AOU Classification Committee – North and Middle America

Proposal Set 2016-B

(a) Move Purple Swamphen *Porphyrio porphyrio* from the Appendix to the Main List
(b) split *P. porphyrio* into six species, thereby removing *P. porphyrio* from the Main List and adding Gray-headed Swamphen *P. poliocephalus*

Background:

The Purple Swamphen *Porphyrio porphyrio* is currently in the Appendix, based on an individual in Delaware in 1990. The text reads:

> An individual thought to be a molting sub-adult and possibly from one of the Middle Eastern subspecies appeared in suburban Wilmington, Delaware, 5 December 1990, and it remained two weeks (1991, Amer. Birds 45: 255). Its origin is questionable, but given the unusual dispersal abilities of many Rallidae, a natural origin cannot be dismissed.

Pranty (2000, 2012) detailed the establishment and quick expansion of a population in southern Florida. In about 1996, Purple Swamphens were first noted in Broward County in southern Florida. They were thought to have been the free-roaming birds of a local aviculturist. They were noted breeding the following year. The populations exploded soon thereafter. By 2006, the Florida Fish and Wildlife Conservation Commission (FFWCC) had determined that the population posed a threat to native species and began a program to eradicate them through shooting. Over two years (October 2006- December 2008), 3100 swamphens were shot. The FFWCC decided at this time to stop the eradication as it was having no effect on the population. The populations appears to be stable in south Florida, and records of dispersing individuals have been noted regularly north to central Florida. The FOSRC voted to add the Purple Swamphen to the Florida list as an established exotic in 2012 (Greenlaw 2014). The ABA-CLC likewise did so in 2013. Pranty (2012) listed the subspecies in Florida as gray-headed *P. p. poliocephalus* from the Indian subcontinent, but the original aviculturists responsible for the introduction said a blue-headed female (not *poliocephalus*) mated and produced offspring with a *poliocephalus* male (Pranty 2012). Specimens at the Florida Museum of Natural History are *P. p. poliocephalus*.

The polytypic and widespread Purple Swamphen is treated as a single species in our Appendix. Dickinson and Remsen (2013) and del Hoyo and Collar (2014) treated it as a single species as well. Recently, Gill and Donsker (2015; the IOC list) and Clements et al. (2015; the Clements list) split *porphyrio* into six species, based largely on Garcia-R and Trewick (2015), who provided a phylogeny of most taxa in the genus based on analyses of analyses of mitochondrial and nuclear DNA (see their tree in Fig. 1 below). Three taxa currently considered species were outgroups to *P. porphyrio*: *P. alleni* (Africa), *P. flavirostris* (South America) and its sister *P. martinicus* (North and South America). Embedded within *P. porphyrio* were two/three taxa considered species: the takahes of New Zealand (*hochstetteri* on the South Island and *mantelli* on the North Island), and the White Swamphen (*P. albus*), on Lord Howe Island. On New Zealand, the takahes are sympatric with the widespread *P. melanotus,* which occurs in

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Australasia and western Oceania. The other major clades were: 2) *P. porphyrio* (SW Europe and NW Africa); (3) *P. indicus* (SE Asia, Indonesia); 4) *P. madagascariensis* (Africa); 5) *P. pulverulentus* (Philippines); and 6) *P. poliocephalus* (Indian subcontinent). They estimated splitting among these major clades at 1.1-2 mya. They do not discuss reproductive isolation or current gene flow between clades, aside from the fact that one specimen from Indonesia (*indicus*) was more closely
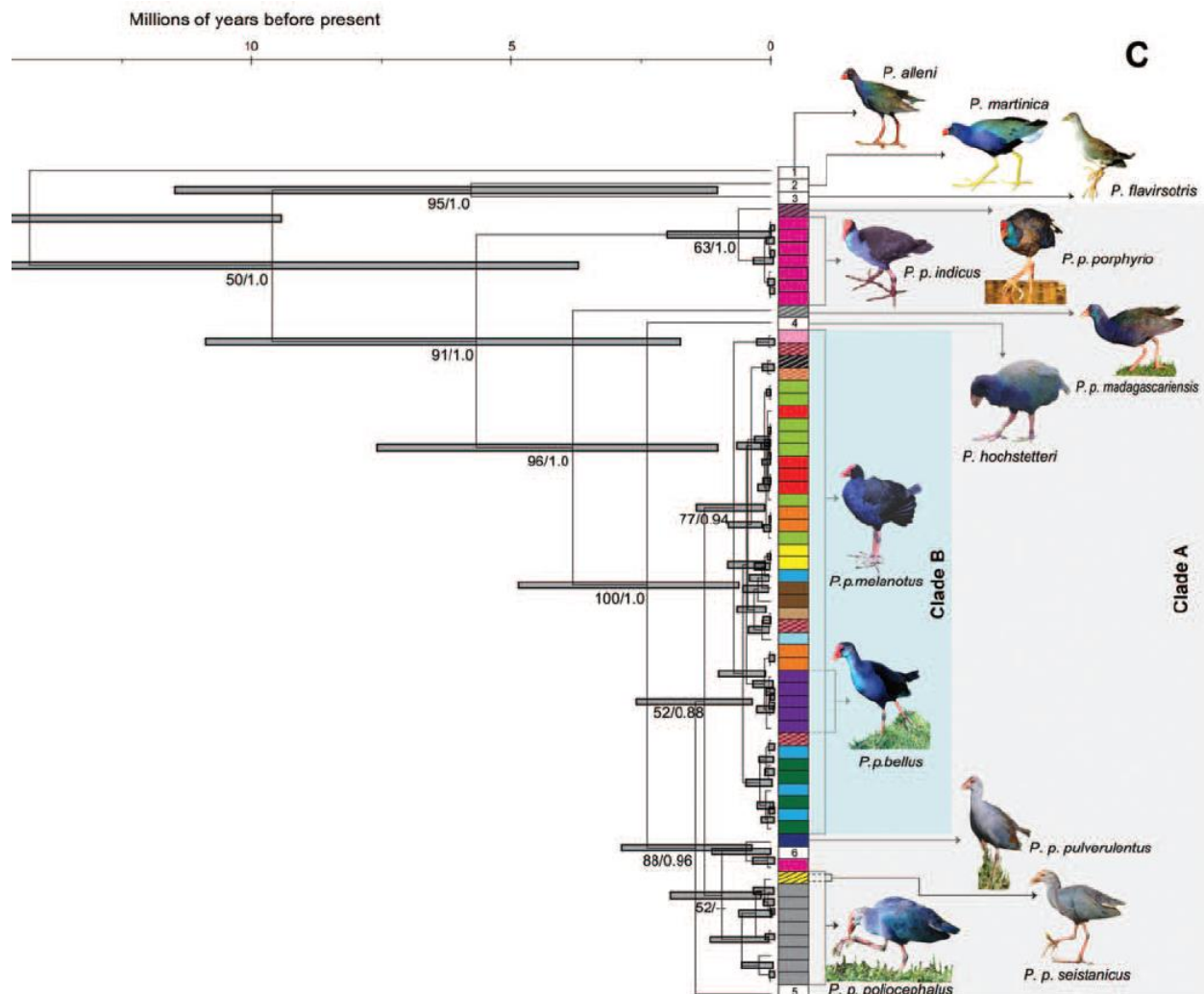
Figure 1. Phylogenetic tree from Garcia-R and Trewick (2015); white rectangles represent species other than *P. porphyrio*. In addition to *P. hochstetteri* (pictured above; white rectangle 4), *P. mantelli* (white rectangle 5) and *P. albus* (white rectangle 6) were also embedded within *P. porphyrio*.

related to the *pulverulentus* clade. The major clades show distinct plumage differences. The English name used for *poliocephalus* in Gill and Donsker (2015; the IOC List) and Clements et al. (2015) is Gray-headed Swamphen; it is also the English name preferred by del Hoyo and Collar (2014) if *poliocephalus* is split.

Recommendation:

I recommend yes votes on both A and B: *Porphyrio porphyrio* (Purple Swamphen) should be removed from the Appendix and *Porphyrio poliocephalus* (Gray-headed Swamphen) added to the Main List. We tend to follow the ABA-CLC in matters of adding of established exotics to the Main List, and the criteria for establishment in both the ABA-CLC and FOSRC are among the strictest in North America. Whether we treat *poliocephalus* as a species-level taxon is somewhat subjective. The takahes exist (or existed) sympatrically with *porphyrio sensu lato* in New Zealand, so they must be considered separate species. That would create a paraphyletic *porphyrio sensu lato*. That, coupled with the rather old diversification and plumage differentiation, indicates that we should probably treat the major clades as separate species, even without analyses of reproductive isolation. Note that Dickinson and Remsen (2013) and del Hoyo and Collar (2014) were written prior to the publication of Garcia-R and Trewick (2015).

Proposed new species account:

Porphyrio poliocephalus (Latham). Gray-headed Swamphen.

> *Gallinula poliocephala* Latham, 1801, Ind. Orn. Suppl., 1801, p. lxviii. (India.)

> **Habitat**.—xxxxxx (xxxxx zones).
> **Distribution**.—*Resident* from central Turkey, Iran, Azerbaijan, Afghanistan, Pakistan, Nepal, Bangladesh, and south central China, south through Syria and Iraq, to the Persian Gulf, throughout the Indian subcontinent, and Myanmar, Thailand, and peninsular Malaysia, and on Sri Lanka and islands in the Andaman Sea.
> Introduced or escaped, and established in southeastern Florida, mainly in Okeechobee, Glades, Hendry, Palm Beach, Broward, and Miami-Dade counties. Casual north to Brevard County. A record from Delaware (1991, Amer. Birds 45: 255) is of questionable origin.
> **Notes**.—Formerly included within an expanded *P. porphyrio* (Purple Swamphen, Linnaeus 1758), but genetic analyses indicate that that species is polyphyletic if some flightless Pacific Ocean taxa are not included (Garcia-R and Trewick 2015).

Literature Cited:

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del Hoyo, J., and Collar, N. J. 2014. HBW and Birdlife International; Illustrated checklist of birds of the World. Volume 1: Non-passerines. Lynx Editions, Barcelona.

Dickinson, E.C., and J. V. Remsen, Jr. 2013. The Howard and Moore complete checklist of birds of the World. 4th edition. Vol. 1. Aves Press, Eastbourne, U.K.

Garcia-R, J C., and S. A. Trewick. 2015. Dispersal and speciation in purple swamphens (Rallidae: *Porphyrio*). Auk 132: 140-155.

Gill, F & D Donsker (Eds.). 2015. IOC World Bird List (v 5.4). doi
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Committee: 2012. Florida Field Naturalist 42: 153-171.
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Pittaway, and D. A. Sibley. 2013. 24th report of the ABA Checklist Committee.
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Pranty, B. 2012. Population growth, spread and persistence of Purple Swamphens
(*Porphyrio porphyrio*) In Florida. Florida Field Naturalist 40: 1-12.

Submitted by: Andrew Kratter
Date of Proposal: 10 November 2015

PROPOSAL 2016-B-1c (addendum):
Add African Swamphen *Porphyrio* [*porphyrio*] *madagascarensis* to main list.

In October, 2009, Andrew Dobson photographed a swamphen in Bermuda (Dobson 2009: http://www.audubon.bm/images/content/Newsletters/Vol._20_No.2.pdf). This throws a monkey wrench into our earlier proposal (2016-B-1) to add Gray-headed Swamphen *Porphyrio* [*porphyrio*] *poliocephalus* to main list, and split *Porphyrio porphyrio* (s.l.) into six species. The Bermuda bird was identified as the African subspecies (*P. p. madagascarensis)* of Purple Swamphen (*P. porpyhrio* s.l.) after consultation (Dobson 2009). *P.* [*p.] madagascarensis* would attain species status if proposal 2016-B-1b passes. The identification as *madagascarensis* looks correct (see Taylor 1998) as the bird has a dark blue head and greenish back and wing coverts. Purple Swamphen (*P. porphyrio* sensu strictu) has a purple back and wing coverts; Gray-headed (*P. poliocephalus*) has a pale blue head and bluish back and wing coverts; Philippine Swamphen (*P. pulverulentus*) has pale head and underparts, brownish back and wings; Australasian Swamphen (*P. melanotus*) has nearly black back and wings; and Indonesian (*P. indicus*) is like *melanotus* with pale blue lesser coverts and a darker bill.   Dobson (2009) listed ship-assistance as probable in this case, although he notes that *madagascarensis* has been recorded as a presumed natural vagrant in Europe as far north as France, Germany, and Austria. The species appears on Bermuda's list. (Bermuda Audubon Society 2015), but that list does not differentiate between established exotics (House Sparrow, Estrildids) and native species. All of the free-flying swamphens in Florida are *P. poliocephalus*. The species (sensu latu) is in our Appendix currently, based on a bird photographed in Delaware in 1990 (American Birds 45:255) of one of the "Middle Eastern subspecies," which are included in *P. poliocephalus*.

Whether the Bermuda record is a wild vagrant or ship-assisted is difficult to determine. The NACC does not seem to have a position stated on whether to include species based on ship-assisted individuals. The ABA-CLC is a bit more explicit and states "An otherwise wild bird that voluntarily uses or is attracted to a feeder, nest box, audio playback, ship at sea, or other nonnatural device, without being captured, is still considered wild."   I don't see any indication of what led Dobson (2009) to the conclusion of ship-assisted, other than it was far out of range. Dobson does not take into account the propensity of rallids to undertake long over water dispersals, which is certainly the case in *P. porphyrio melanotus*, which has colonized such isolated islands as New Zealand, Rennell and Taumako in the Solomon Islands, Vanuatu, Tonga, and Samoa. None of the taxa in this complex are very migratory, though they seem quite capable of long distance vagrancy.

The way I see it, there are four possible outcomes to this proposal if we accept the proposal (Proposal 2016 -B-1a) that the Florida population is established: 1) if we choose to split *P. porphyrio* into six species (Proposal 2016 -B-1b) , then the

acceptance of the Bermuda bird would add another new species to our List; 2) If we accept the split, but do not accept the Bermuda bird as a wild vagrant, then we would add *P. madagascarensis* to the Appendix; 3) if we do not split *P. porphyrio*, but accept the Bermuda bird as a wild vagrant, this would add *P porphyrio* to the main list as a wild vagrant (with introduced population in Florida); or 4) if we do not split *P. porphyrio* and do not accept the Bermuda bird as a wild vagrant, this would add *P porphyrio* to the main list as introduced, noting the record in Bermuda. In the unlikely event that we do not accept the Florida population as established, then *P. porphyrio* would remain in the appendix if not split, or, if split*, P. poliocephalus* and *P. madagascarensis* would be added to the Appendix and *P. porphyrio* removed.

I recommend that we add African Swamphen *Porphyrio* [*porphyrio*] *madagascarensis* to the main list. This would be in conjunction with my recommendation that we add Gray-headed Swamphen *Porphyrio* [*porphyrio*] *poliocephalus* to main list, and that we split *Porphyrio porphyrio* (s.l.) into six species from proposal 2016-B-1.

Literature Cited:

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Dobson, A. 2009. Purple Swamphen – new to Bermuda. Bermuda Audubon Society
        Newsletter 20 (2); 1.
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Submitted by: Andrew Kratter
Date of Proposal: 10 March 2016

Revise the subfamilies of Scolopacidae: (a) eliminate Phalaropodinae, and (b) restructure the family into five subfamilies

Background:

We presently recognize two subfamilies in Scolopacidae: Scolopacinae and Phalaropodinae. A preponderance of evidence indicates that continuing to recognize Phalaropodinae as separate from our Scolopacinae is inappropriate, because its relationship lies deeply within Scolopacinae. In addition, there are other well-supported groups within Scolopacidae for which subfamily-level recognition is warranted. This proposal is in two parts: A) to eliminate Phalaropodinae, and B) to restructure the family into five subfamilies. If A passes but B does not, then we will have no subfamilies of Scolopacidae for awhile (until subfamily limits become clearer at fine scales).

New (and old) information:

A) Evidence for the invalidity of Phalaropodinae as presently conceived in our Check-list is extensive. Jehl (1968), using the downy plumage of chicks, considered Phalaropodinae to be a subfamily of Scolopacidae, most closely related to Tringinae. Sibley and Ahlquist (1990), using DNA-DNA hybridization, found *Phalaropus* to be deeply embedded in Scolopacidae, as did Ericson et al. (2003), Paton et al. (2003), Baker et al. (2007, 2008), and Gibson and Baker (2012) using various DNA sequence datasets. Figure 1 from the latter is copied on the following page. Retention of our present subfamily structure (Scolopacinae and Phalaropidinae) is not supported by these studies.

B) Although Gibson and Baker (2012, Fig. 1, copied on the next page) outlined a possible alternative recognizing eight subfamilies, several uncertainties remain regarding the limits of those groups (which they do not actually discuss as subfamilies). For example, there are some short branches and weakly supported nodes among the topmost two major clades in Fig. 1. It thus might seem prudent to await datasets with more loci and a cogent published discussion of accurate subfamily divisions. However, at present, five clades appear to be robust, congruent with other studies, and of similar evolutionary depth. These are the following clades in the Gibson and Baker (2012) figure: Tringinae (shanks and phalaropes), Scolopacinae (snipe, woodcock, and dowitchers), Arenariinae (sandpipers), Limosinae (godwits), and Numeniinae (curlews). (Note that this is given in the figure order; a different sequence would be needed for the Check-list – see below.)

Baker et al. (2007, 2008) proposed that these are ~Eocene-era groups. In addition to these being old and rather well-defined groups, one argument in favor of a five-subfamily framework (for now, at least) is that there are some obvious morphologically good groups here (e.g., curlews, godwits). In the future, when uncertainties are cleared up (e.g., the relationship between *Phalaropus* and

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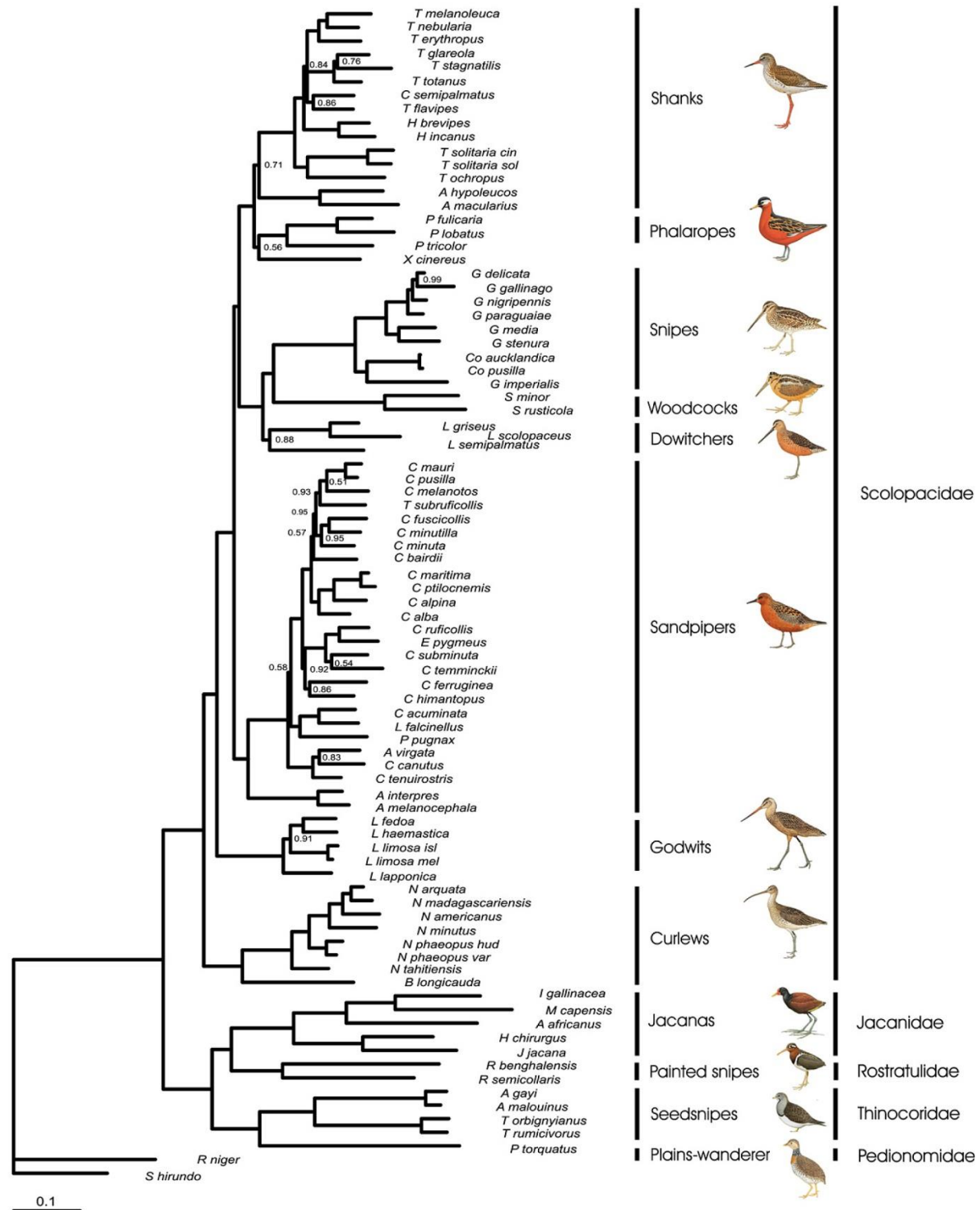
Fig. 1. Phylogeny based on sequences of five genes (RAG1, CYT B, 12S, ND2, and COI) estimated with partitioned Bayesian analysis for 84 species of the Scolopaci. All nodes received a posterior probability of 1.00 unless otherwise labeled.

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Xenus), we could revisit the possibility or desirability of further subfamily-level splits in the Tringinae and Scolopacinae. At present, a five-subfamily solution seems preferable to a no-subfamily or a greater-than-five-subfamily taxonomy.

Van Remsen wrote a similar proposal for SACC, and he included further discussion of possible finer-scale divisions than the five outlined here. See the proposal and the votes and comments here: www.museum.lsu.edu/~Remsen/SACCprop555.html . I refrain from including consideration of finer-scale divisions until a more robust phylogeny definitively elucidates their likely limits (and one would hope that future publication would also discuss subfamilies and perhaps tribes and their limits).

Here is how these changes (A and B) would affect the Check-list (with our present sequence maintained as much as possible within subfamilies); colors reflect Word's Track Changes function (except blue, which reflects our online Check-list format):

The new linear sequence would be as follows (with our present sequence maintained as much as possible within subfamilies):

family: Scolopacidae

- subfamily: Numeniinae
  o genus: *Bartramia*
    - species: *Bartramia longicauda* (Upland Sandpiper, Maubèche des champs)
  o genus: *Numenius*
    - species: *Numenius minutus* (Little Curlew, Courlis nain) A
    - species: *Numenius borealis* (Eskimo Curlew, Courlis esquimau)
    - species: *Numenius phaeopus* (Whimbrel, Courlis corlieu)
    - species: *Numenius tahitiensis* (Bristle-thighed Curlew, Courlis d'Alaska)
    - species: *Numenius madagascariensis* (Far Eastern Curlew, Courlis de Sibérie) N
    - species: *Numenius tenuirostris* (Slender-billed Curlew, Courlis à bec grêle) A
    - species: *Numenius arquata* (Eurasian Curlew, Courlis cendré) A
    - species: *Numenius americanus* (Long-billed Curlew, Courlis à long bec)
- subfamily Limosinae
  o genus: *Limosa*
    - species: *Limosa limosa* (Black-tailed Godwit, Barge à queue noire) N
    - species: *Limosa haemastica* (Hudsonian Godwit, Barge hudsonienne)
    - species: *Limosa lapponica* (Bar-tailed Godwit, Barge rousse)
    - species: *Limosa fedoa* (Marbled Godwit, Barge marbrée)

- subfamily Arenariinae
  - genus: *Arenaria*
    - species: *Arenaria interpres* (Ruddy Turnstone, Tournepierre à collier)
    - species: *Arenaria melanocephala* (Black Turnstone, Tournepierre noir)
  - genus: *Calidris*
    - species: *Calidris tenuirostris* (Great Knot, Bécasseau de l'Anadyr) A
    - species: *Calidris canutus* (Red Knot, Bécasseau maubèche)
    - species: *Calidris virgata* (Surfbird, Bécasseau du ressac)
    - species: *Calidris pugnax* (Ruff, Combattant varié)
    - species: *Calidris falcinellus* (Broad-billed Sandpiper, Bécasseau falcinelle) A
    - species: *Calidris acuminata* (Sharp-tailed Sandpiper, Bécasseau à queue pointue) N
    - species: *Calidris himantopus* (Stilt Sandpiper, Bécasseau à échasses)
    - species: *Calidris ferruginea* (Curlew Sandpiper, Bécasseau cocorli)
    - species: *Calidris temminckii* (Temminck's Stint, Bécasseau de Temminck) A
    - species: *Calidris subminuta* (Long-toed Stint, Bécasseau à longs doigts) N
    - species: *Calidris pygmea* (Spoon-billed Sandpiper, Bécasseau spatule) A
    - species: *Calidris ruficollis* (Red-necked Stint, Bécasseau à col roux)
    - species: *Calidris alba* (Sanderling, Bécasseau sanderling)
    - species: *Calidris alpina* (Dunlin, Bécasseau variable)
    - species: *Calidris ptilocnemis* (Rock Sandpiper, Bécasseau des Aléoutiennes)
    - species: *Calidris maritima* (Purple Sandpiper, Bécasseau violet)
    - species: *Calidris bairdii* (Baird's Sandpiper, Bécasseau de Baird)
    - species: *Calidris minuta* (Little Stint, Bécasseau minute) N
    - species: *Calidris minutilla* (Least Sandpiper, Bécasseau minuscule)
    - species: *Calidris fuscicollis* (White-rumped Sandpiper, Bécasseau à croupion blanc)
    - species: *Calidris subruficollis* (Buff-breasted Sandpiper, Bécasseau roussâtre)
    - species: *Calidris melanotos* (Pectoral Sandpiper, Bécasseau à poitrine cendrée)
    - species: *Calidris pusilla* (Semipalmated Sandpiper, Bécasseau semipalmé) species: *Calidris mauri* (Western Sandpiper, Bécasseau d'Alaska)
- subfamily: Scolopacinae
  - genus: *Limnodromus*
    - species: *Limnodromus griseus* (Short-billed Dowitcher, Bécassin roux)

- species: *Limnodromus scolopaceus* (Long-billed Dowitcher, Bécassin à long bec)
    - o genus: *Lymnocryptes*
        - species: *Lymnocryptes minimus* (Jack Snipe, Bécassine sourde) A
    - o genus: *Gallinago*
        - species: *Gallinago delicata* (Wilson's Snipe, Bécassine de Wilson)
        - species: *Gallinago gallinago* (Common Snipe, Bécassine des marais)
        - species: *Gallinago stenura* (Pin-tailed Snipe, Bécassine à queue pointue) A
        - species: *Gallinago solitaria* (Solitary Snipe, Bécassine solitaire) A
    - o genus: *Scolopax*
        - species: *Scolopax rusticola* (Eurasian Woodcock, Bécasse des bois) A
        - species: *Scolopax minor* (American Woodcock, Bécasse d'Amérique)

- subfamily: Tringinae
    - o genus: *Xenus*
        - species: *Xenus cinereus* (Terek Sandpiper, Chevalier bargette) N
    - o genus: *Actitis*
        - species: *Actitis hypoleucos* (Common Sandpiper, Chevalier guignette) N
        - species: *Actitis macularius* (Spotted Sandpiper, Chevalier grivelé)
    - o genus: *Tringa*
        - species: *Tringa ochropus* (Green Sandpiper, Chevalier cul-blanc) A
        - species: *Tringa solitaria* (Solitary Sandpiper, Chevalier solitaire)
        - species: *Tringa brevipes* (Gray-tailed Tattler, Chevalier de Sibérie) N
        - species: *Tringa incana* (Wandering Tattler, Chevalier errant)
        - species: *Tringa erythropus* (Spotted Redshank, Chevalier arlequin) N
        - species: *Tringa melanoleuca* (Greater Yellowlegs, Grand Chevalier)
        - species: *Tringa nebularia* (Common Greenshank, Chevalier aboyeur) N
        - species: *Tringa semipalmata* (Willet, Chevalier semipalmé)
        - species: *Tringa flavipes* (Lesser Yellowlegs, Petit Chevalier)
        - species: *Tringa stagnatilis* (Marsh Sandpiper, Chevalier stagnatile) A
        - species: *Tringa glareola* (Wood Sandpiper, Chevalier sylvain)
        - species: *Tringa totanus* (Common Redshank, Chevalier gambette) A
    - o genus: *Phalaropus*
        - species: *Phalaropus tricolor* (Wilson's Phalarope, Phalarope de Wilson)

- species: *Phalaropus lobatus* (Red-necked Phalarope, Phalarope à bec étroit)
- species: *Phalaropus fulicarius* (Red Phalarope, Phalarope à bec large)

Recommendation:

SACC voted to recognize these five subfamilies. I recommend YES to both parts. There is a considerable degree of robust morphological and molecular evidence for curlews and godwits (at least) as good subfamily-level taxa. And while more may eventually be done when relationships are fully worked out in the family, this framework seems quite solid.

Literature Cited:

Baker, A. J., S. L. Pereira, and T. A. Paton. 2007. Phylogenetic relationships and divergence times of Charadriiformes genera: multigene evidence for the Cretaceous origin of at least 14 clades of shorebirds. Biology Letters 3:205-209.

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Submitted by: Kevin Winker
Date of Proposal: 23 November 2015

Split Emerald Toucanet *Aulacorhynchus prasinus* into seven species

Background:

The emerald toucanets belonging to the *Aulacorhynchus prasinus* species group are distributed from southern and eastern Mexico south to Bolivia (Puebla-Olivares *et al.* 2008, Bonaccorso 2011), and they present considerable variation in bill shape and color patterns along their range (Haffer 1974, Navarro-Sigüenza *et al.* 2001). Along its distribution, isolated populations of *A. prasinus* on single mountain ranges show considerable differentiation (Puebla-Olivares *et al.* 2008), and most forms replace one another along latitudinal and elevational gradients (Gilbert 2002). Given the known differences, there are 15-17 currently recognized subspecies, distinguished mainly by bill and throat coloration (Peters 1948, Winker 2000). These are characters that have been considered important in reproductive and social behavior in Ramphastidae (Skutch 1967). These differences among the isolated populations of *A. prasinus* throughout its range and the careful analyses of coloration and morphology have led to the consideration of *A. prasinus* to constitute a complex of multiple species (Haffer 1974, Navarro-Sigüenza *et al.* 2001, Ridgely & Greenfield 2001, Clements 2007). Although the most widely adopted taxonomy recognizes *Aulacorhynchus* to consist of six species (*e.g.*, Short & Horne 2002, Dickinson 2003, Remsen *et al.* 2015; *contra* IOC World Bird List 2015), there is strong evidence to support a split of this complex given morphological and molecular analyses of the available data (Puebla-Olivares *et al.* 2008, Bonaccorso 2011, Bonaccorso & Guayasamin 2013).

New Information:

Puebla-Olivares *et al.* (2008) performed an analysis of genetic variation in the *Aulacorhynchus prasinus* complex, using segments of mitochondrial DNA genes (cytochrome *b*, ND2 and ND3), and found seven differentiated populations that are consistent with well-defined biogeographic limits found across the distribution of the complex. This also agrees with the limits previously suggested solely on the basis of morphological evidence. Genetic variation coincides with geographical structuring in the emerald toucanets, which can be appreciated by the average genetic distance and the values of genetic differentiation (*Fst*) and gene flow (*Nm*). The consensus phylogenetic tree obtained, along with the deep divergence values among the subclades of the *"prasinus"* complex, suggests a deep genetic differentiation and supports a split. They suggested, based on the morphological and molecular data, that these clades likely represent species under the evolutionary, biological, and phylogenetic concepts, recognizing four species in Mesoamerica (*A. prasinus, A. wagleri, A. caeruleogularis*, and *A. cognatus*) and three in South America (*A. griseigularis, A. albivitta*, and *A. atrogularis*).

More recently, a molecular study by Bonaccorso *et al.* (2011) on the phylogenetic relationships in the genus *Aulacorhynchus* used the same mitochondrial genes (except ND3) and included two nuclear loci (TGFβ2.5 and βfib7). Their results were consistent with those previously obtained by Puebla-Olivares *et al.* (2008), showing differentiated

clades within the *"prasinus"* complex (although Bonaccorso *et al.* didn't include *A. cognatus* in the sampling).

Given the evidence, current recognition of *A. prasinus* as a single species with a wide distribution doesn't seem to be correct, given the morphological and genetic differentiation within the species.

Recommendation:

Split *Aulacorhynchus prasinus* into seven species. Four of them would have a direct effect on NACC:

(1) ***Aulacorhynchus prasinus* (Gould 1833). Emerald Toucanet.** Northeastern Mexico south to Nicaragua. Includes the subspecies *warneri*, *chiapensis, virescens, stenorhabdus*, and *volcanius*.

(2) ***Aulacorhynchus wagleri* (Sturm and Sturm 1841). Wagler's Toucanet.** Endemic to southern Oaxaca and Sierra Madre del Sur of Guerrero in Mexico.

(3) ***Aulacorhynchus caeruleogularis* (Gould 1854). Blue-throated Toucanet**. Endemic to the montane humid forests of Costa Rica and western Panama. Includes the subspecies *maxillaris*.

(4) ***Aulacorhynchus cognatus* (Nelson 1912). Goldman's Blue-throated Toucanet**. Endemic to the isolated mountains of Darién, in eastern Panama.

The other three species have a direct effect on SACC, and maybe should be treated in another proposal:

(5) ***Aulacorhynchus griseigularis* Chapman 1915. Grey-throated Toucanet.** Endemic to western and central Andes of Colombia.

(6) ***Aulacorhynchus albivitta* (Boissonneau 1840). White-throated Toucanet.** Occurs along the Andes of northern South America, in Venezuela and eastern Colombia.

(7) ***Aulacorhynchus atrogularis* (Sturm and Sturm 1841). Black-throated Toucanet.** Distributed along the eastern slopes of the Andes of Bolivia and Peru. Includes the subspecies *cyanolaemus.*

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Submitted by: Danny Zapata-Henao
Date of Proposal: 23 November 2015

Transfer Yellow-breasted Crake *Porzana flaviventer* to *Hapalocrex* and transfer Laysan Rail *P. palmeri* and Hawaiian Rail *P. sandwichensis* to *Zapornia*

Background:

The AOU Checklist currently lists five species in the genus *Porzana*, as follows:

Porzana palmeri (Laysan Rail) H †
Porzana porzana (Spotted Crake) A
Porzana carolina (Sora)
Porzana sandwichensis (Hawaiian Rail) H †
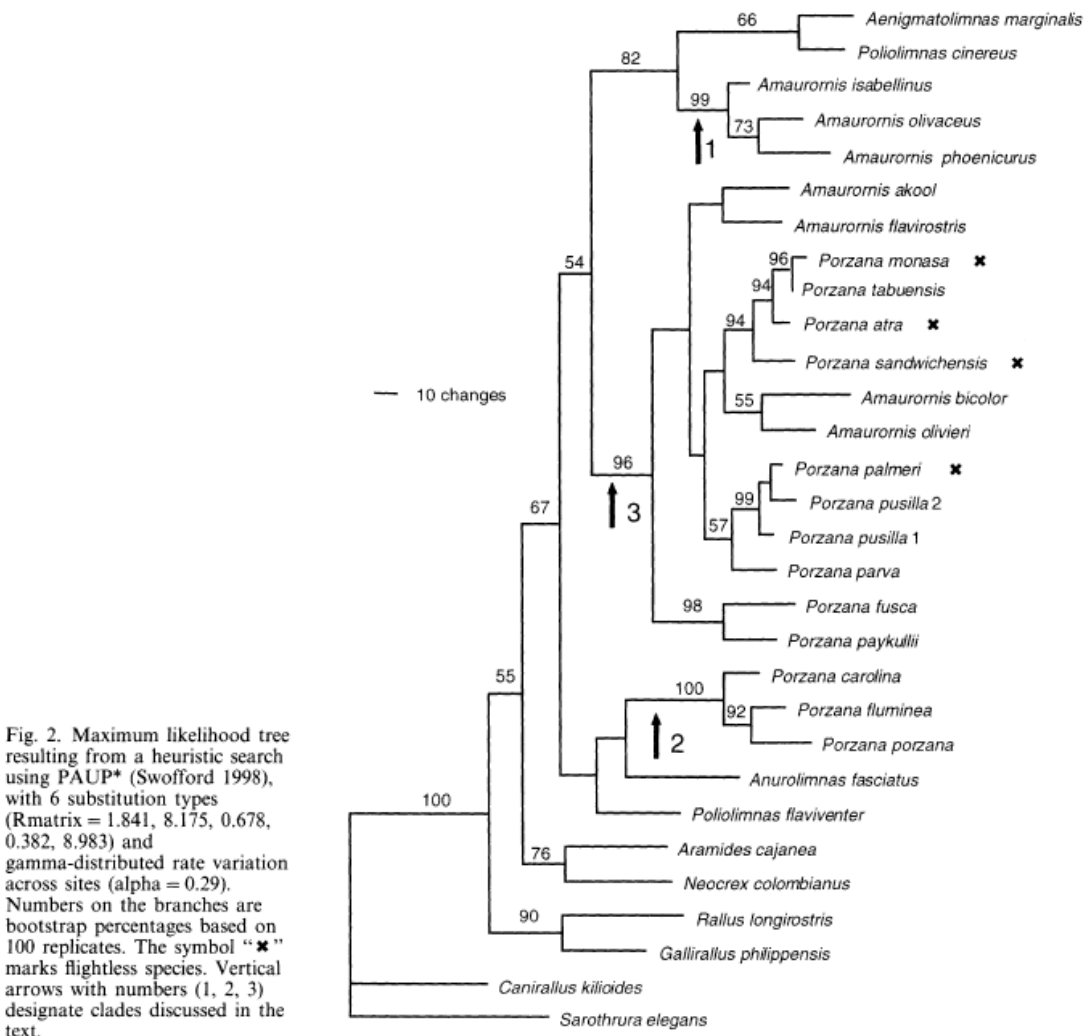*Porzana flaviventer* (Yellow-breasted Crake)

Slikas et al. (2002), in a study focused on the evolution of flightless rails, used ca. 900 bp of mitochondrial DNA to conduct a phylogenetic analysis including of 12 of the 14 species of *Porzana*, seven of the nine species of *Amaurornis*, and 10 other rail species. Their phylogeny provided evidence that neither *Porzana* nor *Amaurornis* is monophyletic (see tree below).

AOU species currently placed in *Porzana* belonged to three lineages: the extinct species *palmeri* and *sandwichensis* grouped with a large number of species of *Porzana* and *Amaurornis* in Clade 3 in their tree, *porzana* and *carolina* grouped into Clade 2, and *flaviventer* (as *Poliolimnas flaviventer*) was the second successive sister to Clade 2. Support for Clade 3 and Clade 2 was strong (96% and 100%, respectively), but support at deeper levels of the tree was generally weaker.

New Information:

Garcia-R et al. (2014) recently published a phylogeny of the Rallidae based on sequences of ca. 2900 bp of mitochondrial DNA and ca. 1900 bp of nuclear DNA. They sequenced some 50% of rail species, including AOU species *porzana, carolina*, and *flaviventer*. They did not sequence extinct species *sandwichensis* and *palmeri*, but included several species (e.g., *P. paykullii*, *fusca*, *tabuensis*, *pusilla*, and *parva*, and *A. akool* and *flavirostris*) that grouped with them in Clade 3 of the Slikas et al. (2002) tree. Their results were very similar to those of Slikas et al. (2002), except that their broader taxon sampling produced even greater separation between the clades containing (1) *porzana* and *carolina*, (2) *palmeri* and *sandwichensis*, and (3) *flaviventer*. The relevant part of their tree is reproduced on the next page. In it, *porzana* and *carolina* are located in the section of the tree colored dark gray whereas *flaviventer* is in the light purple (lavender?) section. Species that formed a clade with *palmeri* and *sandwichensis* in the Slikas et al. tree are in the section colored red. These clades are all strongly supported

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(bootstraps from 95-100%; posterior probabilities all 1.0), although again the deeper branches received noticeably weaker support.

Fig. 2. Maximum likelihood tree resulting from a heuristic search using PAUP* (Swofford 1998), with 6 substitution types (Rmatrix = 1.841, 8.175, 0.678, 0.382, 8.983) and gamma-distributed rate variation across sites (alpha = 0.29). Numbers on the branches are bootstrap percentages based on 100 replicates. The symbol " ✖ " marks flightless species. Vertical arrows with numbers (1, 2, 3) designate clades discussed in the text.

Recommendation: It seems clear that *Porzana*, as currently treated, is polyphyletic. I propose that we split our species into the three groups identified in the phylogenies of Slikas et al. (2002) and Garcia-R et al. (2014). Dickinson and Remsen (2013), in their treatment of the family Rallidae, already made this split based on Slikas et al (2002). The type species of *Porzana* is *porzana*, so *porzana* and *carolina* would remain in *Porzana*. The genus name *Zapornia* (type species *parva*) is available for the clade containing *palmeri* and *sandwichensis*, and the genus name *Hapalocrex* (type *flaviventer*) is available for *flaviventer*.

Relevant section of the tree of Garcia-R et al. (2014):
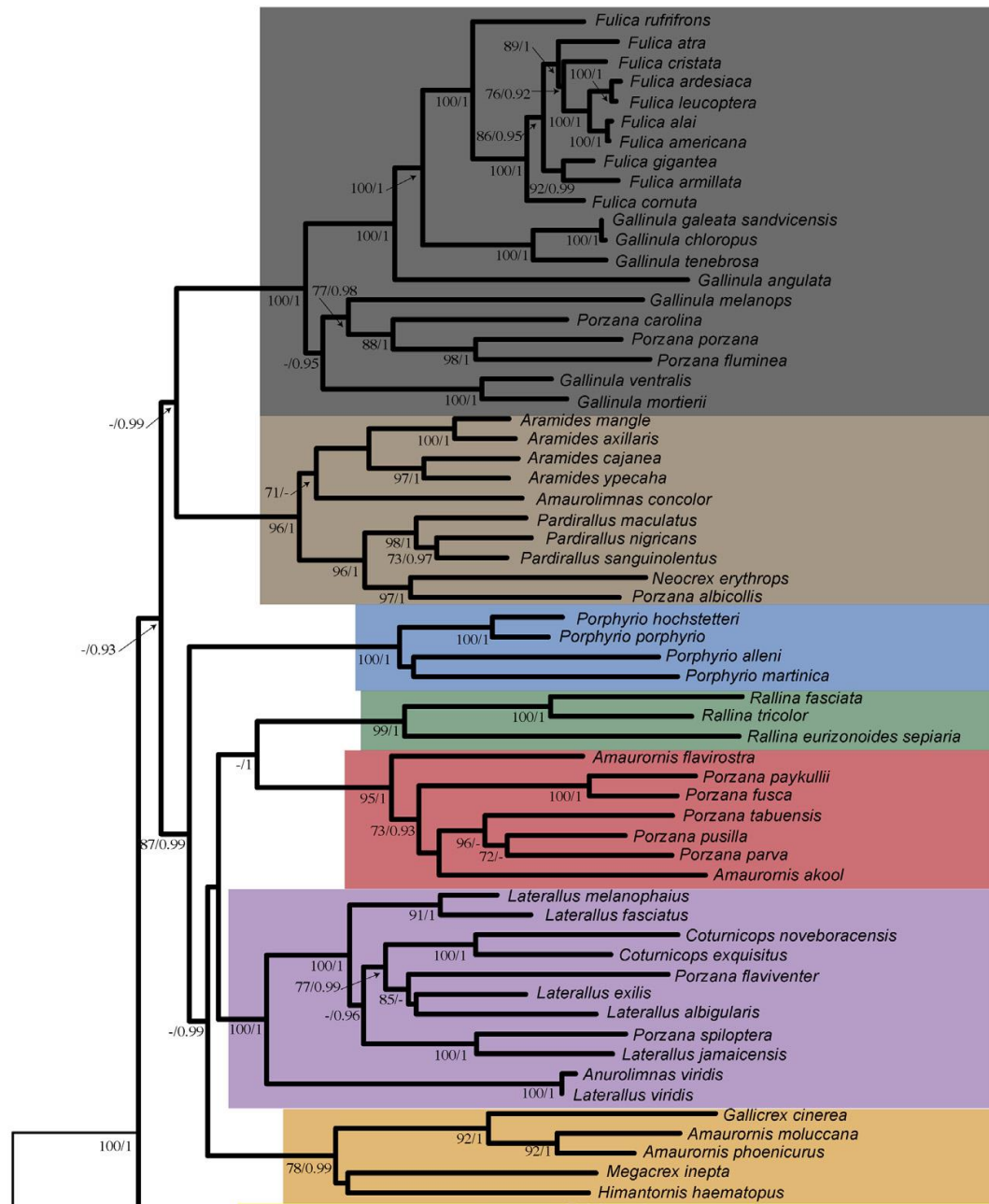
At a minimum, our linear sequence will have to be changed so that species in the same genus are placed together in the sequence. We could also consider more sweeping changes in the linear sequence based on Garcia-R et al. (2014); for example, it seems clear from their tree that *Porzana*, *Gallinula*, and *Fulica* form a well-supported clade, and that *Hapalocrex* forms a well-supported clade with *Laterallus* and *Coturnicops*. However, given the limited support at deeper nodes, we would essentially be placing these and other well-supported clades in a sequence based on very little support. We have a good support for the constituent clades in the Rallidae but a poor idea of how

they fit together, so perhaps it's best if we restrict our attention at the moment to *Porzana*. The limited taxon sampling also makes it difficult to apply our conventions for linear sequences for splitting *Porzana*. However, we can certainly make the following two changes:

(1) move *Zapornia palmeri* to precede *Z. sandwichensis* in our linear sequence. This places our two *Zapornia* species together and also places *Zapornia* adjacent to *Hapalocrex*, which is supported by Garcia-R et al. (2014).

(2) move *Porzana carolina* to precede *P. porzana*. In the trees of both Slikas et al. (2002) and Garcia-R et al. (2014), *carolina* is sister to a clade containing *porzana* and *fluminea*, meaning that *carolina* should precede *porzana* in our sequence.

The new arrangement would therefore be:

Porzana carolina
Porzana porzana
Zapornia palmeri
Zapornia sandwichensis
Hapalocrex flaviventris

Literature Cited:

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Submitted by: Terry Chesser
Date of Proposal: 28 December 2015

Recognize new subfamilies of tanagers

Background:

Tanagers are widely distributed throughout the Neotropics, exhibiting remarkable ecological and phenotypic diversity. The taxonomic limits of the family (Barker et al. 2013) and of genera within Thraupidae have changed frequently (Burns & Racicot 2009, Sedano & Burns 2010, Campagna *et al.* 2011, Mason & Burns 2013, Shultz & Burns 2013). Recently, Burns et al. (2014) produced a near-comprehensive phylogeny for the family that resolved many of these issues. Using this new phylogenetic information, they allocated species into 15 subfamilies, 5 of which were newly described (Burns et al., 2014). These subfamilies are based on the deepest highly supported nodes that descend from a series of short, unresolved internodes near the root of the phylogeny (Fig. 1). Nine of the fifteen subfamilies include species within the geographic scope of the NACC, suggesting that new and rearranged thraupid subfamilies could be recognized to reflect the evolutionary relationships inferred by Burns et al. (2014).

Linear sequence of subfamilies:

Below is a revised linear sequence of thraupid subfamilies based on the findings of Burns et al. (2014) that follows the sequence of genera adopted by Chesser et al. (2015). An asterisk indicates a new subfamily described by Burns et al. (2014).

Thraupinae
 Bangsia
 Paroaria
 Thraupis
 Tangara
Diglossinae
 Conirostrum
 Sicalis
 Haplospiza
 Acanthidops
 Diglossa
Hemithraupinae
 Chlorophanes
 Chrysothlypis
 Heterospingus
 Hemithraupis
Tachyphoninae
 Volatinia
 Eucometis
 Tachyphonus
 Lanio

> *Ramphocelus*

Dacninae

> *Tersina*
> *Cyanerpes*
> *Dacnis*

Coerebinae

> *Coereba*
> *Tiaris*
> *Euneornis*
> *Loxigilla*
> *Melopyrrha*
> *Loxipasser*
> *Melanospiza*
> *Pinaroloxias*

Sporophilinae

> *Sporophila*

Emberizoidinae*

> *Emberizoides*

Saltatorinae

> *Saltator*

Recommendation:

Recognize new and rearranged subfamilies of tanagers to reflect evolutionary relationships within Thraupidae, based on a recent, near-comprehensive phylogeny of the family.

Literature Cited:

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Shultz, A.J. & Burns, K.J. 2013. Plumage evolution in relation to light environment in a novel clade of Neotropical tanagers. *Molecular Phylogenetics and Evolution*, 66, 112–125.

Figure 1:
Phylogeny of Thraupidae with subfamilies shown in different colors (Burns et al. 2014)..
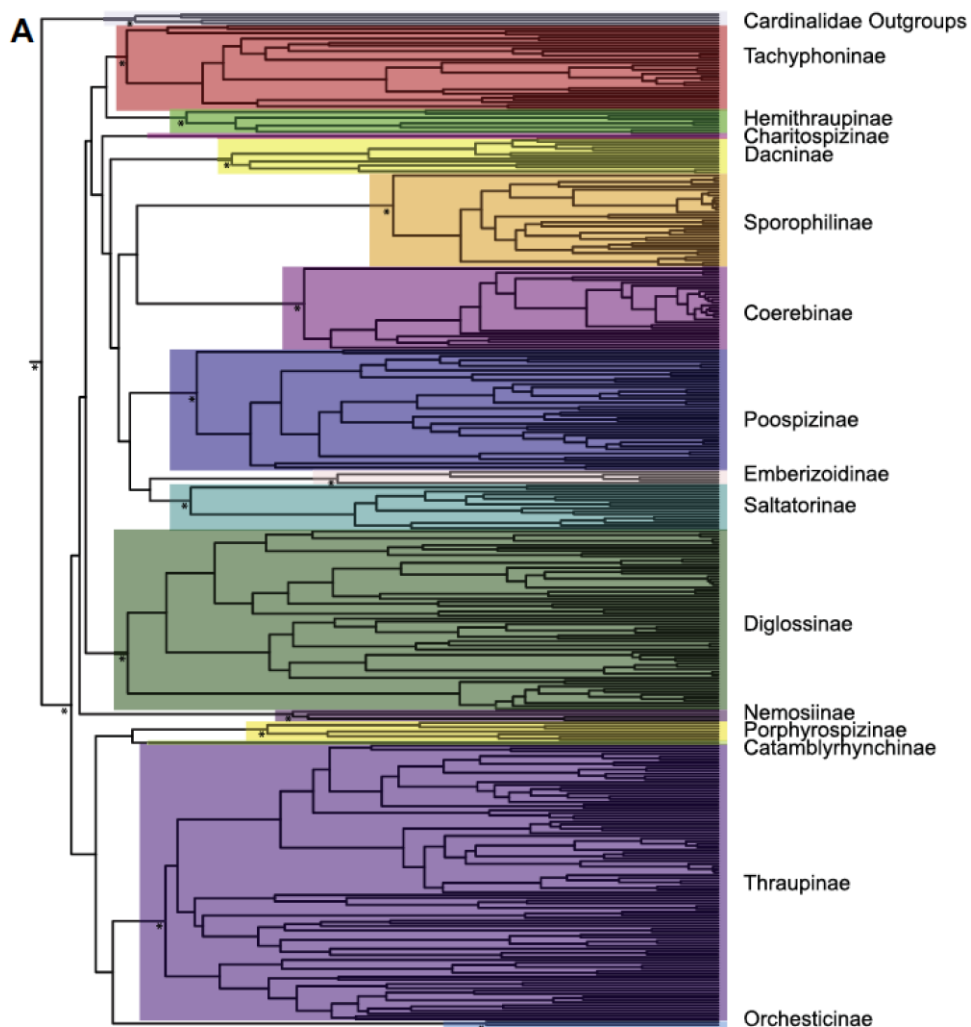
Submitted by: Nicholas A. Mason, Cornell University; Kevin J. Burns, San Diego State University

Date of Proposal: 3 January 2016

Split Costa Rican Warbler *Basileuterus melanotis* and Tacarcuna Warbler *B. tacarcunae* from Three-striped Warbler *B. tristriatus*

Background:

Understory warblers in the *Basileuterus tristriatus* complex inhabit many biogeographic regions in the highlands of Central America and South America (Fig. 1). Preferring mature and secondary forests in the mountains of Costa Rica and much of the Central and Northern Andes, the *B. tristriatus* complex includes fourteen subspecies based largely on phenotypic variation in ventral and facial coloration within two currently recognized species: *B. tristriatus* and *B. trifasciatus* (Howard and Dickinson 2003; Curson 2010; Clements et al. 2015). Geographic barriers separate many differentiated subspecies, and analyses of new molecular (Gutiérrez-Pinto et al. 2012) and vocal data (Donegan 2014) suggest that species limits need reevaluation.

New Information:

Gutiérrez-Pinto et al. (2012) assessed genetic differentiation within the *B. tristriatus* complex, uncovering deep mitochondrial divergences among geographically and phenotypically concordant lineages. Their relatively well-supported mitochondrial gene tree indicated that *B. tristriatus* is paraphyletic with respect to the phenotypically distinct *B. trifasciatus* (of South America) nested within the *tristriatus* clade (Fig. 2). The deep branching order in this reconstruction has *tristriatus melanotis* (*tristriatus tacarcunae* (*trifasciatus* (all remaining *tristriatus*))). Therefore, (1) the two Central American forms of *tristriatus* are outside of the clade formed by *trifasciatus* plus the South American *tristriatus*, and (2) the degree of mitochondrial divergence between these four groups is substantial. Given this deep molecular divergence and the overall phenotypic variation within the complex, (Gutiérrez-Pinto et al. 2012) proposed a taxonomic revision to recognize four species among these ten mitochondrial clades: *melanotis, tacarcunae, trifasciatus*, and *tristriatus*. These authors suggested that genetic divergence should be considered alongside behavioral, phenotypic, and ecological information to delimit species with integrative criteria.

Donegan (2014) later analyzed geographic variation in morphology and vocal displays within the *B. tristriatus* complex. Despite largely undiagnosable variation in morphological characters, Donegan (2014) described diagnosable, qualitative differences in song structure and vocal repertoire concordant with phylogenetic structure inferred by Gutiérrez-Pinto et al. (2012). *Basileuterus tristriatus melanotis* of the Chiriquí-Talamanca highlands of Costa Rica and western Panama sing a rapid, jumbled series of notes and lack the 'rising song' that is present in other *B. tristriatus* repertoires (Donegan 2014). In contrast, the single available recording of *B. t. tacarcunae* reveals an 'incessant and scratchy' song with many more notes than any other lineage in the *B. tristriatus* complex (Donegan 2014). Although Ridgely and

Greenfield (2001) described the songs of *B. tristriatus* and *B. trifasciatus* as 'quantitatively similar', Donegan (2014) noted that the 'slow song' of *B. trifasciatus* is structurally different from all *B. tristriatus* in lacking a long initial trill. Thus, diagnosable, qualitative differences in song structure and repertoire support splitting *B. t. melanotis* and *B. t. tacarcunae* from *B. tristriatus*, resulting in four phenotypically and geographically concordant and monophyletic species within the lineage. In isolation this evidence from partially learned traits might be equivocal, but it is more compelling given the high congruence between the groups delimited by song and mtDNA variation.

Figures:
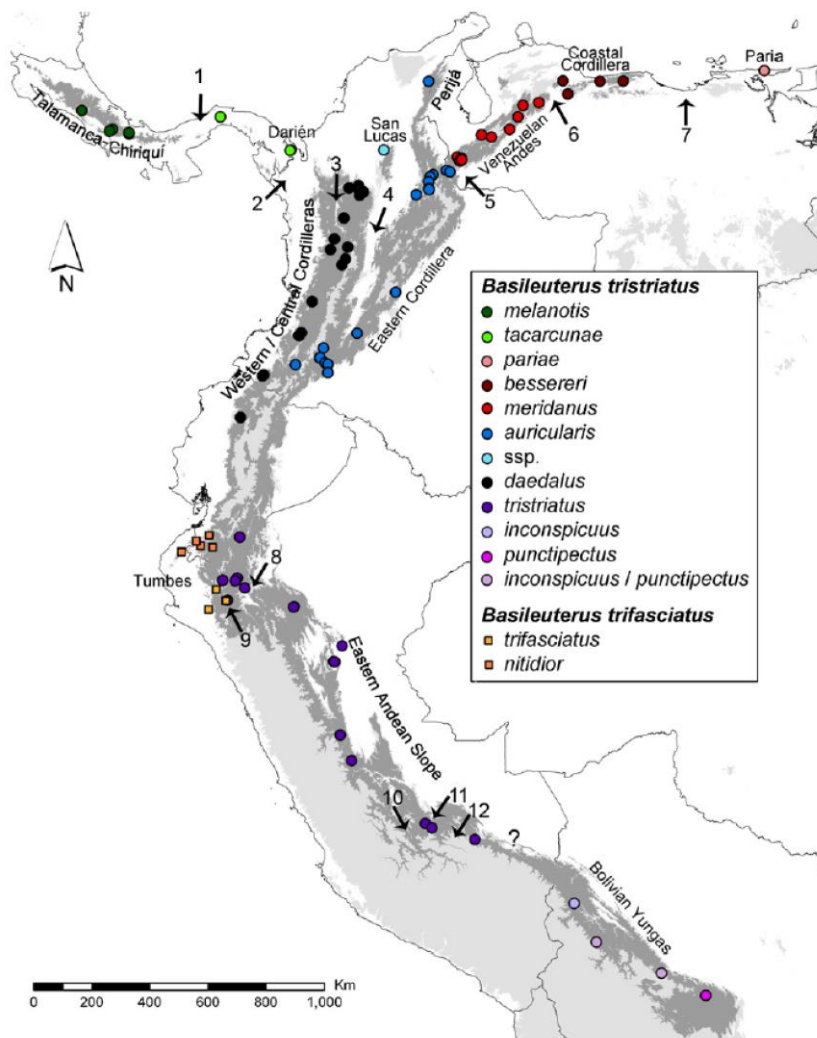
Figure 1: Geographic distribution of *B. tristriatus* complex and sampling localities of Gutiérrez-Pinto et al. (2012).
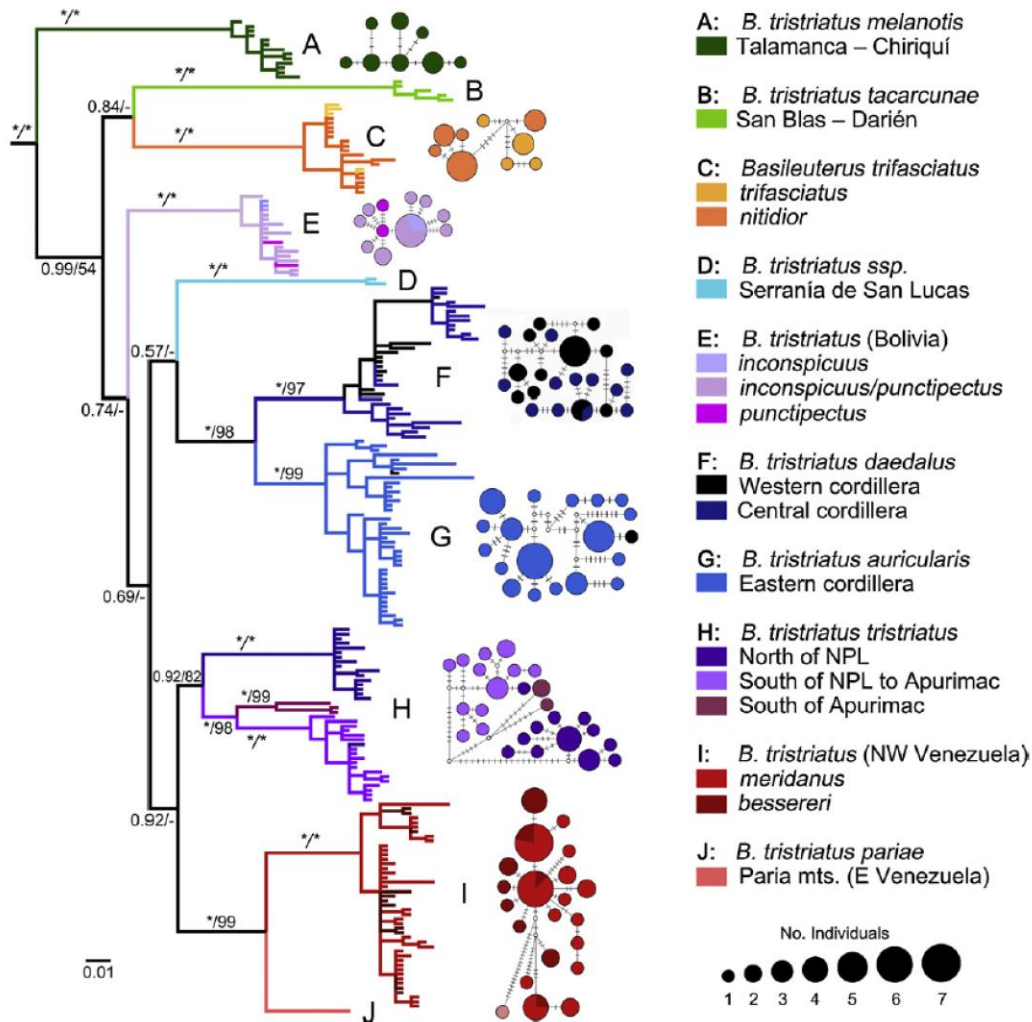
Figure 2: Mitochondrial phylogeny (ND2) of *Basileuterus tristriatus/trifasciatus* complex from Gutiérrez-Pinto et al. (2012).

Recommendation:

Split Costa Rican Warbler *Basileuterus melanotis* and Tacarcuna Warbler *B. tacarcunae* from Three-striped Warbler *Basileuterus tristriatus.*

Literature Cited:

Clements, J. F., T. S. Schulenberg, M. J. Iliff, D. Roberson, T. A. Fredericks, B. L. Sullivan, and C. L. Wood. 2015. The eBird/Clements checklist of birds of the world: v2015. Downloaded from http://www.birds.cornell.edu/clementschecklist/download/

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Donegan, T. M. 2014. Geographical variation in morphology and voice of Three-striped Warbler *Basileuterus tristriatus*. Bulletin of the British Ornithologists' Club 134:79–109.

Gutiérrez-Pinto, N., A. M. Cuervo, J. Miranda, J. L. Pérez-Emán, R. T. Brumfield, and C. D. Cadena 2012. Non-monophyly and deep genetic differentiation across low-elevation barriers in a Neotropical montane bird (*Basileuterus tristriatus*; Aves: Parulidae). Molecular Phylogenetics and Evolution 64:156–165. doi: 10.1016/j.ympev.2012.03.011

Submitted by: Nicholas A. Mason and Irby J. Lovette, Cornell University
Date of Proposal: 5 January 2016

Transfer White-thighed Swallow *Neochelidon tibialis* and Black-capped Swallow *Notiochelidon pileata* to *Atticora*

Effect on NACC: If approved, this proposal would transfer White-thighed Swallow *Neochelidon tibialis* and Black-capped Swallow *Notiochelidon pileata* to *Atticora.* This proposal applies the suggestions of approved SACC proposal #314 to the geographical scope of the NACC. Of the two species considered here, the SACC proposal to merge these species into *Atticora* applied only to *tibialis*, which is found broadly in South America and which enters the NACC region in Panama. Its sister species *pileata* is not found in the South American checklist region, as it is endemic to Mexico and Central America.

Background:

The genus-level classification of swallows has long been troublesome. Morphological criteria from Ridgway (1903, 1904)—particularly foot arrangement and the degree of syndactyly—grouped species into genera for many decades. Over the past two decades or so, a series of molecular studies generated a comprehensive species-level relationships among new world swallows, revealing paraphyly and polyphyly among certain genera (Sheldon et al. 1993, 1995, 2005, Whittingham 2002). This proposal suggests transferring species into monophyletic genera to recognize phylogenetic relationships based on these findings.

The multilocus phylogeny from Sheldon et al. (2005) demonstrates that several swallow genera are not monophyletic. One clade within the 'core martins' includes the genera *Atticora*, *Neochelidon, Notiochelidon, Alopochelidon, Pygochelidon,* and *Haplochelidon* (Fig. 1). Within this clade, *Atticora* is polyphyletic: *A. fasciata* is more closely related to *Notiochelidon pileata* and *Neochelidon tibialis* than it is to *A. melanoleuca.* Similarly, *Notiochelidon pileata* is inferred as sister to *Neochelidon tibialis* rather than its distant congener, *Notiochelidon flavipes.* To resolve this discordance, the SACC adopted a revised genus-level taxonomy with *A. melanoleuca* transferred to *Pygochelidon* Baird 1865 and *Notiochelidon flavipes*, along with *Alopochelidon andecola*, transferred to a resurrected *Orochelidon* Ridgway 1903. To reconcile the clade containing *A. fasciata*, *Neochelidon tibialis,* and *Notiochelidon pileata*, the SACC recommended merging these species into a single genus. *Atticora fasciata* is the type species of *Atticora* Boie 1826, which has priority over its sister genera, *Notiochelidon* Baird 1865 and *Neochelidon* Sclater 1862. Therefore, these three species can be united under the genus *Atticora* in accordance with changes adopted by the SACC.

Figure 1: Phylogeny of core martins within Hirundinidae taken from Sheldon et al. (2005).

The names in the figure above refer to the traditional genera to which these species were assigned. In the same order as presented in the figure, the revision creates monophyletic genera as below:

Original	Revised	relevant Checklist region(s)
Atticora fasciata	*Atticora fasciata*	SA
Notiochelidon pileata	*Atticora pileata*	NA
Neochelidon tibialis	*Atticora tibialis*	NA, SA
Pygochelidon cyanoleuca	*Pygochelidon cyanoleuca*	NA, SA
Atticora melanoleuca	*Pygochelidon melanoleuca*	SA
Alopochelidon fucata	*Alopochelidon fucata*	SA
Notiochelidon murina	*Orochelidon murina*	SA
Haplochelidon andecola	*Orochelidon andecola*	SA

Recommendation:

Transfer White-thighed Swallow (*Neochelidon tibialis*) and Black-capped Swallow (*Notiochelidon pileata*) to *Atticora*.

Literature Cited:

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Sheldon, F. H., L. A. Whittingham, R. G. Moyle, B. Slikas & D. W. Winkler. 2005. Phylogeny of swallows (Aves: Hirundinidae) estimated from nuclear and mitochondrial DNA sequencing. Mol. Phylog. Evol. 35:254-270.

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Submitted by: Nicholas A. Mason and Irby J. Lovette, Cornell University
Date of Proposal: 5 January 2016

Revise the generic classification of 3 species of *Hylophilus*: (a) resurrect *Pachysylvia* and (b) recognize *Tunchiornis* (SACC 656A-B)

Background:

SACC Vireonidae footnotes 11 and 14 read as follows:

11. Genetic data indicate that *Hylophilus* is not monophyletic (Johnson et al. 1988) and that at least three separate genera are required (Slager et al. 2014). The name *Pachysylvia* was formerly (e.g., Ridgway 1904) used for *Hylophilus*. SACC proposal 656 passed to resurrect *Pachysylvia*.

14. Slager et al. (2014) found that inclusion of *ochraceiceps* in *Hylophilus* would make that genus paraphyletic. Slager & Klicka (2014) named a new genus for this species, *Tunchiornis*. SACC proposal 656 passed to adopt *Tunchiornis*.

Other lines of evidence besides phylogenetics also support the polyphyly of *Hylophilus*. As Slager and Klicka (2014) wrote, "[a]lthough *Hylophilus* species do share some common anatomical proportions and plumage features, some striking and concordant differences in habitat, voice, and iris color led Ridgely and Tudor (1989) to posit that the genus might contain sufficient diversity to warrant splitting into multiple genera." Ridgely and Tudor (1989) categorized *Hylophilus* into three groups: The pale-eyed "scrub" group, the dark-eyed "canopy" group, and the "understory" group (*Hylophilus ochraceiceps*).

New Information:

Slager et al. (2014) produced a phylogeny of Vireonidae using mitochondrial (ND2) and nuclear (3 Z-linked loci) data that included 221 samples representing 46/52 currently recognized vireonid species and 14/15 species of *Hylophilus.* The phylogeny of Slager et al. (2014) showed that *Hylophilus* was polyphyletic, composed of 4 clades spread throughout Vireonidae. The four clades are shown in phylogenetic context in Figure 1 of Slager and Klicka (2014).

Hylophilus is clearly polyphyletic based on molecular data (Slager et al. 2014) and four genera are needed to reflect this diversity (Slager and Klicka 2014).

The first clade, containing extralimital *Hylophilus sclateri*, was addressed in a separate SACC proposal (Proposal 655) which passed, transferring *sclateri* to genus *Vireo*.

The second clade, containing the pale-eyed, scrub-dwelling species *H. poicilotis, H. amaurocephalus, H. flavipes, H. olivaceus, H. semicinereus, H. thoracicus, H.*

pectoralis, and *H. brunneiceps,* can remain in the genus *Hylophilus* since the type species of *Hylophilus* is *H. poicilotis.* See paragraph 5 of Slager and Klicka (2014) for more discussion. *H. flavipes* is the only species in this clade on the NACC checklist.

The third clade contains several canopy-dwelling species with dark irides and complex songs: *H. decurtatus*, *H. aurantiifrons*, *H. hypoxanthus*, *H. muscicapinus*, and *H. semibrunneus.* Because *Hylophilus* is in use for the "scrub" greenlets, these canopy species should be transferred to the resurrected genus *Pachysylvia* Bonaparte (type species = *H. decurtatus*), which has priority. See 6th paragraph of Slager and Klicka (2014) for more details. Since *Pachysylvia* is feminine, the specific epithets for *decurtatus*, *hypoxanthus*, *muscicapinus*, and *semibrunneus* should be changed to *decurtata*, *hypoxantha*, *muscicapina*, and *semibrunnea*, respectively. *H. aurantiifrons* and *H. decurtatus* are the two species in this clade on the NACC checklist.

The fourth clade, containing the forest interior understory-dwelling *Hylophilus ochraceiceps*, is sister to (*Vireo* + *Hylophilus sclateri* + *Pachysylvia*) and clearly needs its own genus. Slager and Klicka (2014) described *Tunchiornis* for this purpose. See Slager and Klicka (2014) paragraph 7 and page 2 for details.

Recommendation:

YES votes are recommended (a) to resurrect *Pachysylvia*, and (b) to recognize *Tunchiornis*.

Literature Cited:

Ridgely, R.S. & Tudor, G. (1989) The Birds of South America. Vol. 1. The Oscine Passerines. University of Texas Press, Austin, Texas, 596 pp.

Slager, D.L., Battey, C.J., Bryson, R.W. Jr., Voelker, G., & Klicka J. (2014) A multilocus phylogeny of a major New World avian radiation: the Vireonidae. *Molecular Phylogenetics and Evolution* 80, 95-104.

Slager, D.L. & J. Klicka. (2014). Polyphyly of *Hylophilus* and a new genus for the Tawny-crowned Greenlet (Aves: Passeriformes: Vireonidae). *Zootaxa* 3884:194-196.

Submitted by: David L. Slager, Department of Biology & Burke Museum of Natural History and Culture, Seattle, Washington, USA
Date of Proposal: 4 January 2016

SACC comments

Comments from Stiles: "YES to A and B. The canopy greenlets form a coherent group, with *Pachysylvia* available as the genus name. Clearly *ochraceiceps* also requires its own genus given its remote phylogenetic position."

Comments from Nores: "A-B: NO. I would include *H. ochraceiceps,* "canopy" *Hylophilus,* and *Hylophilus sclateri* within *Vireo.*"

Comments from Zimmer: "YES to A and B. The genetic data are clear that *Hylophilus*, as currently constituted, is polyphyletic. The proposed reclassification would appropriately recognize the two internally coherent groups of pale-eyed (scrub greenlets) versus dark-eyed (canopy greenlets) in separate genera (while employing historically used names), while placing the very different, polytypic *ochraceiceps* in its own, newly erected genus."

Comments from Robbins: "YES to both. Genetic data make this a straightforward decision for erecting two genera for the clades that clearly are not monophyletic with true *Hylophilus* vireos."

Comments from Areta: "YES to A and B. Taxon sampling is excellent, and the phylogenetic grouping of the *Pachysylvia* should be recognized at the genus level. I also agree in that the very distinctive and phylogenetically isolated *ochraceiceps* deserves to be in its own genus. *Tunchiornis* is a fine name."

Revise the linear sequence of Vireonidae (SACC 661)

Background:

Vireonidae is a rather morphologically conserved family that has received relatively little phylogenetic attention over the years.

SACC Vireonidae footnote 13a currently reads as follows:

> 13a. *Hylophilus flavipes* and *H. olivaceus* were considered to form a superspecies by AOU (1983) and Sibley & Monroe (1990) because Zimmer (1942b) considered them conspecific. Slager et al. (2014), however, found that they are not sister species: *H. olivaceus* and *H. pectoralis* are sisters, and *H. flavipes* and *H. semicinereus* are sisters.

New Information:

Slager et al. (2014) produced a phylogeny of Vireonidae using mitochondrial (ND2) and nuclear (3 Z-linked loci) data that included 221 samples representing 46/52 currently recognized vireonid species. SACC proposal 661 passed to modify the linear sequence of the family.

The multilocus and ND2 trees in Slager et al. (2014) provide many new insights on relationships within Vireonidae.

Gene tree conflict occurs at the deepest nodes in Slager et al. (2014). Three Z-linked nuclear loci, concatenated mtDNA + nuclear loci, and species tree analyses of 4 loci place *Cyclarhis* sister to "scrub" *Hylophilus*, which are in turn sister to (*Vireolanius* + the rest of Vireonidae). However, analyzing mitochondrial ND2 sequences alone places *Cyclarhis* sister to the rest of Vireonidae. This proposal uses the former topology since it is the one best supported by multiple loci.

Translating the tree of Slager et al. (2014) into a linear sequence (using their multilocus concatenated/species tree topology for the deeper nodes and their ND2 tree for shallower nodes) yields the following sequence for NACC species:

Cyclarhis gujanensis
Hylophilus flavipes
Vireolanius melitophrys
Vireolanius pulchellus
Vireolanius eximius
Tunchiornis ochraceiceps

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Pachysylvia decurtata
Pachysylvia aurantiifrons
Vireo hypochryseus

(linear sequence for the species below follows AOU, mostly, because of lack of structure)

    Vireo osburni
    Vireo brevipennis
    Vireo atricapilla
    Vireo nelsoni *
    Vireo griseus
    Vireo crassirostris
    Vireo pallens
    Vireo bairdi
    Vireo caribaeus *
    Vireo modestus
    Vireo gundlachii *
    Vireo latimeri
    Vireo nanus
    Vireo bellii
    Vireo vicinior
    Vireo huttoni

Vireo flavifrons
Vireo carmioli
Vireo cassinii
Vireo solitarius
Vireo plumbeus
Vireo philadelphicus
Vireo gilvus
Vireo leucophrys
Vireo olivaceus (ignoring species limits problems)
Vireo flavoviridis
Vireo altiloquus
Vireo magister

Pachysylvia and *Tunchiornis* are new names (see SACC 656 and concurrent NACC proposal).

* unsampled in Slager et al. (2014)

Recommendation:

I recommend a YES vote. Although Slager et al. (2014) does not resolve every node, the proposed linear sequence reflects the current state of knowledge much better than the existing linear sequence.

Literature Cited:

Slager, D.L., Battey, C.J., Bryson, R.W. Jr., Voelker, G., & Klicka J. (2014) A multilocus phylogeny of a major New World avian radiation: The Vireonidae. Molecular Phylogenetics and Evolution 80, 95-104.

Submitted by: David L. Slager, Department of Biology & Burke Museum of Natural History and Culture
Date of Proposal: 4 January 2016

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SACC comments

<u>Comments from Nores</u>: NO. In the phylogeny of Vireonidae (Slager et al. 2014), the taxon that splits first is *Cyclarhis* and must be placed at the top of the sequence. Then, splits the clade containing V*ireolanius* of which *leucotis* splits first and must be placed in that order. Then splits the clade containing several species of scrub-dwelling *Hylophilus* and finally, the clades containing *Hylophilus ochraceiceps,* "canopy" *Hylophilus, Vireo* and *Hylophilus sclateri.* In my opinion *Hylophilus ochraceiceps,* "canopy" *Hylophilus* and *Hylophilus sclateri* could be included within *Vireo*, the linear sequence would be as follows:

   Cyclarhis gujanensis
   Cyclarhis nigrirostris
   Vireolanius leucotis
   Vireolanius eximius
   Hylophilus amaurocephalus
   Hylophilus poicilotis
   Hylophilus olivaceus
   Hylophilus pectoralis
   Hylophilus flavipes
   Hylophilus semicinereus
   Hylophilus brunneiceps
   Hylophilus thoracicus
   Vireo ochraceiceps
    Vireo decurtatus
    Vireo hypoxanthus
    Vireo muscicapinus
    Vireo aurantiifrons

Vireo semibrunneus
Vireo flavifrons
Vireo masteri
Vireo sclateri
Vireo philadelphicus
Vireo leucophrys
Vireo olivaceus
Vireo gracilirostris
Vireo flavoviridis
Vireo altiloquus

Comments from Stiles: YES, with the minor tweak suggested by Manuel. However, I do think that it would be important to sequence *V. masteri* in particular (see my comment on prop. 658).

Comments from Jaramillo: YES - I see no problems with the new proposed linear order, some fine-tuning on the species level stuff is of course necessary.

Additional comments from Remsen: Concerning Manuel's objection to the proposed sequence, see the second paragraph under Analysis above.

Comments from Pacheco: YES. I choose the exact sequence in Slater's proposal, considering the comments of Remsen.

Revise the classification of the Apodiformes

This proposal would elevate the hummingbirds Trochilidae to the status of order as Trochiliformes, thereby recognizing its level of taxonomic distinctness as commensurate with that of groups formerly treated within Caprimulgiformes but which will now be treated (if Proposal 2016-A-14 has passed) at the ordinal level.

Background:

The hummingbirds have long been treated as a family within the Apodiformes, based on several shared anatomical characters, although some authors have considered certain or all of these characters to be due to convergent adaptations for their extreme flight styles. The Apodiformes has also long been considered likely the closest relatives of Caprimulgiformes. Several molecular phylogenetic analyses have now confirmed this basic picture.

New Information:

In Proposal 2016-A-14, the AOU-CLC voted on recognizing Steatornithidae and Nyctibiidae as orders rather than families within the Caprimulgiformes. The proposal's author (Remsen) and other voting committee members noted during this process that, while clearly sister groups, the split between the hummingbirds Trochilidae and the swifts Apodidae and Hemiprocnidae is almost as deep as that for the Steatornithidae and Nyctibiidae in a recent higher-order avian phylogeny (Prum et al. 2015). However, Proposal 14 was concerned solely with the proposed revision of Caprimulgiformes *sensu lato*, and a split of Apodiformes was therefore not an option. In Jarvis et al. (2014), which shows only one member of each order, the divergence time between Trochilidae and Apodidae was later than for other traditionally recognized orders except for Piciformes and Coraciiformes, which are hypothesized therein to have diverged during approximately the same time intervals as Trochilidae-Apodidae.

Conversely (as mentioned by Van), Cracraft (2013) expanded Caprimulgiformes to include all present members of Apodiformes, which were united within the Superfamily Trochiloidea. This treatment is simple but does not standardize taxonomic level with divergence times, and Cracraft (2013) did not clearly explain the rationale for choosing this option. Winkler et al. (2015), citing Hackett et al. (2008) and Jarvis et al. (2014) as the phylogenetic hypotheses followed, also retained all these groups (including traditional Apodiformes) in Caprimulgiformes. But as Van pointed out in Proposal 2016-A-14, several erstwhile Caprimulgiform lineages are older than several other groups traditionally (and still) treated as orders. This proposal is a follow-up to Remsen's Caprimulgiformes proposal, even using some of the same images (thanks, Van).
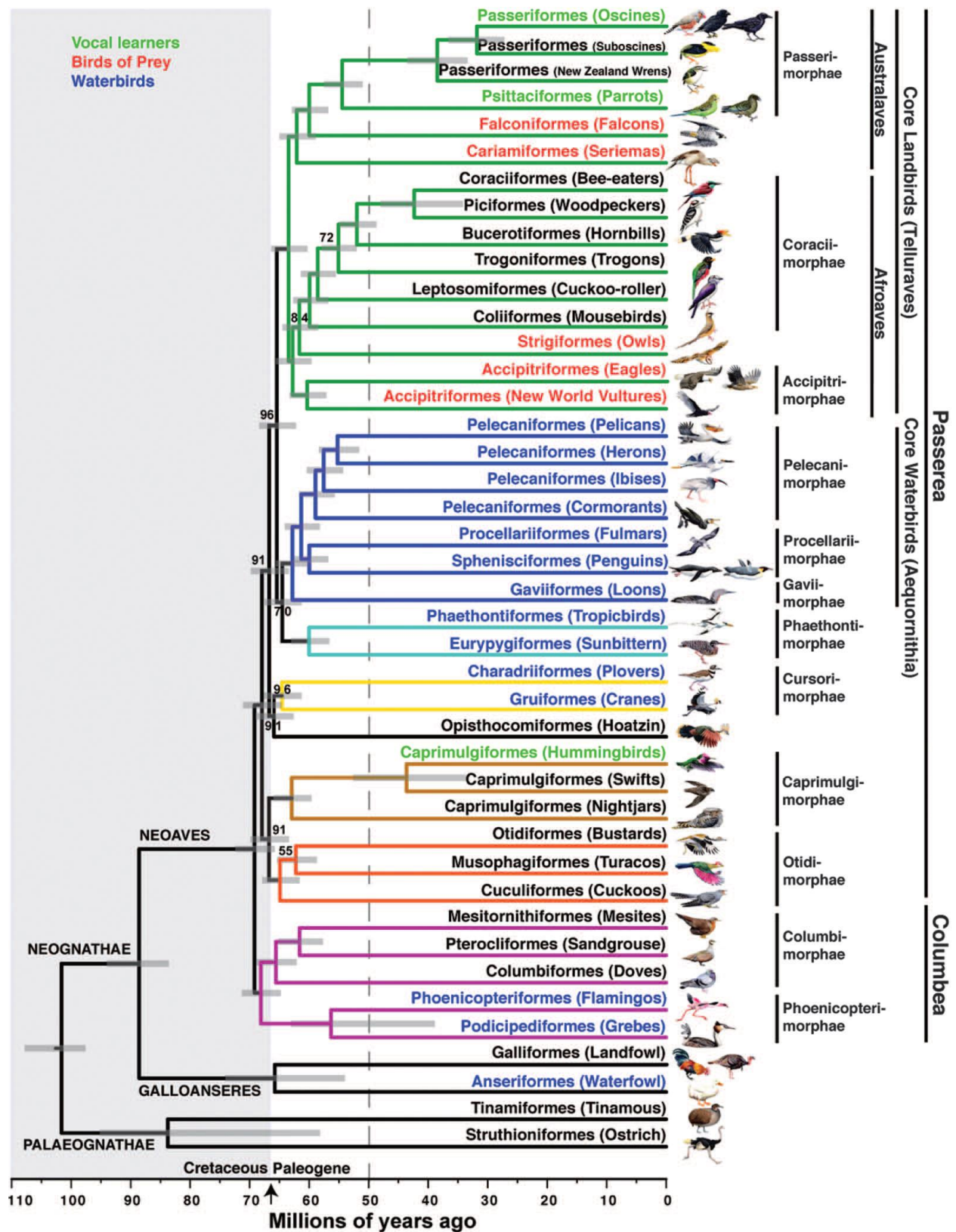
36

From Hackett et al. (2008):
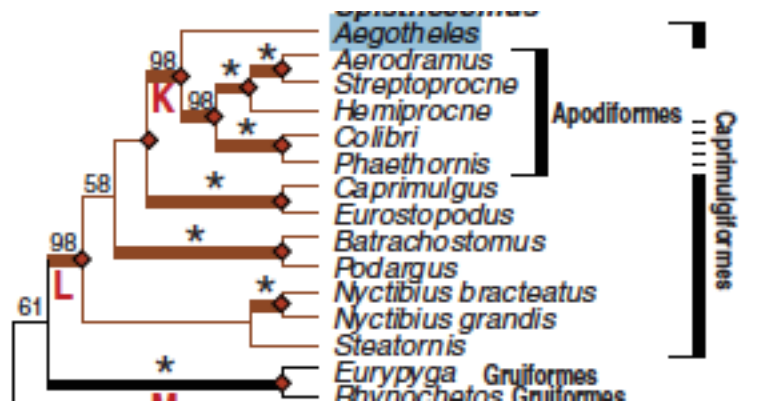
and Prum et al. (2015):
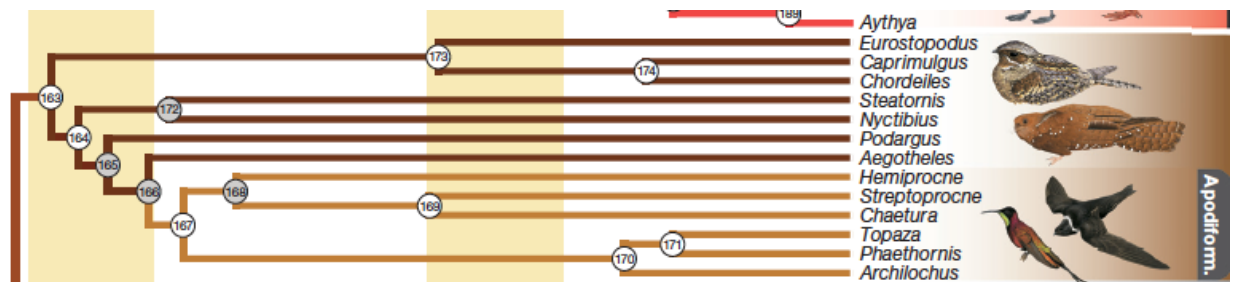
From Jarvis et al. (2014):

If we are elevating Steatornithidae and Podargidae to order level, then it seems that for the sake of consistency we should elevate Trochiliformes as well.

Recommendation:

I recommend a YES vote for treating Trochilidae as a family within the order Trochiliformes, sister to Apodiformes. The alternative, a NO vote, would maintain Trochilidae within the traditional Apodiformes.

Literature Cited:

Cracraft, J. 2013. Avian higher-level relationships and classification: nonpasseriforms. Pp. xxi-xli in: Dickinson, E.C. and J. V. Remsen, Jr. (Eds.) 2013. *The Howard and Moore Complete Checklist of the Birds of the World. 4th ed. Vol. 1.* Aves Press, Eastbourne, UK.

Hackett, S. J., R. T. Kimball, S. Reddy, R. C. K. Bowie, E. L. Braun, M. J. Braun, J. L. Choinowski, W. A. Cox, K.-L. Han, J. Harshman, C. J. Huddleston, B. D. Marks, K. J. Miglia, W. S. Moore, F. H. Sheldon, D. W. Steadman, C. C. Witt, and T. Yuri. 2008. A phylogenomic study of birds reveals their evolutionary history. Science 27: 1763-1768.

Jarvis, E. D., et al. 2014. Whole-genome analyses resolve early branches in the tree of life of modern birds. Science 346: 1320-1331.

Prum, R. O., J. S. Berv, A. Dornburg, D. J. Field, J. P. Townsend, E. M. Lemmon, and A. R. Lemmon. 2015. A comprehensive phylogeny of birds (Aves) using targeted next-generation DNA sequencing. Nature 526: 569-573.

Winkler, D. W., S. M. Billerman, and I. J. Lovette. 2015. *Bird Families of the World: An Invitation to the Spectacular Diversity of Birds.* Lynx Edicions, Barcelona.599 pp.

Submitted by: Pam Rasmussen
Date of Proposal: 11 January 2016

Recognize *Psittacara maugei* as a separate species from Hispaniolan Parakeet *P. chloropterus*

Background:

See Olson (2015) for an extremely detailed and informative summary of the history of this taxon and location of specimens of the extinct Puerto Rican Parakeet. It is known from just three study skins and several fragmentary fossil and archeological specimens. Through most of its taxonomic history, it has been treated as a subspecies of *P. chloroptera* of Hispaniola, often as doubtfully distinguishable despite Ridgway's (1916) statement that it "seems really different from true *A. chloroptera*". I looked at Ridgway myself; his key provides obvious, diagnostic characters for separating *maugei* from *chloropterus*. Thus, this is yet another case of copy-cat perpetuation of erroneous conclusions (i.e. "doubtfully distinct" copied over and over through the years) without consulting a reliable source such as Ridgway; see Olson for details.

New Information:

Olson (2015) studied the last specimen (Mona Island, 1892; FMNH; WW Brown), fragmentary fossils and archeological specimens, photos of the original painting for the type description, and photographs of a mounted specimen. The differences he found between this and *P. chloropterus* confirmed Ridgway's synopsis and led Olson to conclude that *maugei* should certainly be treated as a separate species. The main differences are:

1. strong differences in bill morphology, including lack of a "tooth" on the maxilla.

2. bill tip shaped differently: "ventral surface of the premaxilla in *P. maugei* is much wider and longer and the concavity at the base is much less distinct, and the tip of the rostrum is again seen to be much less ventrally hooked than in *P. chloroptera*."

3. nostrils "larger, rounder, and are oriented markedly more dorsally, as opposed to laterally in *P. chloroptera*."

4. bill color darker.

5. absence of red on leading edge of wing (conspicuous in *P. chloropterus*).

6. Underwing coverts red (olive greenish in *P. chloropterus*).

Recommendation:

This proposal would elevate to species rank an extinct taxon currently considered a subspecies of *Psittacara chloropterus*. This taxon differs as much in plumage and morphology from *P. chloropterus* as many taxa traditionally ranked as species in the "*Aratinga*" (s.l.) group of parakeets. Olson pointed out that its bill shape is the outlier in the West Indian *Psittacara* and made a case for adaptation to a different diet. Olson has made a solid case for species rank, and in my opinion, burden of proof falls squarely on the case for treating it only as a subspecies. Thus, I recommend a YES vote to treat *Psittacara maugei* as a separate species.

English name: Olson also shows that the species was found on Puerto Rico, probably widely, not just on Mona Island as is usually assumed; he makes a case that Mona Island was just its last stronghold after eradication from the main island. Therefore, the English name "Puerto Rican Parakeet", as used by Olson, makes sense, especially with its presumed sister *P. chloropterus* being called "Hispaniolan Parakeet" and closely related *P. euops* being called "Cuban Parakeet". Ridgway (1916) called it Mauge's Paroquet, but I suspect "Mauge's Parakeet" would lose badly in a vote vs. Puerto Rican Parakeet.

Literature Cited:

Olson, S. L. 2015. History, morphology, and fossil record of the extinct Puerto Rican Parakeet *Psittacara maugei* Souancé. Wilson Journal of Ornithology, 127(1):1-12.

Submitted by: Van Remsen
Date of Proposal: 15 January 2016

Split *Sirystes albogriseus* from *S. sibilator*

Background:

The cross-Andean split of Western Sirystes *S. albogriseus* from Eastern Sirystes *S. sibilator* is widely recognised following Ridgely & Tudor (1994) and Ridgely & Greenfield (2001). This split is supported by long-known and striking differences in vocalizations. Donegan (2013)'s study of vocal variation in the genus supported the West/East split, but also a further three-way split of eastern populations, all of which have now been accepted by AOU-SACC (Proposal 610). This present proposal affords AOU-NACC with an opportunity to align its taxonomy with AOU-SACC and also adopt a new vernacular name with respect to the sole form found in the NACC area, namely *albogriseus*, which extends into southernmost Panama.

New Information:

Ridgely & Greenfield (2001), followed by Jahn *et al.* (2002), Hilty (2003), Gill & Wright (2006), Ridgely & Tudor (2009), McMullan & Navarrete (2013) and others all treat *S. albogriseus* ("Western Sirystes") as a species separate from a broadly defined *S. sibilator* including all remaining taxa ("Eastern Sirystes"), based mainly on differences in vocalisations discussed in Ridgely & Tudor (1994).

Western Sirystes gives only short chips whilst Eastern Sirystes vocalisations involve longer notes that are more complex.

Western: http://www.xeno-canto.org/species/Sirystes-albogriseus?view=3

Eastern: http://www.xeno-canto.org/species/Sirystes-sibilator?view=3

In Donegan (2013), voice of *Sirystes* throughout its range was studied in detail, as well as some specimens and other sources of records. It was concluded in the abstract that: "The widely recognized split of Western Sirystes *S. albogriseus* of the Chocó (Panama, Colombia and Ecuador) from the more widespread Eastern Sirystes *S. sibilator* is strongly supported by differences in vocal repertoire and quantitative vocal differentiation." And in the text: "Western Sirystes" *S. albogriseus* has a dramatically different vocal repertoire from all populations East of the Andes. Western Sirystes has a different sort of primary vocalization from all other populations, and no recordings include whistles, chattering songs or downstroke songs. All available recordings involve repeated short notes, which can appear almost vertical on sonagrams. Recordings from across the species' range in Panama, Colombia and Ecuador are similar in this respect (Figs. 1A-E). Notes are quickly delivered downstrokes with a small initial upstroke (Fig. 1AE). A comparison of the most similar call notes of the proximate (Western Amazonian) population – the second or third notes in the "*wheer-péw*" or "*wheer-péw-péw*" call – reveals statistical diagnosability in note length (Fig. 5B, App. 2-3). The small number of short note recordings in other populations occurring east of the Andes

similarly show no overlap for note length. The vocal differences between Western and Eastern birds are substantial, with voices of the two being virtually unrecognizable from one another to the human ear or using sonagrams. These differences give strong support to Ridgely & Greenfield (2001)'s proposed split."

Figure 5B of Donegan (2013) illustrates these differences. Here, there is a plot of vocal variables of acoustic frequency and call length for "short notes". This was produced by measuring the shortest notes from within the more complex vocalisations of eastern populations and ignoring longer notes given in sequence with such shorter notes. Even based on this conservative comparative analysis, western populations are diagnosable by their shorter notes. Appendices 3-4 of Donegan (2013) set out full details of the quantitative and qualitative vocal differences between described *Sirystes* populations.
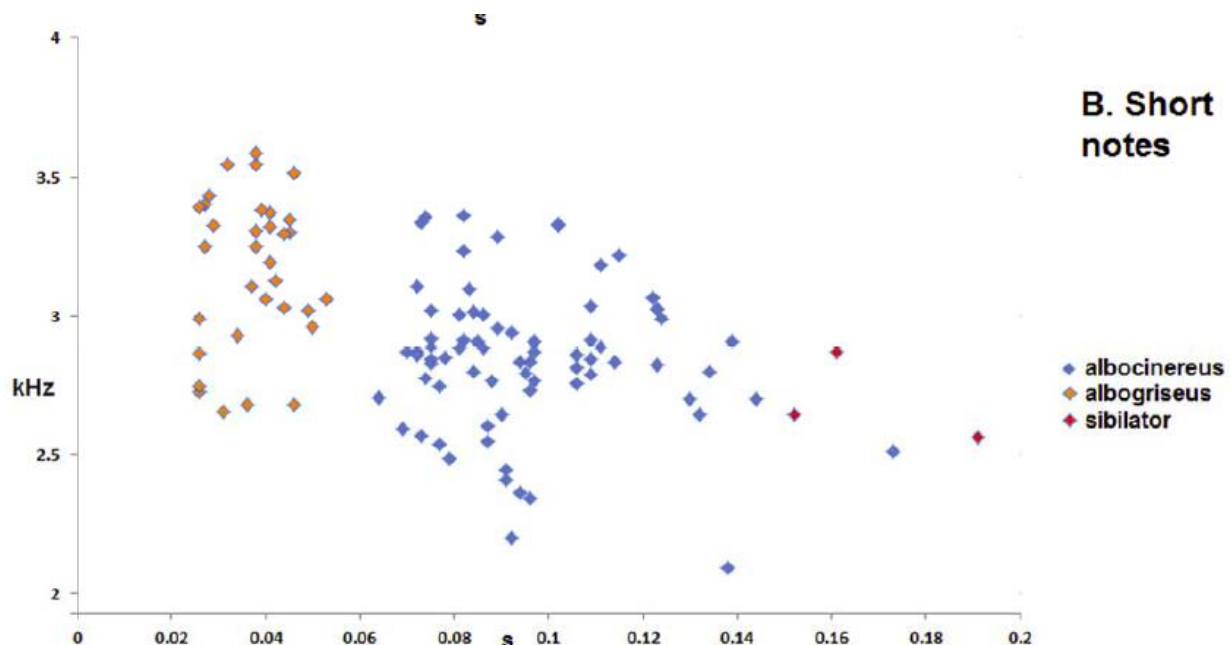
In plumage, *albogriseus* has more extensive white markings on the wing coverts and tail tip compared to all other populations (see Appendix 5 of Donegan 2013). These differences are noteworthy in the context of the genus' closest relatives being in the morphologically cryptic genus, *Myiarchus*. The plate below is replicated from Figure 3 of Donegan (2013). The two specimens on the left are of *albogriseus*; the others are of eastern populations.
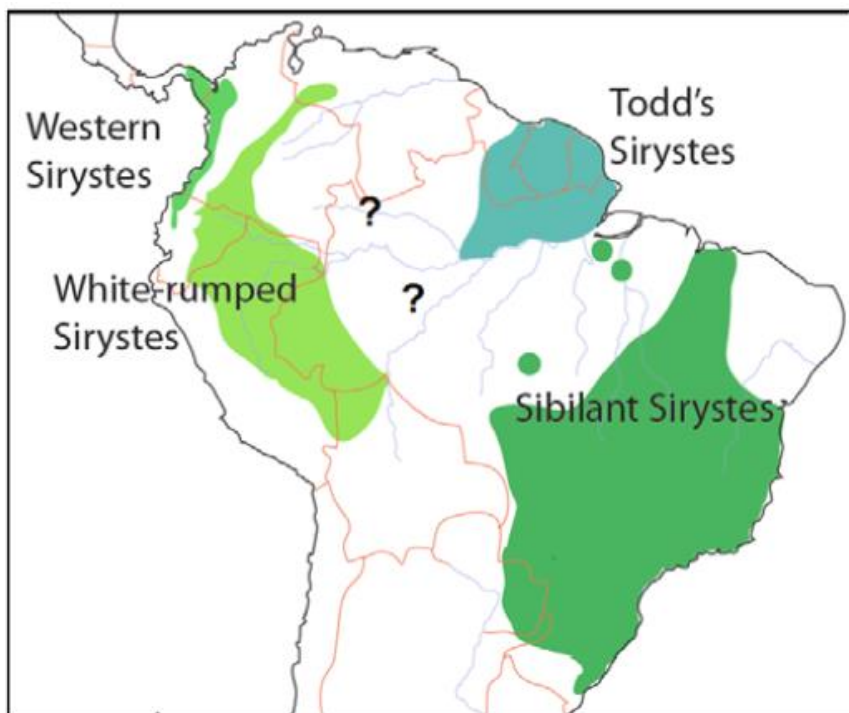
English names: "Western Sirystes" was coined by Ridgely & Greenfield (2001) for *albogriseus*, under their two-way split. Ridgway (1907) and Hellmayr (1927) used "Panama Sirystes" previously. In Donegan (2013), I proposed "Choco Sirystes" instead, which seems more appropriate following the four-way split (see distribution map below). "Choco Sirystes" was accepted by AOU-SACC and is proposed here.

The other eastern splits do not require to be considered by NACC, because none of the taxa occur in the AOU-NACC region. The name *albogriseus* and distribution of the Choco Sirystes would be unaffected by how eastern taxa are arranged.

Recommendation:

The Check-list entry for *Sirystes* would be amended and rewritten, by replacing the account for Sirystes *Sirystes sibilator* with one labelled as Choco Sirystes *Sirystes albogriseus*. This species occurs in primary forests in the Chocó region of Panama, Colombia and Ecuador. Ridgely & Greenfield (2001) and Donegan (2013) should be cited as authority for the split.

Literature Cited:

Donegan, T.M. 2013. Vocal variation and species limits in the genus Sirystes (Tyrannidae). *Conservación Colombiana* 19: 11-30. http://www.proaves.org/birds-of-colombia-2013/?lang=en
Ridgley, R.S. & Greenfield, P.J. 2001. *The birds of Ecuador*. Cornell Univ. Press, Ithaca.

Other references are cited in the above papers.

Submitted by: Thomas Donegan
Date of Proposal: 20 January 2016

Comments on SACC Proposal 610 are appended below. The split of the western population (A) and the three-way split of the eastern populations (B) both passed:

Comments from Remsen: YES to both A and B. Donegan's published analyses shows that multiple species should be recognized.

Comments from Stiles: A definite YES to part A: this split is well documented and widely accepted. For part B, given their vocal distinctiveness and relatively less extreme plumage differences as well as the convincing analogy with the closely related *Myiarchus,* I think that the burden of proof has shifted towards those who would treat all three as a single species, so YES.

Comments from Pacheco: Yes (A) due to of reasons given by Donegan's paper, in accordance with the existing literature data. A Yes (B) also based on that article and my own experience.

Comments from Nores: A: YES. B: NO. I repeat here what I put in proposal 49: Separar especies por suaves diferencias en el canto no me parece bien. Recientemente estuve en el noreste de Brasil y me llamó la atención lo diferente que son los cantos de algunas subespecies de allá con respecto a las poblaciones del sur de Sudamérica. Por

ejemplo, *Thraupis sayaca* tiene un canto mucho mas potente y mas variado que las razas del sur y *Turdus rufiventris* emite un llamado permanente que nunca se lo escuchó a la subespecie de esta latitud. Otro notable ejemplo es *Vanellus chilensis*, del cual la raza del sur de Argentina y Chile emiten un canto bastante diferente (parece un loro) que la raza que habita el norte y centro de Argentina hasta Amazonas. Esto no significa para mi que haya que elevar las subespecies a especies."

Comments from Zimmer: YES to both A and B. The vocal distinctions between the various populations of *Sirystes* have long been obvious to those with the required geographic breadth of field experience, and Donegan has done a good job of detailing that in his paper. He has also done a good job of highlighting the apparent patchy distribution of *Sirystes* as a whole, something that squares with my experience, but which flies counter to most published range descriptions. These are suboscine birds (unlike the examples of *Thraupis* and *Turdus* mentioned by Manuel), and I see no reason not to treat their diagnosably different vocalizations as hard-wired, genetically based characters that are at least on a par with any plumage characters as being reflective of species-level relationships (or lack thereof).

Comments from Robbins: YES, to recognizing four *Sirystes* species. I did not appreciate that the distribution of the cis-Andean taxa was far more restricted than what the literature has indicated. Differentiation in plumage and vocalizations are indeed analogous to *Myiarchus* species.