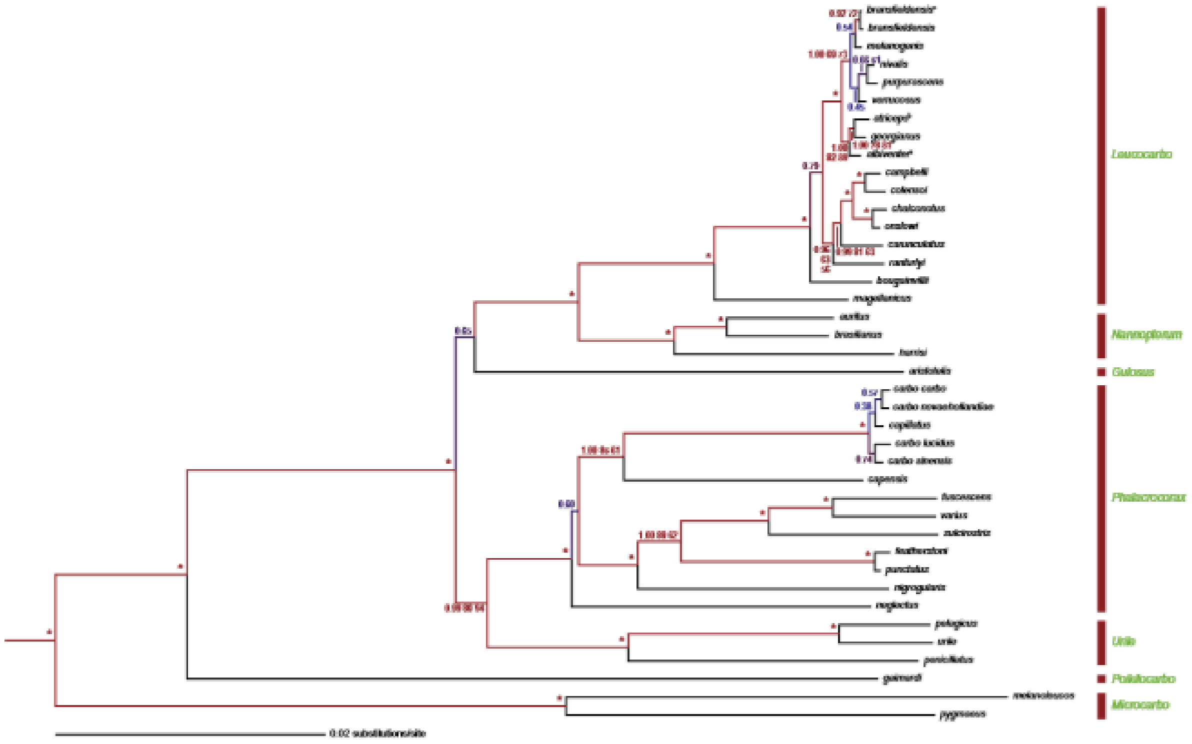
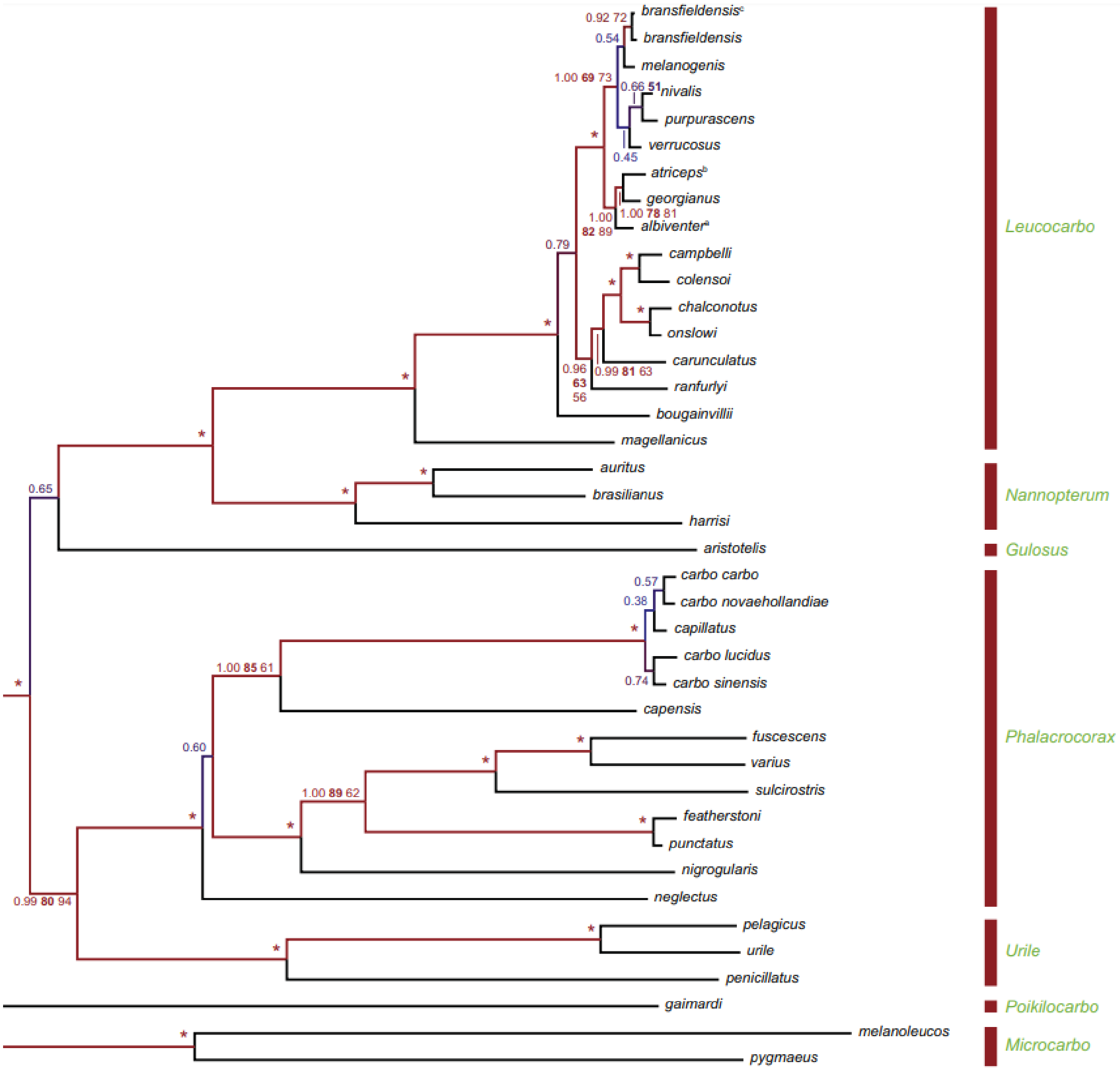


Fig. 1. The Bayesian phylogram for the combined dataset (outgroups not shown, for the phylogram including the outgroups see Fig. S1). The numbers associated with the branches represent posterior probabilities from Bayesian MCMC searches, ML bootstrap values (bold), and equally weighted MP bootstrap values. Bootstrap values ≥50% are shown. Branch and number color represent the Bayesisan posterior probability on a gradient of red (very high) to blue (low) as applied in FigTree 1.3.1 (tree.bio.ed.ac.uk/software/figtree/). Black branches are terminal. The asterisks indicate strong support from all of these measures, i.e., a Bayesian posterior probability of 0.95 and above and bootstrap values of 90% and above. Our classification is shown. $^{a-c}$As in Table 2. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

Because this tree is virtually illegible at this scale, the next page contains an enlarged version of the most relevant section of the tree:



I submitted a SACC proposal (648; see below) to follow Kennedy and Spencer's recommended classification. The proposal to split *Phalacrocorax* into 7 genera did not pass, but by only 1 vote (6 YES, 4 NO), and I still favor recognizing 7 genera (see SACC proposal and comments below). However, I will restrict the proposal just to the linear sequence changes required by the phylogeny. Nonetheless, if I receive sufficient encouragement from NACC members, especially Pam, to submit a proposal on generic limits, I will do so.

For now, I propose only that we modify our sequence as follows. Below is the SACC proposal graphic, with taxa from the NACC area in black (extralimital = gray), but using the Kennedy-Spencer classification at the genus level.

Microcarbo
Poikilocarbo gaimardi
Urile penicillatus
Urile urile
Urile pelagicus
Phalacrocorax carbo
Gulosus
Nannopterum auritus
Nannopterum brasilianus
Leucocarbo magellanicus
Leucocarbo bougainvillii
Leucocarbo atriceps
[many extralimital *Leucocarbo*]

This translates to a modified NACC sequence as follows using standard conventions for linear sequencing:

Phalacrocorax penicillatus
Phalacrocorax urile
Phalacrocorax pelagicus
Phalacrocorax carbo
Phalacrocorax auritus
Phalacrocorax brasilianus

Note that by convention, in the sister taxa *urile* and *pelagicus*, the northwesternmost one is listed first; ditto *auritus* and *brasilianus.*

Recommendation:

I recommend altering our linear sequence as per above. These linear sequence changes are basically bookkeeping but are needed to improve the information content of our classification by more accurately portraying the phylogenetic relationships of our taxa (within the constraints of a linear sequence).

Literature Cited:

Kennedy, M., and H. G. Spencer. 2014. Classification of the cormorants of the world. Molecular Phylogenetics and Evolution 79: 249-257.

Submitted by: Van Remsen

Date of Proposal: 3 September 2019

Proposal (648) to South American Classification Committee

Revise the classification of the Phalacrocoracidae

Background: Our current SACC footnote is as follows:

> **8. Although the monophyly of the Phalacrocoracidae has never been questioned, treatment within the family has ranged from subfamilies and multiple genera, e.g., *Hypoleucus, Stictocarbo*, *Leucocarbo, Notocarbo* (Siegel-Causey 1988) to all species in a single genus, *Phalacrocorax* (e.g. Dickinson 2003). Kennedy et al. (2009) showed that the subfamilies and most genera of Siegel-Causey were not monophyletic. Dickinson & Remsen (2013), using the data in Kennedy et al. (2000, 2009), resurrected *Microcarbo* for a group of five Old World species, but all New World species remained in *Phalacrocorax*. Kennedy and Spencer (2014), using additional new genetic data, split *Phalacrocorax* into seven genera, restricting *Phalacrocorax* to a group of Old World species, and placing South American taxa into *Nannopterum* (for *brasilianus* and *harrisi*), *Poikilocarbo* (for *gaimardi*), and *Leucocarbo* (for *magellanicus*, *bougainvillii*, *atriceps*). SACC proposal badly needed.**

New information: Kennedy and Spencer (2014) sampled 40 taxa of cormorants and sequenced over 8000 bp of mtDNA (5 loci) and nuDNA (5 loci). (However, except for a few samples obtained from LSU and AMNH, all samples are unvouchered blood or feather samples; the lack of anomalous results and Kennedy's extensive experience with the family indicate no misidentifications).

Their Figure 1 is pasted in below (for better resolution see the original – pdf available from me if needed):

[Here deleted --- moved directly to NACC proposal]

Kennedy and Spencer used the tree topology to recommend recognition of 7 genera (by resurrecting old generic names) for their 7 well-differentiated clades, as you can see from the figure, and the effect that adoption of their classification is reflected in the SACC note above.

Although estimated lineage ages are not included in the figure, from the text the estimates are as follows: (1) extralimital *Microcarbo* vs. the rest, 13-15 mya; (2) *Poikilocarbo*, 12-13.5 mya; (3) extralimital *Urile* vs. *Phalacrocorax*, 9-10 mya; and (4) *Nannopterum* vs. *Leucocarbo*, no figure given but crudely extrapolating from the other nodes, probably 6-7 mya. (Note the irony that *Nannopterum*, described solely on the basis of its flightlessness and reduced wings, is resurrected and survives as the oldest name for the two most widespread species in the W. Hemisphere; it is also of interest that *N. harrisi* is sister to the ancestor of *olivaceus* + *auritus*, as previously found by Kennedy et al. (2009); I would have predicted that it was recently derived from one of the two extant species.)

Analysis and recommendation: The genetic data look solid, and the 7 groups have been evolving as separate lineages for a long time. The Phalacrocoracidae must be one of the most homogenous families in terms of superficial external morphology, and so I suspect most were comfortable with but a single genus for the entire family, as in the Peters' Check-list (1979) (and even the 1931 Peters' CL recognized only 3 genera). (The tiny African Pygmy Cormorant looks to me basically like a dwarf *P. olivaceus*.) However, those who have studied cormorant skeletal morphology closely (Siegel-Causey 1990, Worthy 2011) have advocated multiple genera (although their groupings did not show much concordance with the Kennedy-Spencer tree).

If the 7 lineages were of comparatively recent origin, say within the last 5 million years, I would oppose elevating each of the groups to genus rank. However, because these lineages are old, all likely evolving independently since the Miocene, I personally favor following the Kennedy-Spencer recommendations exactly.

Converting their tree to a linear sequence with the usual sequencing conventions produces the following classification, with indentations used to signal nodes, with extralimital taxa in gray:

- *Microcarbo*
  - *Poikilocarbo gaimardi*
    - *Urile*
    - *Phalacrocorax*

    - *Gulosus*
      - *Nannopterum harrisi*
        - *Nannopterum auritus*
        - *Nannopterum brasilianus*
      - *Leucocarbo magellanicus*
        - *Leucocarbo bougainvillii*
          - *Leucocarbo atriceps*
          - Many extralimital *Leucocarbo*

Let's divide the proposal into two parts because even if one votes against the new classification, there remains the issue of linear sequencing of species taxa to match the tree topology.

Part A. Recognize the generic boundaries proposed by Kennedy and Spencer (2014), which would place all South American species in one of the three resurrected genera as per above. I recommend a YES.

Part B. Revise the linear sequence to reflect the phylogeny of Kennedy and Spencer (2014), as outlined above, regardless of passage of Part A. I recommend a YES on this.

Literature Cited

KENNEDY, M., AND H. G. SPENCER. 2014. Classification of the cormorants of the world. Molecular Phylogenetics and Evolution 79: 249-257.

KENNEDY, M., C. A. VALLE, AND H. G. SPENCER. 2009. The phylogenetic position of the Galapagos Cormorant. Molecular Phylogenetics and Evolution 53: 94-98.

SIEGEL-CAUSEY, D. 1988. Phylogeny of the Phalacrocoracidae. Condor 90: 885–905.
WORTHY, T.H. 2011. Descriptions and phylogenetic relationships of a new genus and two new species of Oligo-Miocene cormorants (Aves: Phalacrocoracidae) from Australia. Zool. J. Linn. Soc. 163, 277–314.

Van Remsen, September 2014

Comments from Stiles: "Although the resulting genus name is rather unfortunate, the phylogenetic data look solid, so:

A. YES, as this does maintain consistent ages for the genera of cormorants.
B. YES, this follows from A.

Comments from Stotz: "A. Modified YES. Right now I can't vote for a split into 7 genera. I would personally favor, *Phalacrocorax* for old world taxa (plus *Urile*) and *Leucocarbo* for New World taxa, recognizing *Poikilocarbo* for *gaimardi* and *Microcarbo* for Old World pygmy cormorants. The European Shag is a problem; I could go with *Leucocarbo* (not sure what the oldest name is), but I guess I am inclined to recognize *Gulosus*. So for SA taxa, I would say Yes to *Poikilocarbo*, and *Leucocarbo*, but NO to the splitting out of *Nannopterum*. B. YES. This seems straightforward."

Comments from Nores: "NO. I prefer to be conservative. For this reason, I would place all South American cormorants, except *gaimardi*, in the genus *Leucocarbo*:

Poikilocarbo gaimardi
Leucocarbo harrisi
Leucocarbo brasilianus
Leucocarbo magellanicus
Leucocarbo bougainvillii
Leucocarbo atriceps"

Comments from Zimmer: "Part (A): YES. Although the thought of 7 genera of cormorants is pushing it, even for someone like myself, who prefers more internally cohesive, narrowly defined genera. Uugh! Part (B): YES."

Comments from Pacheco: "A – YES; Because the results of Kennedy/Spencer point to ancient lineages, I consider inescapable accept the arrangement proposed in three genera to the South American taxa.
B – YES"

Comments from Areta: "A-YES. Tough decision! To make genetic differentiation of clades including multiple species more consistent, *Nannopterum* should be merged with *Leucocarbo*, thus resembling differentiation within *Phalacrocorax* as defined by Kennedy & Spencer (2014). However, an alternative treatment would be to recognize *Nannopterum* and to split

Phalacrocorax in two or three genera following the branching pattern, making the degree of differentiation within genera more consistent. I incline toward recognizing *Nannopterum*, given that morphological analyses have also recovered this clade, it is an old split and it provides interesting clues on the evolution of *harrisi*. Recognition of *Poikilocarbo* is also reasonable given its phylogenetic position and degree of differentiation. B-YES."

Comments from Jaramillo: "A – NO but only with respect to *Nannopterum*, as others have suggested it is more internally consistent to include it with *Leucocarbo* -- at least to be consistent with the treatment of *Phalacrocorax*. Not sure which name is older, *Leucocarbo* or *Nannopterum*? I assume the former? Separating *Poikilocarbo* is fully justified. B – YES."

Comments from Cadena: "NO. I am not sure I fully understand the situation here. Specifically, why exactly is it *necessary* to split the clade sister to *Microcarbo* into multiple genera? If I understand this correctly, all the taxa in this clade are recognized as members of a single genus by Dickinson and Remsen and in our baseline list; because all the taxa in this genus are descended from a single ancestor (i.e., the genus is monophyletic), I see no need to change. Sure, there are deep divisions within the genus, but this is true of many other genera. Van's points about the ages of lineages are interesting, but as far as I know, clade age is not a criterion we have consistently followed to establish ranks above the species level. Absent a policy of naming/ranking clades based on their age, I think we should only fiddle with classification above the species level when absolutely necessary due to non-monophyly of taxa. Am I missing something?"

2020-A-13 N&MA Classification Committee various pages

Modify various linear sequences to reflect new phylogenetic data

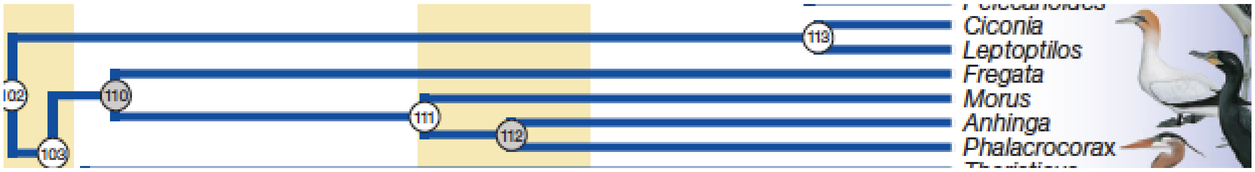
Under the umbrella of this proposal, I collected a batch of minor linear sequence changes that reflect new phylogenetic data and have already been passed by SACC (proposal 735). This is just drudgery bookkeeping that has to be done, but hopefully only once, and so we won't have to fiddle with it again (the Rallidae a likely exception). I don't like the instability, but if we have rules, we should follow them. I restricted this proposal to nonpasserines just to cut it down in size. I did not present much in the way of methods in each case; these can be found in the cited papers if interested. In each case, the sequences follow the standard convention of listing first the branch with the fewest species, and in the case of sisters, the northwestern-most taxon is listed first.

I recommend a YES on all of them (unless of course someone finds a mistake), although I'm not 100% certain in the case of the *Chloroceryle* proposal.

A. Sequence of families in Suliformes
B. Sequence of species and genera in Cathartidae
C. Sequence of genera in Rallidae
D. Invert Laridae and Rynchopidae
E. Sequence of species in *Chloroceryle*
F. Sequence of species in *Forpus*

A. Sequence of families in Suliformes

Our current sequence of families in the Suliformes is Fregatidae, Sulidae, Phalacrocoracidae, and Anhingidae. A minor correction needs to be made to follow standard conventions for sequencing. All recent data point to a sister relationship between Phalacrocoracidae and Anhingidae, e.g., here's the figure from Prum et al. (2015):



Anhingidae having fewer species means that it should precede its sister taxon Phalacrocoracidae. Pretty exciting stuff, I know.

B. Sequence of species and genera in Cathartidae

Our current linear sequence is as follows:

Coragyps atratus Black Vulture
Cathartes aura Turkey Vulture
Cathartes burrovianus Lesser Yellow-headed Vulture
Gymnogyps californianus California Condor
Sarcoramphus papa King Vulture

Johnson et al. (2016) published a phylogeny of the Cathartidae with the following tree:

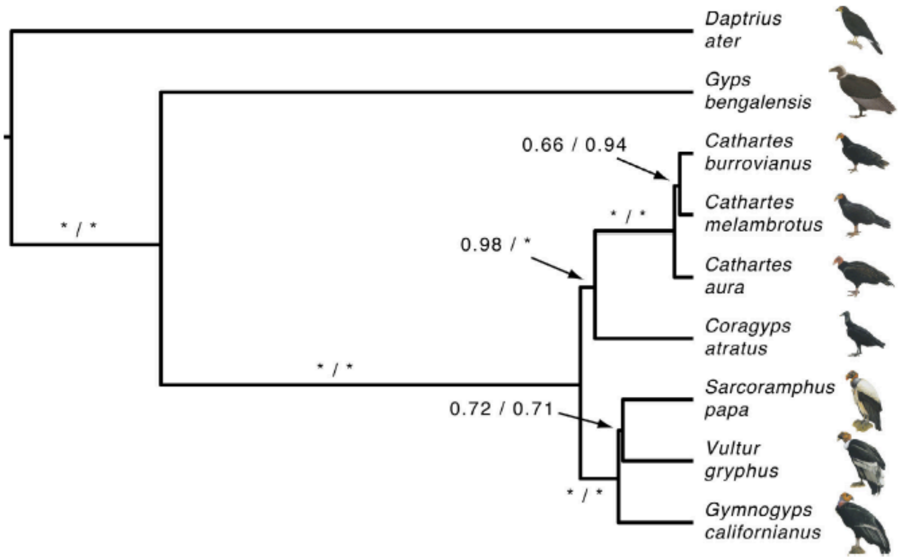


Fig. 1. *BEAST maximum clade credibility cathartid species tree. Posterior nodal support values correspond with the (5nuc/2mt)/(9nuc/2mt) datasets; *, maximum nodal support. Species tree generated using an uncorrelated lognormal relaxed clock applied separately for each locus. Bird images modified from Houston (1994).

Converting this to a linear sequence produces the following (treating *Cathartes* as a polytomy):

Gymnogyps californianus California Condor
Sarcoramphus papa King Vulture
Coragyps atratus Black Vulture
Cathartes aura Turkey Vulture
Cathartes burrovianus Lesser Yellow-headed Vulture

C. Sequence of genera in Rallidae

Our current sequence of genera, based mostly on historical momentum, is as follows:

RALLIDAE (RAILS)
  Coturnicops
  Micropygia
  Laterallus
  Crex
  Rallus
  Aramides

Amaurolimnas
Porzana
Zapornia
Hapalocrex
Neocrex
Cyanolimnas
Pardirallus
Porphyrio
Gallinula
Fulica

García-R et al. (2014; *MPE* 81: 96-108) published a phylogeny that lacks a lot of oddball genera, as you can imagine from such a globally distributed family, but included most genera in the NACC area. See their tree on the following page (note that *Porzana flaviventer* on their tree is *Hapalocrex flaviventer* on the NACC list). The big differences from traditional relationships are that *Porphyrio* is not closely related to *Gallinula*, and that true *Porzana* are in the same lineage *Gallinula* and *Fulica*. They found strong support for the following relationships (extralimital taxa pruned), with indentations used to indicate relationships:

Rallus
Crex

- *Porphyrio*
  - *Coturnicops*
    - *Hapalocrex*
    - *Laterallus*

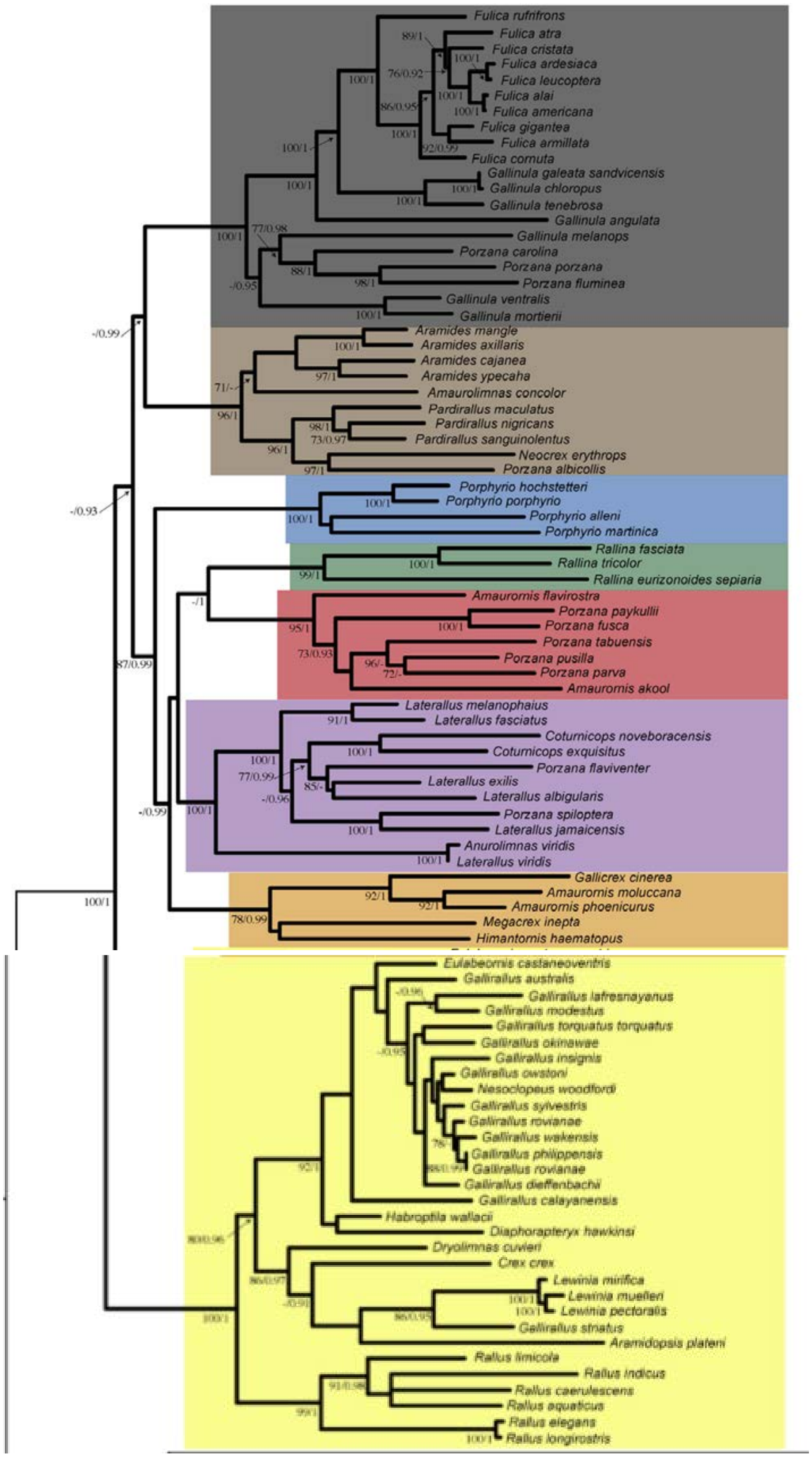
- *Neocrex*
- *Pardirallus*

- *Amaurolimnas*
- *Aramides*

- *Porzana*

- *Gallinula*
- *Fulica*

They did not have a sample of *Micropygia*, so we could keep it next to *Coturnicops* to reflect traditional ideas on its relationship. They did not have a sample of *Zapornia* (Laysan and Hawaiian rails), but we placed this genus to follow *Porzana* in 57th Supplement. They did not have a sample of *Cyanolimnas* (Zapata Rail). Olson (1973) summarized the similarities between *Cyanolimnas* and *Neocrex* + *Pardirallus* (presumably the rationale for their current proximity in the linear classification), and Livezey's (1997) analysis also placed them in a monophyletic group; therefore, continued placement of *Cyanolimnas* near those genera is the safest solution for now. Because of the polyphyly of genera such as *Laterallus*, *Porzana*, and even *Gallinula*, and the limited number of species sampled, I suspect we may have to do more


Fulica rufrifrons
89/1
Fulica atra
Fulica cristata
100/1
Fulica ardesiaca
76/0.92
Fulica leucoptera
100/1
100/1
Fulica alai
86/0.95
100/1
Fulica americana
Fulica gigantea
100/1
Fulica armillata
92/0.99
100/1
Fulica cornuta
Gallinula galeata sandvicensis
100/1
100/1
Gallinula chloropus
100/1
Gallinula tenebrosa
Gallinula angulata
100/1
77/0.98
Gallinula melanops
Porzana carolina
88/1
Porzana porzana
98/1
Porzana fluminea
-/0.95
Gallinula ventralis
100/1
Gallinula mortierii
-/0.99
Aramides mangle
100/1
Aramides axillaris
Aramides cajanea
97/1
Aramides ypecaha
71/-
Amaurolimnas concolor
96/1
Pardirallus maculatus
98/1
Pardirallus nigricans
73/0.97
Pardirallus sanguinolentus
96/1
Neocrex erythrops
97/1
Porzana albicollis
Porphyrio hochstetteri
-/0.93
100/1
Porphyrio porphyrio
100/1
Porphyrio alleni
Porphyrio martinica
Rallina fasciata
100/1
Rallina tricolor
99/1
Rallina eurizonoides sepiaria
-/1
Amaurornis flavirostra
Porzana paykullii
95/1
100/1
Porzana fusca
Porzana tabuensis
87/0.99
73/0.93
Porzana pusilla
96/-
72/-
Porzana parva
Amaurornis akool
Laterallus melanophaius
91/1
Laterallus fasciatus
Coturnicops noveboracensis
100/1
Coturnicops exquisitus
100/1
Porzana flaviventer
77/0.99
85/-
Laterallus exilis
-/0.96
Laterallus albigularis
-/0.99
100/1
Porzana spiloptera
100/1
Laterallus jamaicensis
Anurolimnas viridis
100/1
Laterallus viridis
Gallicrex cinerea
100/1
92/1
Amaurornis moluccana
92/1
Amaurornis phoenicurus
78/0.99
Megacrex inepta
Himantornis haematopus
Eulabeornis castaneoventris
Gallirallus australis
-/0.96
Gallirallus lafresnayanus
Gallirallus modestus
Gallirallus torquatus torquatus
Gallirallus okinawae
-/0.95
Gallirallus insignis
Gallirallus owstoni
Nesoclopeus woodfordi
Gallirallus sylvestris
Gallirallus rovianae
Gallirallus wakensis
78/-
Gallirallus philippensis
88/0.99
Gallirallus rovianae
92/1
Gallirallus dieffenbachi
Gallirallus calayanensis
Habroptila wallacii
80/0.96
Diaphorapteryx hawkinsi
Dryolimnas cuvieri
86/0.97
Crex crex
Lewinia mirifica
100/1
Lewinia muelleri
-/0.91
100/1
Lewinia pectoralis
100/1
86/0.95
Gallirallus striatus
Aramidopsis plateni
Rallus limicola
Rallus indicus
91/0.98
Rallus caerulescens
Rallus aquaticus
99/1
Rallus elegans
100/1
Rallus longirostris

fiddling with this sequence once the family is more broadly sampled. Nonetheless, the sequence above will be much closer to the eventual final sequence than our current one.

Putting all this together creates the following revised sequence

Rallus
Crex
Porphyrio
Coturnicops
Micropygia
Hapalocrex
Laterallus
Neocrex
Cyanolimnas
Pardirallus
Amaurolimnas
Aramides
Porzana
Zapornia
Gallinula
Fulica

D. Reverse Laridae and Rynchopidae

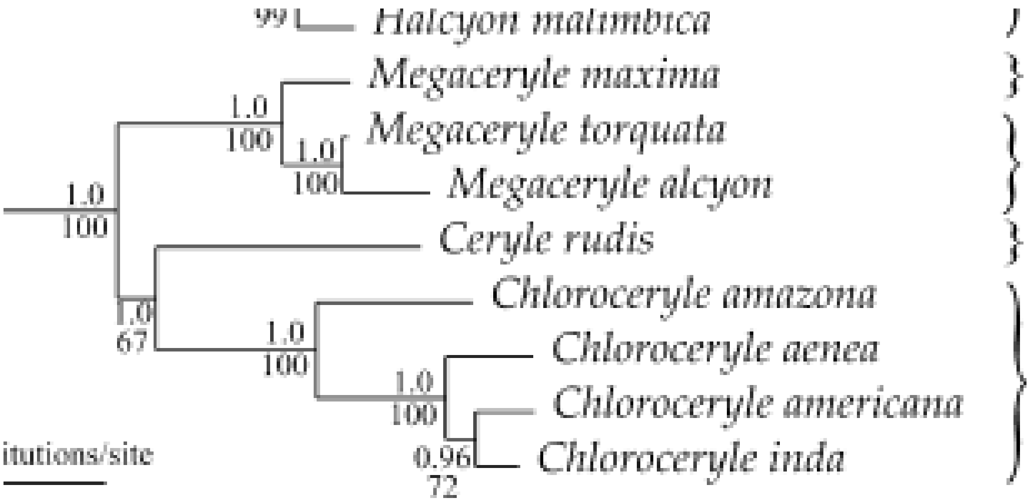
All data indicate that the Laridae and Rynchopidae are sister families (and Rynchopidae likely embedded within Laridae as currently defined). If linear sequences are to follow conventions, rather than tradition, Rynchopidae should clearly precede the much more diverse group Laridae, and the sequence of the two should be reversed.

E. Sequence of species in *Chloroceryle*

Our current sequence is as follows

Chloroceryle amazona Amazon Kingfisher
Chloroceryle americana Green Kingfisher
Chloroceryle inda Green-and-rufous Kingfisher
Chloroceryle aenea American Pygmy Kingfisher

Moyle et al. (2006), however, found the following relationships:



Thus, to make the sequence reflect these data, *C. aenea* needs to be moved, as follows:

Chloroceryle amazona Amazon Kingfisher
Chloroceryle aenea American Pygmy Kingfisher
Chloroceryle americana Green Kingfisher
Chloroceryle inda Green-and-rufous Kingfisher

Note that support for the *americana-inda* sister relationship is not rock solid, and so that could be a reason to vote for stability until support for that node solidifies.

F. Sequence of species in *Forpus*

Our current sequence in Forpus is as follows:

Forpus passerinus Green-rumped Parrotlet
Forpus cyanopygius Mexican Parrotlet
Forpus conspicillatus Spectacled Parrotlet

Smith et al. (2013) found the following relationships:

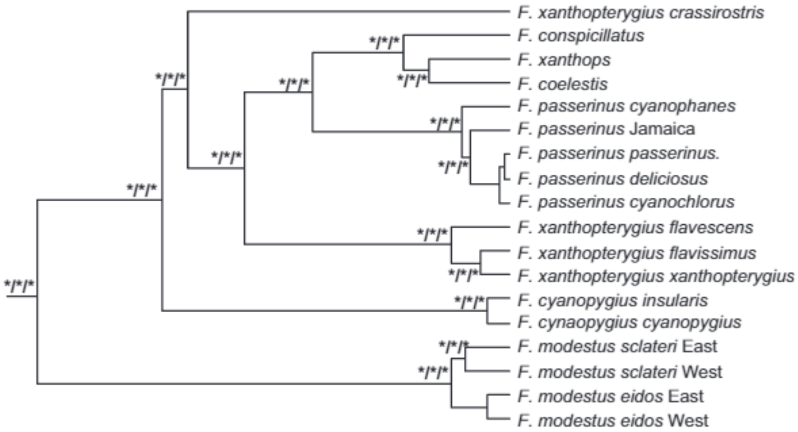


Fig. 3 Species tree of *Forpus* showing speciation posterior probabilities from BP&P. Nodes show posterior probabilities using three different prior combinations: 1st—large ancestral N_e and deep divergences; 2nd—small ancestral N_e and shallow divergences and 3rd—large ancestral N_e and shallow divergences. Nodes that did not have high speciation probabilities using all three prior combinations are not labelled: *Forpus passerinus cyanochlorus*: PP = 0.09/0.15/0.12; *Forpus passerinus passerinus* and *Forpus passerinus deliciosus*: PP = 0.02/0.08/0.04; *Forpus modestus scalteri* East and *F. modestus scalteri* West: PP = 0.39/0.92/0.38.

Converting this to a linear sequence produces the following:

Forpus cyanopygius Mexican Parrotlet
Forpus passerinus Green-rumped Parrotlet
Forpus conspicillatus Spectacled Parrotlet

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