

N&MA Classification Committee: Proposals 2010-B

No.	Page	Title
01	2	Transfer eight species from the Turdidae to the Muscicapidae
02	8	Transfer three species of muscicapids to different genera
03	10	Revise two type localities
04	11	Change <i>Amazilia chionopectus</i> to <i>Amazilia brevirostris</i>
05	12	Create a new order, Pteroclidiformes, for the sandgrouse
06	14	Recognize <i>Anas diazi</i> as a species—again
07	17	Change the linear sequence of the furnarioid families
08	20	Recognize the Bahama Warbler <i>Dendroica flavescens</i> as a distinct species
09	21	Recognize <i>Geothlypis (aequinoctialis) chiriquensis</i> as a distinct species
10	23	Adopt a new generic classification for the Parulidae
11	27	Restore authority for the genus name <i>Peucedramus</i> to Coues
12	29	Split Mexican Jay <i>Aphelocoma ultramarina</i> into two species
13	34	Lump <i>Ramphastos swainsonii</i> with <i>R. ambiguus</i>

Transfer eight species from the Turdidae to the Muscicapidae

Description of the problem:

Relationships of the thrushes, chats, Old World flycatchers, and relatives (Turdidae and Muscicapidae) have been notoriously difficult to resolve. Certain groups and genera of birds have been moved between these two families repeatedly, due in part to a lack of good morphological characters that distinguish the two groups, much like the traditional Sylviidae and Timaliidae. In their study using DNA-DNA hybridization, Sibley and Ahlquist (1990) grouped the thrushes, chats, and Old World flycatchers into a single family, the Muscicapidae. Within that family, the chats were more closely related to the Old World flycatchers than to the thrushes. Other arrangements of the larger group have included the chats and their allies within the Turdinae (Ripley 1963) or Turdidae (AOU 1998, Collar 2005), generally on the basis of shared morphology and ecology. In the current AOU Checklist, the Old World flycatchers, chats, and robins (not including the “traditional” thrushes, such as *Turdus*, which are not considered in this proposal) are arranged as follows:

Muscicapidae:

Narcissus Flycatcher (*Ficedula narcissina*)
Mugimaki Flycatcher (*Ficedula mugimaki*)
Taiga Flycatcher (*Ficedula albicilla*)
Dark-sided Flycatcher (*Muscicapa sibirica*)
Gray-streaked Flycatcher (*Muscicapa griseisticta*)
Asian Brown Flycatcher (*Muscicapa dauurica*)
Spotted Flycatcher (*Muscicapa striata*)

Turdidae:

Rufous-tailed Robin (*Luscinia sibilans*)
Siberian Rubythroat (*Luscinia calliope*)
Bluethroat (*Luscinia svecica*)
Siberian Blue Robin (*Luscinia cyane*)
Red-flanked Bluetail (*Tarsiger cyanurus*)
White-rumped Shama (*Copsychus malabaricus*)
Northern Wheatear (*Oenanthe oenanthe*)
Stonechat (*Saxicola torquatus*)

New information:

A number of recent studies have used DNA sequence data to investigate relationships within these groups. Cibois and Cracraft (2004) used sequence data from RAG-1 (a nuclear exon) to study relationships within the large superfamily Muscicapoidea of Sibley and Ahlquist (1990). They found, as had Sibley and Ahlquist, that the chats of the tribe Saxicolini were sister to the Muscicapini, and that these two groups (the Muscicapinae) were in turn sister to the thrushes. This result received very strong (100% bootstrap) support. Further studies with larger sample sizes have revealed that this finding, although largely correct, is an over-simplification, and that the Old World flycatchers (Muscicapini) and the chats and robins (Saxicolini) are not themselves monophyletic groups, but instead are paraphyletic with respect to each other.

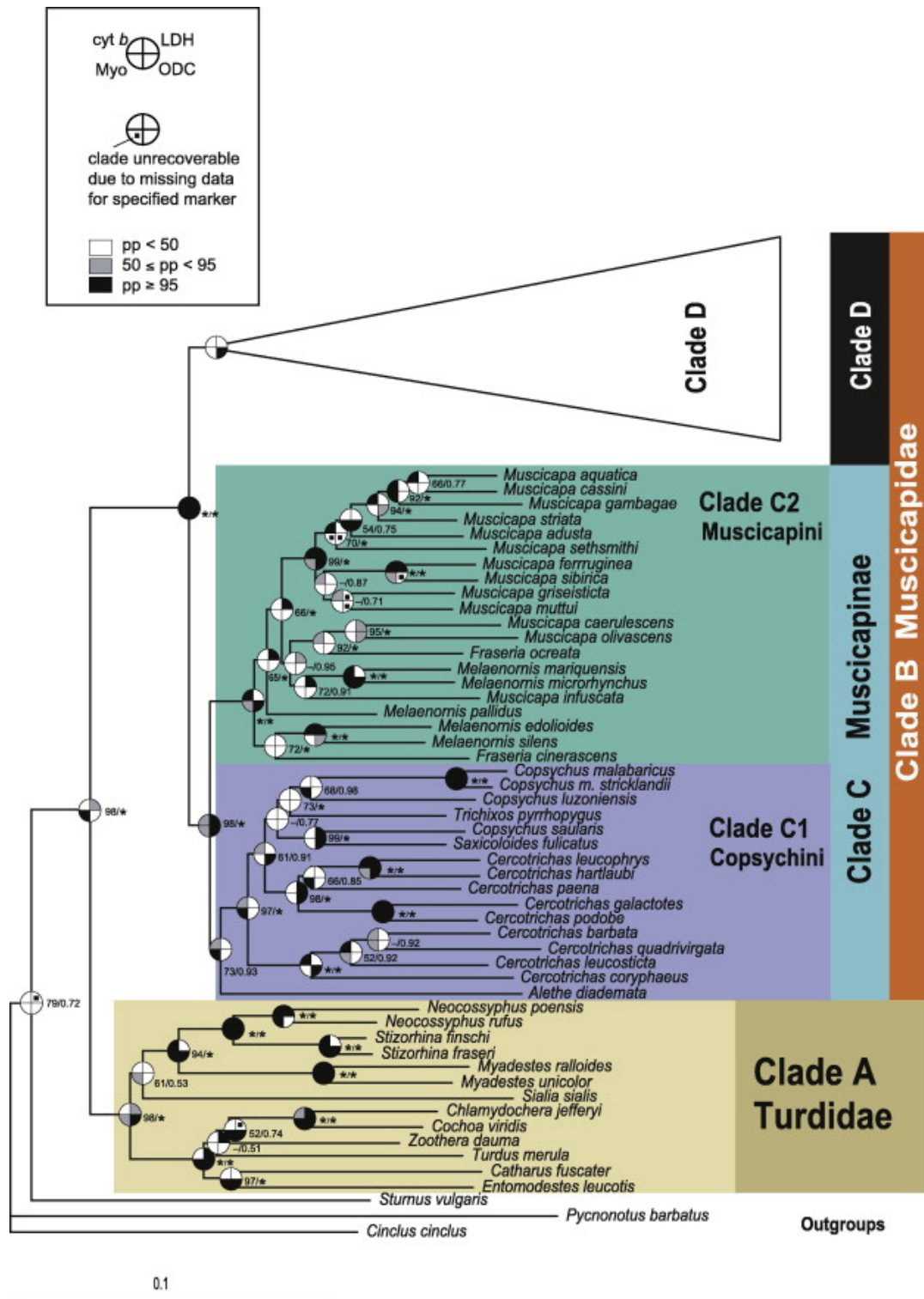
Other studies provide further support for the inclusion of the chats and robins in the Muscicapidae and insight into relationships within the Muscicapidae generally. In Sangster *et al.* (2010 – see trees appended below), four subfamilies of muscicapids were proposed. The first consisted of the tribes Muscicapini (mostly *Muscicapa* flycatchers) and Copsychini (which includes *Copsychus*, among other genera). Sister to the Muscicapinae was a clade consisting of the other three subfamilies, the Niltavinae, the Erithacinae, and the Saxicolinae (which includes the genera *Luscinia*, *Tarsiger*, *Ficedula*, *Oenanthe*, *Saxicola*, and others). Within this group, the Erithacinae and Saxicolinae were sisters, and these in turn were sister to the Niltavinae. Bootstrap support for these clades and relationships among them was moderate to strong (65-100% ML bootstraps, 0.84-1.0 Bayesian posterior probabilities). The Muscicapidae, as defined here, was found to be sister to the Turdidae (98% ML, 1.0 pp). These same basic clades and relationships were also recovered in the muscicapid phylogeny of Zuccon and Ericson (2010). Although their sampling was not as extensive, support values in Zuccon and Ericson (73-100% ML bootstraps, 0.99-1.0 pp) were somewhat improved over those in Sangster *et al.* (2010).

Recommendation:

Based on the recent published genetic work, which includes data from several nuclear and mitochondrial genes, the species listed above in the Turdidae should be transferred to the Muscicapidae, *Copsychus malabaricus* should be moved to follow *Muscicapa* in the muscicapine part of the sequence, and the three species of *Ficedula* known from the AOU area should be moved to the saxicoline part of the sequence, following *Tarsiger cyanurus*.

If this is accepted, the Muscicapidae will include the following species, in the following sequence:

Gray-streaked Flycatcher (*Muscicapa griseisticta*)
Asian Brown Flycatcher (*Muscicapa dauurica*)
Spotted Flycatcher (*Muscicapa striata*)
Dark-sided Flycatcher (*Muscicapa sibirica*)
White-rumped Shama (*Copsychus malabaricus*)
Rufous-tailed Robin (*Luscinia sibilans*)
Siberian Rubythroat (*Luscinia calliope*)
Bluethroat (*Luscinia svecica*)
Siberian Blue Robin (*Luscinia cyane*)
Red-flanked Bluetail (*Tarsiger cyanurus*)
Narcissus Flycatcher (*Ficedula narcissina*)
Mugimaki Flycatcher (*Ficedula mugimaki*)
Taiga Flycatcher (*Ficedula albicilla*)
Northern Wheatear (*Oenanthe oenanthe*)
Stonechat (*Saxicola torquatus*)



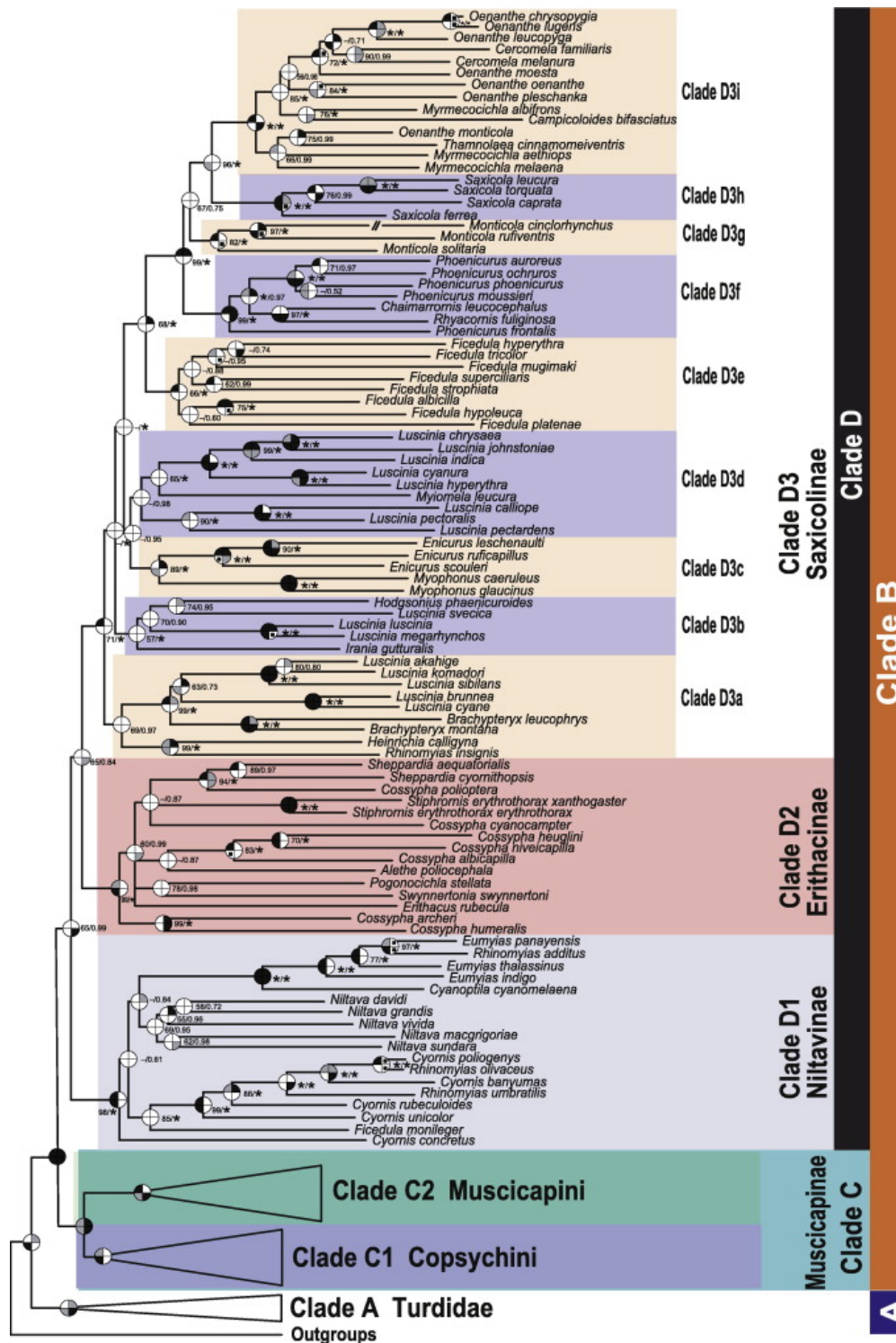


Fig. 1. Relationships of Muscicapidae and Turdidae based on Bayesian analysis of combined mitochondrial cytochrome *b*, and nuclear ODC, myoglobin and LDH intron sequences (3240 bp) divided into two partitions analyzed under the GTR + G + I model (cyt *b* and ODC), one partition analyzed under the GTR + G model (LDH) and one partition analyzed under the HKY + G model (myo). Maximum Likelihood bootstrap

values and Bayesian posterior probabilities, respectively, are given for each clade. An asterisk denotes a bootstrap value of 100% or a posterior probability of 1.0. A ‘-’ indicates that the node was not recovered by Maximum Likelihood analysis. The pie diagrams indicate support from individual gene trees. The names referring to the marked clades are the ones proposed here.

Literature Cited:

- American Ornithologists' Union. 1998. Check-list of North American birds. 7th edition. – American Ornithologists' Union, Washington, D.C.
- Christidis, L. and W.E. Boles. 2008. *Systematics and Taxonomy of Australian Birds*. CSIRO Publishing, Melbourne
- Cibois, A. and J. Cracraft. 2004. Assessing the passerine “Tapestry”: phylogenetic relationships of the Muscipoidea inferred from nuclear DNA sequences. *Molecular Phylogenetics and Evolution* **32** 264-273
- Collar, N.J. 2005. Family Turdidae (Thrushes). In del Hoyo, J., Elliott, A. and Sargatal, J. eds. *Handbook of the Birds of the World, Volume 10, Cuckoo-shrikes to Thrushes*. Lynx Edicions, Barcelona, pp. 514-811
- Ripley, D.S. Subfamily Turdinae in *Check-list of Birds of the World, Vol. 10*. Museum of Comp. Zoology, Cambridge, Massachusetts
- Sangster, G., P. Alström, E. Forsmark, U. Olsson. 2010. Multi-locus phylogenetic analysis of Old World chats and flycatchers reveals extensive paraphyly at family, subfamily and genus level (Aves: Muscicapidae). *Molecular Phylogenetics and Evolution* **57** 380-392
- Sibley, C.G. and Ahlquist, J.E. 1990. *Phylogeny and classification of birds*. Yale. Univ. Press, New Haven, Connecticut
- Zuccon, D. and P.G.P. Ericson. 2010. A multi-gene phylogeny disentangles the chat-flycatcher complex (Aves: Muscicapidae). *Zoological Scripta*

Submitted by: Shawn Billerman and Terry Chesser

Date of Proposal: 21 Oct 2010

Transfer three species of muscicapids to different genera

Description of the problem:

Recent genetic studies have shed light on the complex relationships within the Muscicapidae, showing that the chats and wheatears (among others) are more closely related to the Old World flycatchers than to the thrushes (Turdidae) (Cibois and Cracraft 2004, Sangster *et al.* 2010, Zuccon and Ericson 2010). In addition to clarifying the family level relationships within this large group, genera-level relationships have also been clarified. Several studies have shown that many genera, especially larger genera, are not monophyletic. In particular, it has been shown that the various “types” of birds in this large group (for example, the flycatchers or the chats) are not monophyletic (Sangster *et al.* 2010, Zuccon and Ericson 2010).

New information:

To eliminate paraphyly in selected muscicapid genera, Sangster *et al.* (2010 – see trees in Proposal 2010-B-1) recommended resurrecting several genera no longer in general use. Of relevance to this committee, they recommended that the genus *Luscinia* be split into four genera (one of which, *Tarsiger*, is already recognized by the AOU). Three species of *Luscinia* known from the AOU Check-list region would be affected by the proposed taxonomic changes. These species are:

Rufous-tailed Robin (*Luscinia sibilans*), to be transferred to *Larvivora*
Siberian Blue Robin (*Luscinia cyane*), to be transferred to *Larvivora*
Siberian Rubythroat (*Luscinia calliope*), to be transferred to *Calliope*

If Proposal 2010-B-1 is accepted, the four species currently in *Luscinia* would be positioned immediately following *Copsychus malabaricus* and preceding *Tarsiger cyanurus*. The sequence of these species and *Luscinia svecica*, which would remain in *Luscinia*, would be altered as follows:

Siberian Blue Robin (*Larvivora cyane*)
Rufous-tailed Robin (*Larvivora sibilans*)
Bluethroat (*Luscinia svecica*)
Siberian Rubythroat (*Calliope calliope*)

Although the topology of the tree in Zuccon and Ericson (2010) is generally consistent with the taxonomic revisions suggested by Sangster *et al.*, only one of the species listed above (*L. sibilans*) was included in their study.

Recommendation:

For lower-level taxonomy of birds that do not occur regularly in our area, the AOU has traditionally deferred to counterparts that deal more directly with Old World taxa, especially the BOU. However, none of the species listed above are normally found in the BOU area. Although many of the deeper nodes in the Saxicolinae receive only moderate support (Sangster *et al.* 2010, Zuccon and Ericson 2010), the groups of *Luscinia* are separated by well-supported nodes in more shallow parts of the tree and almost certainly belong to three distinct clades. As far as we can tell, the proposed names appear to be stable, although details of the composition of these clades may be subject to change. A case can certainly be made for adoption of new genera for the three species listed above. On the other hand, this is not a pressing issue for our area and we may wish to wait to see whether these names are adopted by others with a more direct interest in these taxa.

Literature Cited:

- Cibois, A. and J. Cracraft. 2004. Assessing the passerine "Tapestry": phylogenetic relationships of the Muscipoidea inferred from nuclear DNA sequences. *Molecular Phylogenetics and Evolution* **32** 264-273
- Sangster, G., P. Alström, E. Forsmark, U. Olsson. 2010. Multi-locus phylogenetic analysis of Old World chats and flycatchers reveals extensive paraphyly at family, subfamily and genus level (Aves: Muscicapidae). *Molecular Phylogenetics and Evolution* **57** 380-392
- Zuccon, D. and P.G.P. Ericson. 2010. A multi-gene phylogeny disentangles the chat-flycatcher complex (Aves: Muscicapidae). *Zoological Scripta*

Submitted by: Shawn Billerman and Terry Chesser

Date of Proposal: 2 Nov 2010

Revision of two type localities

1. The type locality of *Aethia pygmaea* has been revised as "Unalaska Island, Aleutian Islands, Alaska." Gibson, D. D., and R. C. Banks. 2010. Revised type locality of the Whiskered Auklet *Aethia pygmaea* [Aves: Alcidae]. Proc. Biol. Soc. Wash. 123(3):193-195.
2. The type locality of *Spizella breweri* has been redefined as "Black Hills, Dak[ota Territory] = Laramie Range, Albany County, Wyoming." Banks, R. C., and D. D. Gibson. 2007. The correct type locality of *Spizella breweri*. Auk 124:1083-1085.

I propose that the cited revised type localities for *Aethia pygmaea* and for *Spizella breweri* be accepted by AOUCCLC.

Submitted by: Dan Gibson

Date of Proposal: 1 Dec. 2010

Change *Amazilia chionopectus* to *Amazilia brevirostris*

The White-chested Emerald, a South American hummingbird, is in our Appendix by virtue of four MCZ specimens labeled “Grenada” but that are presumed to be mislabeled. The species is known from Trinidad.

For some time there has been a question of species limits and the priority of names of taxa in the group of *Amazilia* that includes *chionopectus*, *brevirostris*, and *versicolor*. This has recently been resolved by Weller and Schuchmann (2009). Their results show that *brevirostris* and *chionopectus* are conspecific as the White-chested Emerald and form a superspecies with *versicolor*. Of the former, *brevirostris* Lesson, 1829 has priority over *chionopectus* Gould, 1859 and therefore is the valid name for this species. SACC has accepted this.

Weller and Schuchmann (2009, and in HBW) use the generic name *Agyrtria* for these species. We have not accepted Weller’s subdivision of the genus *Amazilia*.

I propose that our Appendix entry and citation be changed to:

Amazilia brevirostris (Lesson). White-chested Emerald.

Ornismya brevirostris Lesson, 1829, Hist. Nat. Ois.-Mouches, p. xxv, pl. 77. (Guiana.)

A sentence or two should be added to the text: Formerly listed as *Amazilia chionopectus* (Gould). Some authors place the species in the genus *Agyrtria*.

Literature Cited:

Weller, A-A., and K.-L. Schuchmann. 2009. Re-evaluation of *Agyrtria brevirostris* Lesson (Aves, Trochilidae), with notes on its taxonomic status and relationships to *A. chionopectus* Gould and *A. versicolor* Vieillot. *Zoosystematics and Evolution* 85: 143-149.

Submitted by: Richard C. Banks

Date of Proposal: 16 December 2010

Create a new order, Pteroclidiformes, for the sandgrouse

Description of the Problem:

The taxonomic affinities of the Pteroclididae (sandgrouse) have long been uncertain. The family has been associated with different groups, including grouse (Galliformes), doves (Columbiformes) and shorebirds (Charadriiformes) (Cracraft 1981, Livezey and Zusi 2001, 2007). They are currently in the AOU checklist as *incertae sedis* between the Charadriiformes and the Columbiformes (AOU 1998). One piece of evidence supporting the sandgrouse-dove relationship was the observation that sandgrouse drink, as do doves, by continuously sucking up water through their bill without the need to tip back their head to swallow. However, careful observation in the 1960s showed that sandgrouse instead must tilt their head back to swallow water (Cade *et al.* 1966).

New Information:

Recent molecular work has shed some light on the relationships of Pteroclididae. Although studies have failed to definitively place the sandgrouse on the avian tree, several hypotheses have been falsified; for example, the sandgrouse have been shown to be unrelated to the Charadriiformes or Galliformes (Ericson *et al.* 2003, Ericson *et al.* 2006, Baker *et al.* 2007, Fain and Houde 2007, Hackett *et al.* 2008). Current evidence suggests that the Pteroclididae are an old group, not closely related to any other, that may form part of a radiation that includes the tropicbirds (Phaethontidae), grebes (Podicipedidae), flamingos (Phoenicopteridae), doves and pigeons (Columbidae), and mesites (Mositornithidae), i.e. part of the Metaves of Fain and Houde (2004). Support values for the Metaves and for relationships among groups within this proposed radiation are poor, and the sandgrouse may or may not be sister to the Columbiformes. The most data-rich study (Hackett *et al.* 2008) places them as sister to a Columbiformes + Mesitornithidae clade, but with poor support. The AOU has recently been according order status to distinctive lineages within the proposed Metaves. For example, we created new orders for the tropicbirds (Phaethontiformes) and the Sunbittern and Kagu (Eurypygiformes) in the most recent supplement (Chesser *et al.* 2010).

Recommendation:

Recent genetic data, while failing to place the sandgrouse definitively, have shown that placing these birds within the Charadriiformes or Galliformes is incorrect (Ericson *et al.* 2006, Baker *et al.* 2007, Fain and Houde 2007, Hackett *et al.* 2008). Instead, they may

belong to a small clade including the doves and pigeons, mesites, tropicbirds, grebes, and flamingos (Ericson *et al.* 2006, Hackett *et al.* 2008). Their relationships within this group are uncertain; tree structure is characterized by long branches leading to individual groups and short internodes between groups. Because of the age of the Pteroclididae and its uncertain affinities, we propose a new order for the sandgrouse, the Pteroclidiformes. Within the AOU Check-list, the sandgrouse would be placed between the Phaethontiformes) and the Columbiformes.

Literature Cited:

- American Ornithologists' Union. 1998. Check-list of North American birds. 7 edition. – American Ornithologists' Union, Washington, D.C.
- Baker, A.J., Pereira, S.L., Paton, T.A. 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.
- Cade, T.J., Willoughby, E.J., MacLean, G.L. 1966. Drinking behavior of sandgrouse in the Namib and Kalahari Deserts, Africa. *The Auk*. 83 124-126.
- Chesser, R. T., R. C. Banks, F. K. Barker, C. Cicero, J. L. Dunn, A. W. Kratter, I. J. Lovette, P. C. Rasmussen, J. V. Remsen, Jr., J. D. Rising, D. F. Stotz, and K. Winker. 2010. Fifty-first supplement to the American Ornithologists' Union *Check-list of North American Birds*. *The Auk*. 127 726-744.
- Cracraft, J. 1981. Toward a phylogenetic classification of the recent birds of the world (class Aves). *The Auk*. 98 681-714.
- Dickinson, E.C. ed. 2003. *The Howard and Moore Complete Checklist of the Birds of the World*. 3rd Edition. Christopher Helm, London.
- Ericson, P.G.P., Anderson, C.L., Britton, T., Elzanowski, A., Johansson, U.S., Källersjö, M., Ohlson, J.I., Parsons, T.J., Zuccon, D., and Mayr, G. 2006. Diversification of Neoaves: integration of molecular sequence data and fossils. *Biol. Lett.* 2 543-547
- Fain, M.G. and Houde, P. 2004. Parallel radiations in the primary clades of birds. *Evolution*. 58 2558-2573.
- Fain, M.G. and Houde, P. 2007. Multilocus perspectives on the monophyly and phylogeny of the order Charadriiformes (Aves). *BMC Evolutionary Biology*. 7:35.
- Hackett, S.J., Kimball, R.T., Reddy, S., Bowie, R.C.K., Braun, E.L., Braun, M.J., Chojnowski, J.L., Cox, W.A., Han, K., Harshman, J., Huddleston, C.J., Marks, B.D., Miglia, K.J., Moore, W.S., Sheldon, F.H., Steadman, D.W., Witt, C.C., and Yuri, T. 2008. A phylogenetic study of birds reveals their evolutionary history. *Science*. 320 1760-1768.
- Livezey, B.C. and Zusi, R.L. 2001. Higher-order phylogenetics of modern Aves based on comparative anatomy. *Netherlands Journal of Zoology*. 51(2) 179-205.
- Livezey, B.C. and Zusi, R.L. 2007. Higher-order phylogeny of modern birds (Theropoda: Aves: Neornithes) based on comparative anatomy. II. Analysis and discussion. *Zoological Journal of the Linnean Society*. 149 1-95.

Submitted by: Shawn Billerman and Terry Chesser

Date of Proposal: 21 Dec 2010

Proposal: Recognize *Anas diazi* as a species—again**Description of the Problem:**

Anas platyrhynchos diazi was recognized as a full species, the Mexican Duck, until the AOU merged it with the Mallard (AOU 1983) on the basis of studies by Hubbard (1977), who detailed large-scale hybridization in the southwestern United States and northern Mexico. Present concepts of hybridization (AOU 1998:xiv) weaken that argument as do new realizations of the extent of hybridization in the mallard complex (Kulikova et al. 2004).

New Information:

Livezey's (1991) cladistic analysis using plumage, soft parts, and anatomical characters of ducks showed a trichotomy of *Anas diazi*, *fulvigula*, and *rubripes*, with *platyrhynchos* (as well as *wyvilliana*, *laysanensis*, and *oustaleti*) derived from them.

Johnson and Sorenson (1999) did a molecular phylogeny (mtDNA) of dabbling ducks and found *diazi*, *fulvigula*, and *rubripes* allied to one of two haplotype groups of Mallard, *platyrhynchos*. The other haplotype group of mallards is closer to Asian taxa.

A mtDNA study by McCracken et al. (2001) on the Mottled Duck, *A. fulvigula*, ($n=219$) sampled both populations (Florida and Gulf Coast) and also *A. rubripes* ($n=13$), *A. platyrhynchos* ($n=10$), and *A. diazi* ($n=4$). 57 unique haplotypes were identified. Neighbor-joining analysis showed a large clade of 52% of *fulvigula* sampled composed of two reciprocally monophyletic clades of Mottled Duck haplotypes, one endemic to Florida and one endemic to the Texas-Louisiana population. These were sister to a clade of Mexican Duck haplotypes. Next was a clade of multi-species haplotypes shared by the rest of the *fulvigula* and a few *rubripes* and *platyrhynchos*, and finally a clade of Mallards. This shows that the two *fulvigula* populations are largely isolated, and that they and *diazi* are more closely related to *rubripes* than to *platyrhynchos*. The idea is that *fulvigula* and *diazi* are off-shoots of an early population of *rubripes* before the area was invaded by the dimorphic Mallard. (This sounds to me very much like Palmer, but I have not re-read his waterfowl volume.)

The taxonomic recommendation of McCracken et al. (2001) is that *fulvigula* and *diazi* should be recognized as species, most closely related to each other, and placed next to the Black Duck, *rubripes*. Kulikova et al. (2004) found that *fulvigula*, *diazi*, and *rubripes*

are closely related to Asian *Anas zonorhyncha*, which is closer to them than it is to Asian Mallards. Another waterfowl mtDNA study (Gonzalez et al. 2009) studying higher level relationships, shows in the cladogram that *diazi*, *rubripes*, and *fulvigula* form a trichotomy, sister to *platyrhynchos*, but do not discuss the situation; *zonorhyncha* apparently was not included.

The IOC English names species list (Gill et al., second edition) has accepted this split of *diazi* from *platyrhynchos*, as have Navarro-Siguënza and Peterson (2004).

It seems to me that other interpretations of these data are possible. For one, the two populations of *fulvigula* could be considered distinct; they are isolated with no contact and each has a large suite of haplotypes not found in the other, or any other taxon studied. For another, both *fulvigula* and *diazi* could be considered subspecies of *rubripes* rather than as species.

Recommendation:

I recommend that *Anas diazi* be split from *A. platyrhynchos* and recognized as the Mexican Duck (its former English name) and listed near *A. rubripes* and *A. fulvigula*. A suggested sequence of the mallard group taxa on our list might be: *zonorhyncha*, *rubripes*, *fulvigula*, *diazi*, *platyrhynchos*, *wywilliana*, *laysanensis*—although the latter may not belong in that group.

Literature Cited:

- AOU 1983, 1998. Check-list, 6th and 7th editions
Gill et al. IOC name list
Gonzalez, J., H. Düttman, and M. Wink. 2009. Phylogenetic relationships based on two mitochondrial genes and hybridization patterns in Anatidae. *Journal of Zoology* 279:310-318 (not fully seen).
Hubbard, J. P. 1977. The biological and taxonomic status of the Mexican Duck. *Bull. New Mexico Dept. Game and Fish* 16.
Johnson, K. P., and M. D. Sorenson. 1999. Phylogeny and biogeography of dabbling ducks (genus: *Anas*): A comparison of molecular and morphological evidence. *Auk* 116:792-805.
Kulikova, I.V., Y. N. Zhuravlev, and K.G. McCracken. 2004. Asymmetric hybridization and sex-biased gene flow between Eastern Spot-billed Ducks (*Anas zonorhyncha*) and Mallards (*A. platyrhynchos*) in the Russian far east. *Auk* 121:930-949.
Livezey, B. C. 1991. A phylogenetic analysis and classification of Recent dabbling ducks (Tribe Anatini) based on comparative morphology. *Auk* 108: 471-507.

McCracken, K. G., W. P. Johnson, and F. H. Sheldon. 2001. Molecular population genetics, phylogeography, and conservation biology of the Mottled Duck (*Anas fulvigula*). *Conservation Genetics* 2:87-102.

Navarro-Sigüenza, A. G., and A. T. Peterson. 2004. An alternative species taxonomy of the birds of Mexico. *Biota Neotropica* 4:1

Submitted by: Richard C. Banks, with help from M. Ralph Browning

Date of Proposal: 27 Dec 2010

Change the linear sequence of the furnarioid families

Description of the Problem:

The current sequence of furnarioid families in the AOU Check-list is:

- Furnariidae
 - Sclerurinae
 - Furnariinae
 - Dendrocolaptinae
- Thamnophilidae
- Formicariidae
- Conopophagidae
- Grallariidae
- Rhinocryptidae

This sequence, although modified to reflect the recent division of the antbirds into three families (Thamnophilidae, Formicariidae, and Grallariidae), is in other respects a holdover from the pre-genetic era of systematics. Sibley and Ahlquist (1990), for example, found that the typical antbirds were not closely related to the ground antbirds, but instead were sister to the rest of the furnarioid families. Although separation of the thamnophilids is now reflected in the AOU classification, the position of the Thamnophilidae as sister to the other furnarioids is not. In part this is because relationships among the furnarioid groups have been difficult to resolve. For example, a study of suboscine relationships based on DNA sequence data (Chesser 2004) found that the Thamnophilidae and Conopophagidae were sisters and that this clade, rather than the Thamnophilidae alone, was sister to the rest of the furnarioids. In fact, none of the relationships within furnarioids found by Sibley and Ahlquist (1990) were recovered in this sequencing study. Nevertheless, particular findings, such as the distinctiveness of the Thamnophilidae relative to the Furnariidae, Formicariidae, Grallariidae, and Rhinocryptidae, have been common to these and most other recent studies of furnarioid relationships (e.g., Irestedt et al. 2002).

New Information:

The most comprehensive genetic study of furnarioids to date (Moyle et al. 2009) indicated that the following sequence (excluding the family Melanopareidae, which does not occur in our area) best reflects their evolutionary relationships:

Thamnophilidae
Conopophagidae
Grallariidae
Rhinocryptidae
Formicariidae
Scleruridae
Dendrocolaptidae
Furnariidae

Support for the clade containing the final six families is very high (1.00 posterior prob., 95% ML bootstrap, 93% MP bootstrap). There is relatively weak support within this clade for a sister relationship between the Grallariidae and Rhinocryptidae (0.93/75/68), but somewhat stronger support for the sister relationship between the Formicariidae and Scleruridae/ Dendrocolaptidae/ Furnariidae (1.00/84/77). The relationships among the Thamnophilidae, the Conopophagidae, and the extralimital Melanopareiidae are largely unresolved, but these families are clearly positioned outside of the six-family clade mentioned above. The best ML tree indicates that the Thamnophilidae is sister to the remaining furnarioids (as in Sibley and Ahlquist 1990) and that the Melanopareiidae and Conopophagidae are successive sisters to the clade consisting of the final six families listed above (Grallariidae through Furnariidae).

Recommendation:

I recommend that we adopt the sequence of Moyle et al (2009) while maintaining our current family and subfamily rankings. Support for the phylogenetic tree that underpins this linear sequence is not uniformly strong, but the sequence of families should be relatively robust and is the best information currently available and likely to be available in the near future. Adoption of this proposal would result in the following linear sequence:

Thamnophilidae
Conopophagidae
Grallariidae
Rhinocryptidae
Formicariidae
Furnariidae
 Sclerurinae
 Dendrocolaptinae
 Furnariinae

If there is support in the committee for elevating the furnariid sub-families to family rank (as in Moyle et al. 2009), this could also be entertained.

Literature Cited:

- Chesser, R. T. 2004. Molecular systematics of New World suboscine birds. *Molecular Phylogenetics and Evolution* 32: 11-24.
- Irestedt, M., J. Fjeldså, U. S. Johansson, and P. G. P. Ericson. 2002. Systematic relations and biogeography of the tracheophone suboscines (Aves: Passeriformes). *Molecular Phylogenetics and Evolution* 23: 499-512.
- Moyle, R. G., R. T. Chesser, R. T. Brumfield, J. G. Tello, D. J. Marchese, and J. Cracraft. 2009. Phylogeny and phylogenetic classification of the antbirds, ovenbirds, woodcreepers, and allies (Aves: Passeriformes: Furnariides). *Cladistics* 25: 386-405.
- Sibley, C. G., and J. E. Ahlquist. 1990. *Phylogeny and Classification of Birds*. Yale Univ. Press, New Haven, CT.

Submitted by: Terry Chesser

Date of Proposal: 27 Dec 2010

Recognize the Bahama Warbler *Dendroica flavescens* as a distinct species**Description of the Problem:**

The presently considered Yellow-throated Warbler population on the Bahamas (Abaco and Grand Bahama) was described as a species, *Dendroica flavescens*. It was lumped with the Yellow-throated Warbler, *D. dominica*, by Bond (1930) on the basis that the trinomial would indicate relationships, and has been treated as a subspecies since.

New Information:

McKay et al. (2010) have shown that *flavescens* is morphologically, vocally, ecologically, and genetically distinct from mainland populations of *D. dominica*. It can be distinguished by color (more extensively yellow ventrally and other characters), nesting ecology (restricted to mature Caribbean pine forests), vocalizations (ascending rather than descending trill), and genetics (unique mtDNA haplotype).

McKay et al. (2010) suggest that the Bahama population be recognized at the species level as *Dendroica flavescens*, and further suggest the English name Bahama Warbler (as the original Yellow-breasted Warbler is in use for an Asian species).

Recommendation:

I recommend that we accept both parts of this suggestion (keeping in mind that the generic name will change if Proposal 2010-B-10 is accepted, in which case this species should be placed next to *S. dominica*).

Literature Cited:

- Bond, J. 1930. The resident West Indian warblers of the genus *Dendroica*. Proceedings of the Academy of Natural Sciences of Philadelphia 82:329-337.
- McKay, B. D., M. B. J. Reynolds, W. K. Hayes, and D. S. Lee. 2010. Evidence for the species status of the Bahama Yellow-throated Warbler (*Dendroica "dominica" flavescens*). Auk 127: 932-939.

Submitted by: Richard C. Banks

Date of Proposal: 27 Dec 2010

Recognize *Geothlypis (aequinoctialis) chiriquensis* as a distinct species

Description of the Problem:

This form of yellowthroat is found only in western Chiriquí, Panama, and immediately adjacent southwestern Costa Rica. It is similar in color pattern to 3 distant disjunct populations, all considered *G. aequinoctialis*, in northern, southern, and southwestern South America, but has a slightly larger bill, duller coloration, and more black on the forecrown (Wetmore et al. 1984). It was named as a species (of course) and apparently maintained in that status until lumped with *aequinoctialis* of South America by Hellmayr (1935). Lowery and Monroe (1968) considered it a species. AOU 1983 and 1998 merged it with *aequinoctialis* although the latter noted that Escalante-Pliego (1991) suggested that that species might include more than one taxon, on the basis of allozymic divergence.

New Information:

Escalante et al. (2009) used sequence data from 3 mtDNA genes to construct a phylogeny of the genera *Oporornis* and *Geothlypis*, which they ended up merging. The Central American taxon fell into a different clade from *aequinoctialis*, and was in fact embedded in a clade with *G. semiflava*, also known from Costa Rica and (disjunctly) South America. They state: "Given that *chiriquensis* is morphologically distinctive enough to have been traditionally assigned to another species group, merging it into *semiflava* . . . seems inappropriate" and suggested that it be raised to species status. Superficially, this seems reasonable, even probable.

However, the sentence in which this suggestion is made is, to me, ambiguous. It says: "we suggest that *chiriquensis* be raised to species status, along with the genetically disjunct and allopatric Central (*G. bairdi*) and South American (*G. semiflava*) forms of *semiflava*." In their Figure 2, what seem to be *chiriquensis* and *bairdi* are linked (right at the top) as sister taxa, and together are sister to Ecuadorian *semiflava*. I am not sure if they are recommending that all three be considered individual species, or if all should be one species, or if the two Costa Rican taxa should be one species distinct from *semiflava*.

Further, their Appendix A indicates that the samples of *chiriquensis* and *bairdi* were taken only 5 days apart, both in Costa Rica. Because they are so similar in Fig. 2, I wondered if there was any possibility of misidentifying one of them. It seems to my untrained eye that if *chiriquensis* and *bairdi* are distinct, they should not come out so

close in the figure. Later studies of the Parulidae (e.g., Lovette et al. 2010) do not resolve this because those groups were not sampled.

I raised this point with John Klicka, one of the authors. It turns out that he had asked the same question and was assured that the specimens, from opposite sides of Costa Rica, were properly identified. I have now looked at our few specimens and see that *chiriquensis* and Costa Rican *semiflava* (= *bairdi*) are readily distinguishable. Klicka suggests that *chiriquensis* is recently derived of Central American *semiflava* stock with a coincidental convergent resemblance to *aequinoctialis*. Considering the color differences, it may be an early offshoot, isolated on Volcán de Chiriquí for a long time.

Recommendation:

I recommend that we recognize *Geothlypis chiriquensis* as a species distinct from *aequinoctialis*, as Escalante et al. (2009) recommend.

Literature Cited:

- Escalante 1991 a paper in IOC, not seen. Cited in AOU 1998
Escalante, P., L. Márquez-Valdelamar, P. de la Torre, J. P. Lacleste, and J. Klicka.
2009. Evolutionary history of a prominent North American warbler clade: the
Oporornis-Geothlypis complex. *Molecular Phylogenetics and Evolution* 53: 668-678.
Hellmayr 1935
Lovette, I., et many al. 2010. A comprehensive multilocus phylogeny for the wood-
warblers and a revised classification of the Parulidae (Aves). *Molecular
Phylogenetics and Evolution* 57:753-770.
Lowery and Monroe 1968. *Peters* vol. 14
Wetmore, A., et al. 1984. *Birds of Panama* vol. 4

Submitted by: Richard C. Banks

Date of Proposal: 27 Dec 2010

Adopt a new generic classification for the Parulidae

Description of the Problem:

Recent years have seen several partial reclassifications of the Parulidae (e. g., Klein et al. 2004, Escalante et al. 2009), and we have responded to some of them. Finally, now, there is one that is based on a thorough DNA analysis of the entire family (minus only a few species/subspecies). This is the analysis by Lovette et al. (2010).

New Information:

Using both mitochondrial and nuclear DNA, Lovette et al. used several analyses to establish a phylogenetic hypothesis for all genera and nearly all species of the family. This new classification recognizes 14 genera corresponding to well-supported clades (see tree below). Several long recognized generic names fall by the wayside, but there have been at least hints of some of these changes in the past. For example, *Oporornis* falls into *Geothlypis* (as in Escalante et al. 2009), *Parula* and *Dendroica* are subsumed into *Setophaga*, and *Wilsonia* disappears into *Myioborus* and *Setophaga*. Sequence within some genera also changes. This analysis also shows that some genera and species generally believed to be parulids actually have relationships elsewhere. These include the genera *Icteria*, *Teretistris*, *Microligea*, *Xenoligea*, *Granatellus*, and *Zeledonia*.

Recommendation:

I propose that we adopt this classification, which is shown on the next page. For the N&MA committee, only those forms that occur in our territory are pertinent. This includes everything from the top through all *Setophaga*, *Myiothlypis fulvicauda*, all *Basileuterus* except *hypoleucus* and *trifasciatus*, plus *ignota* next to *melanogenys*, all *Cardellina*, and *Myioborus pictus*, *miniatus*, and *torquatus*. Fortunately, none of this requires any gender changes in specific (or subspecific) names and no homonymies are created.

If Proposal 2010-B-9 on recognizing *Geothlypis chiriquensis* is accepted, that name would replace *G. aequinoctialis* and be moved to a position next to *G. semiflava*, at least tentatively—or perhaps incertae sedis in the genus.



Literature Cited:

- Escalante, P., L. Márquez-Valdelamar, P. de la Torre, J. P. Lacleste, and J. Klicka. 2009. Evolutionary history of a prominent North American warbler clade: the *Oporornis-Geothlypis* complex. *Molecular Phylogenetics and Evolution* 53: 668-678.
- Klein, N. K., K. J. Burns, S. J. Hackett, and C. S. Griffiths. 2004. Molecular phylogenetic relationships among the wood warblers (Parulidae) and historical biogeography in the Caribbean basin. *Journal of Caribbean Ornithology* 17:3-17.
- Lovette, I. J., J. I. Pérez-Emán, J. P. Sullivan, R. C. Banks, I. Fiorentino, S. Córdoba-Córdoba, M. Echeverry-Galvis, F. K. Barker, K. J. Burns, J. Klicka, S. M. Lanyon, and E. Bermingham. 2010. A comprehensive multilocus phylogeny for the wood-warblers and a revised classification of the Parulidae (Aves). *Molecular Phylogenetics and Evolution* 57: 753-770.

Submitted by: Richard C. Banks

Date of Proposal: 29 Dec 2010

Adopt a new generic classification for the Parulidae - Amendments**Amendment #1 – Retain *Leucopeza semperi* and *Oporornis agilis* in their current genera, rather than lumping them into *Geothlypis* as indicated in the main proposal**

Keep the two monotypic genera as noted above to retain some degree of morphological consistency for *Geothlypis*. *Leucopeza*: there is nothing in the plumage, morphology, or known behavior that suggests a relationship to any other member of this clade; to include it in *Geothlypis* violates any subjective notion of continuity in parulid genera. *Oporornis*: not so clear in this case, but the phylogeny requires for consistency retaining this as a monotypic genus if *Leucopeza* also retained. *Oporornis agilis* has long been recognized as an oddball despite the plumage similarities to *philadelphia+tolmiei* – it is one of the only parulids that walks on the ground. Overall rationale is to avoid relegating genus-level boundaries to nodes based solely on DNA sequence data.

One counter-argument is that there is really no support for these two NOT being nested within one of the other clades; the branching pattern suggests that they are not but without strong statistical support.

Amendment #2 – Retain *Catharopeza bishopi* in its current genus, rather than lumping it into *Setophaga* as indicated in the main proposal

Catharopeza bishopi is sister to the rest of the expanded *Setophaga*, and the node uniting it with the rest of *Setophaga* is deeper than that uniting *Leucopeza+O. agilis* with the rest of *Geothlypis*. The mitochondrial and combined data trees in Lovette et al. (2010) provide strong support for *Catharopeza* as sister to the rest of the expanded *Setophaga*. Phenotypic arguments similar to those made above for retaining *Leucopeza* can also be made for retaining the distinctive *Catharopeza*, which stands out from the rest of the expanded *Setophaga* (even though the expanded *Setophaga* is more phenotypically diverse than is the expanded *Geothlypis*).

Restore authority for the genus name *Peucedramus* to Coues

The genus *Peucedramus* was erected in Henshaw's ornithological chapter in the report of the Geographical and Geological Explorations and Surveys West of the 100th Meridian, for the species described as *Sylvia olivacea* / *Sylvia taeniata* (Henshaw 1875). However, the description of the new genus consisted entirely of a quotation from a manuscript attributed to Coues and the genus was listed as "**PEUCEDRAMUS, Coues, nov. gen.**" (Henshaw 1875, p. 201). Following the description, Henshaw made the following statement, "I called the attention of my friend Dr. Elliott Coues to these ["certain peculiarities of the bird"], and, as a result of his examination of the specimens, ***he has erected the genus as above given***" [bold italics added].

It seems clear that *Peucedramus* should be attributed to Coues in Henshaw (as in Ridgway 1902) or, following AOU practice, simply to Coues. This situation is covered explicitly in section 50.1.1 of the International Code of Zoological Nomenclature (ICZN 1999). The relevant passage states that "if it is clear from the contents that some person other than an author of the work is alone responsible both for the name or act and for satisfying the criteria of availability other than the actual publication, then that other person is the author of the name or act." Moreover, an example is provided (p. 52) that is entirely analogous to the situation with *Peucedramus*.

Interestingly, the name was correctly attributed in the first and second editions of the AOU Check-list, in which *Peucedramus* was considered a subgenus, but the authority was inexplicably changed to Henshaw in the third edition and has remained so in all subsequent editions. The page number was also changed in the third edition, from p. 201 to p. 156; this obvious error was finally corrected in the sixth edition of the Check-list, but Henshaw continued to be cited as the authority. Unfortunately, no explanation for any of these changes was provided.

We recommend that the authority for the genus name *Peucedramus* be restored to Coues, in keeping with the original description in Henshaw and Henshaw's own statements.

Literature Cited:

Henshaw, H. W. 1875. Chapter III (Report upon the ornithological collections) *in* Geographical and Geological Explorations and Surveys West of the 100th Meridian, Vol. 5 – Zoology. Government Printing Office, Washington, DC.

ICZN. 1999. International Code of Zoological Nomenclature, 4th edition. International Trust for Zoological Nomenclature, London.

Ridgway, R. 1902. Birds of North and Middle America. Bull. U.S. Natl. Mus. 50, Pt. 2.

Submitted by: Terry Chesser and Alan Peterson

Date of Proposal: 29 Dec 2010

Split Mexican Jay *Aphelocoma ultramarina* into two species

Description of the problem:

Although *A. ultramarina* (Mexican Jay) has long been considered to harbor unusually high diversity for a single species (Pitelka 1951), taxonomy has been stable, with one species recognized. Pitelka (1951) conducted an intensive study of morphological variation and recognized three groups that he felt merited greater recognition than that afforded by the subspecies designation. The “Wollweberi” group inhabits the Sierra Madre Occidental and includes subspecies (north to south) *arizonae*, *wollweberi*, and *gracilis*. The “Sordida” group inhabits the Sierra Madre Oriental and includes subspecies (north to south) *couchii* and *sordida*. The “Ultramarina” group inhabits the Transvolcanic Range and includes subspecies (west to east) *colimae* and *ultramarina*. Pitelka (1951) offered two suggestions for species limits in *A. ultramarina*. If proof of the cessation of gene flow were needed, he suggested the species be kept unified. If some gene flow in secondary contact were permitted, he recommended elevating the three groups to species level.

The 7th edition of the AOU (1998) check-list maintained *A. ultramarina* as one species. Reasons given for maintaining *A. ultramarina* as one species were the existence of a “broad intermediate area where the groups meet in central Mexico”. This refers to the study of Peterson (1991) that found clinal change in onset of bill color maturation among northern lineages, but subspecies *ultramarina* and *colimae* in the Transvolcanic Belt were found to all have delayed bill color maturation. Splitting was also deferred because of genetic evidence from allozymes suggesting the species might be paraphyletic (Peterson 1992).

The Ultramarina group is the most phenotypically divergent group among Mexican Jays (Pitelka 1951) and prior allozyme work has suggested that it is the first-diverging member of Mexican Jays, with a long history of isolation (Peterson 1992). The question of whether it is completely genetically isolated and divergent from other Mexican Jays has not been examined in detail until recently.

New information:

Since the last checklist, there have been one phylogeographic study of *A. ultramarina* (McCormack et al. 2008) and two phylogenies for *Aphelocoma* (Rice et al. 2003, McCormack et al. 2011) bearing on the species status of the Ultramarina group (*A.*

ultramarina ultramarina + *A. ultramarina colimae*). Of genus-level phylogenies, one was based on mtDNA only and used one individual per lineage to reconstruct a basic evolutionary history (Rice et al. 2003), whereas the other was based on longer mtDNA fragments from two different genes and two nuclear genes and also included nearly 80 individuals representing the full range of variation known from previous genetic, phenotypic, and geographic study (McCormack et al. in press).

Rice et al. (2003) provided the first assessment of DNA sequence differences within *A. ultramarina*. This study established that Uicolored Jays, Scrub Jays, and Mexican Jays were indeed monophyletic groups, contrary to allozyme results that suggested paraphyly of Mexican Jays (Peterson 1992). This study also suggested that the Ultramarina group was monophyletic and had a long history of isolation from other Mexican Jays.

McCormack et al. (2008) analyzed mitochondrial DNA (mtDNA) and 14 microsatellite markers of 482 individuals from throughout the range of *A. ultramarina*, including all known repositories of geographic, genetic, and phenotypic diversity. The sampling distribution was geographically broad and included >10 individuals for 19 of the 27 sampling locations (24 populations had more than one individual). This made it highly likely that if shared genetic markers existed due to either gene flow or recency of ancestry, even at somewhat low levels, they would have been detected.

Results from McCormack et al. (2008) showed that there were at least four highly divergent mtDNA lineages of *A. ultramarina* inhabiting the major mountain massifs of northern Mexico, including the Ultramarina Group, which was confirmed to be an endemic lineage of the Transvolcanic Belt of central Mexico. The other lineages were a *wollweberi* group (*A. u. arizonae* + *wollweberi* + *gracilis*) in the Sierra Madre Occidental, a *couchii* group (*A. u. couchii*) in the Sierra Madre Oriental, and a *potosina* group (*A. u. potosina*) in the Central Plateau and parts of the southern Sierra Madre Oriental. The Ultramarina group (which was given the geographic moniker Transvolcanic) showed no mtDNA haplotypes in common with other groups, and was ~9% divergent in corrected genetic distance. ND2 and control region data both placed the Ultramarina group as the first-diverging lineage within Mexican Jays on a long branch. Preliminary relaxed-clock divergence dating (based on the 2% Rule) placed divergence of the Ultramarina group in the late Miocene. Results from microsatellite markers also supported current genetic isolation of the Ultramarina group from other Mexican Jays in that all individuals were assigned with high probability to a single genetic cluster using the program STRUCTURE. Finally, phenotypic results on morphological traits and spectral analysis of plumage color showed that the Ultramarina group was easily diagnosable and nearly as divergent from other *A. ultramarina* as it was from Uicolored Jays, with which it

occurs sympatrically. Nearly all individuals could be assigned correctly to the Ultramarina group on the basis of a discriminant function analysis of phenotypic traits.

A recently accepted paper on the phylogeny of *Aphelocoma* (McCormack et al. 2011) bolsters evidence for species status of the Ultramarina group by adding 2 nuclear genes, each of which indicates monophyly of the Ultramarina group, both when analyzed individually and when analyzed together with mtDNA in a species-tree analysis. More detailed divergence dating for *Aphelocoma* using fossil calibration on the species tree still supports divergence of the Ultramarina group in the late Miocene.

Recommendation:

We recommend that the Ultramarina group of Pitelka (1951) be considered a separate species (*A. ultramarina*) comprised of two subspecies, *A. ultramarina ultramarina* and *A. ultramarina colimae*. The astonishingly high genetic divergence in both mtDNA and nuclear genes, the lack of evidence for gene flow in mtDNA and nuclear microsatellite markers, the disjunct range borders, and the phenotypic distinctness of this group make a strong case for species status under virtually all species concepts. They may come into contact with northern groups in a handful of locations (Pitelka 1951), but also notable is that they have maintained their genetic distinctiveness throughout the Pleistocene glacial cycles, which undoubtedly shifted their elevational distributions lower to some extent, potentially putting them into contact with other lineages. They also seem to inhabit a higher-elevation pine forest than other Mexican Jays (Pitelka 1951); however, extreme ecological divergence of the Ultramarina group compared to other Mexican jays may have been overstated (Rice et al. 2003; McCormack et al. 2010).

Recommended English names:

We recommend Transvolcanic Jay for this species to underscore that it is endemic to the Transvolcanic Belt and to draw further attention to this region of high endemism in Mexico. Other lineages would retain the name Mexican Jay.

Intraspecific taxonomy:

The Transvolcanic group (*A. ultramarina*) contains two subspecies, (west to east) *colimae* and *ultramarina*. These subspecies are modestly divergent in genetic markers (McCormack et al. 2008) and phenotype (Pitelka 1951), but differences appear to be clinal. More study is needed of intermediate populations in Michoacán.

Position in the Check-list

Following the convention of basal taxa first, we have inserted *A. ultramarina* before other Mexican Jays.

Effect on the Check-list:

We suggest the following revisions to the account for *Aphelocoma ultramarina*:

Aphelocoma ultramarina (Bonaparte). Transvolcanic Jay.

Corvus ultramarinus Bonaparte, 1825, J. Acad. Nat. Sci. Philadelphia 4: 387. (No locality given = Temascáltepec, México.)

Habitat.- Pine Forest, Pine-Oak Forest (900-3400m; Subtropical Zone).

Distribution.- Resident of Transvolcanic Belt from Colima east through southern Jalisco, northern Michoacán, México, northern Morelos, Puebla, and west-central Veracruz.

Notes.- *A. ultramarina* and *A. wollweberi* were formerly considered a single species. Recent genetic study (McCormack et al. 2008; McCormack et al. 2010) and data on morphology, plumage, and voice (Pitelka 1951, McCormack et al. 2008, Brown and Horvath 1989) support a long history of isolation of the two groups.

Aphelocoma wollweberi (Kaup). Mexican Jay.

Aphelocoma wollweberi Kaup, 1854, J. für Ornith. 2: suppl., xlvii-lvi. (No locality given = Zacatecas, México.)

Habitat.- Pine-Oak Forest, Galley Forest, Pine Forest (1200-3400 m; Subtropical and Temperate zones).

Distribution.- Resident [*wollweberi* group] from central Arizona and isolated mountain ranges of southeastern Arizona, southwestern New Mexico, and northern Sonora south throughout Sierra Madre Occidental in Sonora, western Chihuahua, Durango, Zacatecas, and northern Jalisco, and west to Nayarit, and [*couchii* group] from southwestern Texas (Chisos Mountains) and isolated mountains of northern Coahuila south throughout Sierra Madre Oriental in southeastern Coahuila and northwestern Nuevo León, south to western Veracruz, and east to western Tamaulipas, and [*potosina* group] in central Mexican Plateau in San Luis Potosí, Querétaro, Guanajuato, and eastern Jalisco.

Notes.- Formerly considered conspecific with *A. ultramarina* but differs in genetics and phenotype (McCormack et al. 2008) as well as voice. Consists of at least three distinct mitochondrial DNA lineages, but nuclear markers indicate some gene flow

among *couchii* and *potosina* groups (McCormack et al. 2008; McCormack et al. in press), which are not identified as sister taxa by mitochondrial DNA. All molecular markers and phenotype support the *wollweberi* group as distinct, but elevation of this group to species would render the rest of the species paraphyletic. Further investigation is warranted to determine the level of gene flow among *couchii* and *potosina* groups.

Literature cited: * = new literature for species account

- A.O.U. 1998. Check-list of North American Birds. 7th edition. American Ornithologists' Union, Washington, D.C.
- Brown, J. L., and E. G. Horvath. 1989. Geographic variation of group size, ontogeny, rattle calls, and body size in *Aphelocoma ultramarina*. *Auk* 106:124-128.
- *McCormack, J. E., A. T. Peterson, E. Bonaccorso, and T. B. Smith. 2008. Speciation in the highlands of Mexico: genetic and phenotypic divergence in the Mexican jay (*Aphelocoma ultramarina*). *Mol. Ecol.* 17:2505-2521.
- *McCormack J. E., AJ Zellmer & LL Knowles. 2010. Does niche divergence accompany allopatric divergence in *Aphelocoma* jays as predicted under ecological speciation?: Insights from tests with niche models. *Evolution* 64:1231-1244.
- *McCormack JE, J Heled, KS Delaney, AT Peterson, and LL Knowles. 2011. Calibrating divergence times on species tree versus gene trees: implications for speciation history of *Aphelocoma* jays. *Evolution* 65:184-202.
- Peterson, A. T. 1991. Geographic variation in the ontogeny of beak coloration of gray-breasted jays *Aphelocoma ultramarina*. *Condor* 93:448-452.
- Peterson, A. T. 1992. Phylogeny and rates of molecular evolution in the *Aphelocoma* jays (Corvidae). *Auk* 109:133-147.
- Pitelka, F. A. 1951. Speciation and ecological distribution in American jays of the genus *Aphelocoma*. University of California Press, Berkeley & Los Angeles, CA.
- *Rice, N. H., E. Martinez-Meyer, and A. T. Peterson. 2003. Ecological niche differentiation in the *Aphelocoma* jays: a phylogenetic perspective. *Biol. J. Linn. Soc.* 80:369-383.

Submitted by:

John McCormack, Louisiana State University
A. Townsend Peterson, Kansas University
Carla Cicero, University of California Berkeley

Date of proposal: 9 Jan 2011

Lump *Ramphastos swainsonii* with *R. ambiguus***Description of the Problem:**

NACC and SACC differ currently in ranking of taxa in the *Ramphastos ambiguus* group. SACC considers them all conspecific, whereas NACC treats *swainsonii* as a separate species. A proposal from Thomas Donegan to SACC to recognize *R. swainsonii* as a separate species and thus bring SACC and NACC into alignment was just rejected. I think many of us on SACC were predisposed to recognize the split, given the absence of real data one way or another, but by the time the existing evidence was laid out, SACC reaffirmed its position that the current information is consistent with treating them as subspecies of the same species because of lack of any vocal differences and because of hints of intergradation where they are parapatric. The only solid difference between them, facial skin and bill color, is known *not* to be a barrier to gene flow in other parapatric toucans that differ only in bill color. Therefore, I am submitting this proposal to NACC by using Donegan's SACC proposal, pasted in below, along with all the comments.

A YES vote would, therefore, revise NACC classification to consider them conspecific, and a NO vote would maintain the NACC status quo, i.e. two species. However, be sure to note that SACC members so far are more or less evenly split on this one.

Submitted by: Van Remsen

Date of Proposal: 11 January 2011

Proposal (440) to [South American Classification Committee](#)**Split *Ramphastos swainsonii* from *R. ambiguus***

Effect of Proposal: If it passes, this proposal would result in recognition of *Ramphastos swainsonii* (subspecies *swainsonii* and *abbreviatus*) (Chestnut-mandibled Toucan) as a species separate from *Ramphastos ambiguus* (Black-mandibled Toucan). This treatment is reflected in most modern literature. We recently reviewed the basis for split and lumped treatments in Donegan et al. (2010). By way of background, we moved the Colombian checklist to generally follow SACC treatments as from 2007, but did not accept this SACC lump as one of a handful of exceptions.

Discussion: In Donegan et al. (2010), we reviewed the literature on this species and studied a good sample of sound recordings from across the range of the greater *ambiguus* group. We stated as follows:

“Many authors, particularly in the field guide literature, treat Chestnut-mandibled Toucan *Ramphastos swainsonii* as separate from Black-mandibled Toucan *R. ambiguus*, (e.g. Meyer de Schauensee 1964, 1966, Hilty & Brown 1986, Fjeldså & Krabbe 1990, Ridgely & Gwynne 1989, Dunning 1987, Howell & Webb 1995, Ridgely & Greenfield 2001, Stotz et al. 1996, Dickinson 2003, Krabbe & Nilsson 2003, Hilty 2003, Restall et al. 2006, AOU 1998, 2019, Salaman et al.. 2000, 2007, 2008a, 2009; and Gill & Donkser 2010, the latter considering the split to be “accepted by all except SACC”). Despite the latter assertion, some other authorities treat them as lumped (e.g. Short & Horne 2001, 2002; Erize et al. 2006; Remsen et al. 2010; and post-2006 journal papers that require Remsen et al. 2010 to be followed, e.g. Donegan et al. 2007, Patané et al. 2010).

“*R. swainsonii* (subspecies: *swainsonii* and *abbreviatus*) occurs west of the Andes into the Magdalena valley, whereas *R. ambiguus* occurs on the east slope of the Andes. All three taxa were lumped by Haffer (1974) who noted overlaps in biometrics and plumage, based largely on studies of specimens. An inspection of specimens at BMNH gives some insights to this treatment. Once bare skin and bill coloration are lost, as occurs on specimens of a certain age, individuals are difficult to assign to one or other subspecies (except by collecting locality), because biometrics (bill, tail and wing length) overlap and plumage is essentially identical. Despite this, based on the literature review above, it is evident that Haffer (1974)’s lump has not been widely followed.

“The English names also correctly reflect the differences in bill coloration, with *ambiguus* being black-billed and *abbreviatus* / *swainsonii* being dark chestnut brown. As pointed out by Stiles et al. (1999), *abbreviatus* is a valid taxon and is closer to *swainsonii* in its morphology, habitat requirements, and range. The morphological differences between the *swainsonii* and *ambiguus* groups are rather striking when individuals are observed in the field.

“A recent molecular study showed *R. ambiguus* to be a monophyletic group based on the individuals sampled. There was 1.35% mtDNA variation between *swainsonii* and *ambiguus*, suggesting a Pleistocene divergence (Patané et al. 2010). Whilst this was a relatively high value for intraspecific mtDNA variation for a toucan, it amounts to only modest variation and was based on limited sampling (not including *abbreviatus*). On its own, this data forms no basis for either lumping or splitting a species and the authors suggested no such action.

“Turning to voice, Stiles et al. (1999) elucidated small differences between recordings from Colombia and a single recording then available of *ambiguus* from Peru. Recordings available today include good numbers and broad geographical sampling of all populations. An inspection of sonograms of available recordings was

carried out (recordings inspected: all those in Krabbe & Nilsson (2003, Ecuador: 5 *swainsonii*, 2 *ambiguus*), Alvarez et al. 2007 (Colombia: 2 *ambiguus*), Jahn et al. 2001 (Ecuador: 1 *swainsonii*), Boesman 1999 (Venezuela: 2 x *ambiguus*) and www.xeno-canto.org as of 16 April 2010 (various countries: 13 *swainsonii*, 3 *abbreviatus*, 5 *ambiguus*); totals 19 *swainsonii*, 11 *ambiguus*, 3 *abbreviatus*. Both groups give two phrases in their songs, commonly transcribed as: “Dios te de” and “Dios te de te de”. Several recordings of *ambiguus* sound more hurried (hence, shorter) and higher than some recordings of the *swainsonii* group (as noted by Stiles et al. 1999). However, there is overlap, with slower *ambiguus* falling in the range of faster *swainsonii* (including if only “Dios te de” recordings are compared). It is possible that there are average differences in some acoustic variables (this was not tested statistically), but there would not appear to be diagnostic differences in note shape, song length, or acoustic frequency for any particular population. Ridgely & Greenfield (2001) previously noted that populations do not appear fully diagnosable on the basis of voice, a conclusion consistent with ours.

“A rationale for treating *swainsonii* as separate from *ambiguus* would be based on allopatric distributions, diagnostic differences in bare skin and bill coloration, moderate mtDNA variation, and average differences in biometrics and possibly song speed. *R. swainsonii* is clearly a phylogenetic species but is a questionable biological species. Despite these only moderate differences, votes on the Colombian checklist forum were strongly in favour of maintaining species rank for *swainsonii*, with 12-1 votes in favour, perhaps reflecting the status quo of treatments in the vast majority of leading texts.

“We see no strong reasons either to split or lump these taxa based on available studies and materials. Although the split is not strongly supported, the proposition that Remsen et al. (2010)’s lump treatment represents the “status quo” is also weakly supported. The SACC list is supposedly based on Meyer de Schauensee (1970) and Dickinson (2003), who both split this group, as does the AOU’s North American checklist committee (AOU 2010). For whatever reason, Haffer (1974)’s lump has not been widely followed. In accordance with the prevailing treatment in leading texts and the votes received on the checklist forum, we therefore tentatively maintain our current treatment but with little enthusiasm.”

Recommendation: Complete ambivalence. This is an old chestnut of allopatric populations that are easily diagnosable based on few characters. Different authorities have taken different views over the years on this point, although the split treatment prevails. SACC has had this issue down as requiring a proposal for many years. The lack of diagnosable vocal differences and moderate mtDNA variation do not mandate any split. On the other hand, the differences in bare skin and bill coloration between these populations are striking and might influence mate selection if populations were ever to occur together (which seems unlikely). For whatever reason, Haffer (1974)’s treatment has not been widely followed, and SACC’s current (lumped) position for these birds is *contra* most of the field guide literature and the North American AOU. With little

enthusiasm for either treatment, we decided to maintain this split on the somewhat flimsy basis that it better reflects the status quo for Neotropical ornithology. This may be a rare instance where “YES” means “NO” and “NO” means “YES” (i.e. a “YES” vote would maintain a status quo treatment notwithstanding the SACC baseline). “YES” is to split; “NO” is to lump.

References:

Donegan, T., Salaman, P., Caro, D. & McMullan, M. 2010. Revision of the status of bird species occurring in Colombia 2010. *Conservación Colombiana* 13: 25-54.

Other references are cited in this paper.

Thomas Donegan, May 2010

Note: The shade of greenish/yellowish in the cere varies between some populations, but the reference in some field guide and other literature to *ambiguus* having a blue cere (repeated in our 2010 paper) would appear to be in error.

Comments from Robbins: “NO. I’m on the fence on this one. Given that there isn’t a strong argument to overturn our current treatment, I’ll vote “no” for now.”

Comments from Stotz: “YES. I have to admit that until this proposal I could not have told you that SACC lumped *ambiguus* and *swainsoni*. This isn’t quite a novel treatment, but it has only been followed by a few independent sources. It is not the treatment followed by Dickinson, which was largely the original base list for SACC. Unfortunately, the evidence does not strongly point to either treatment as the appropriate one. Vocal differences are clearly weak. The only significant differences are in soft part colors. There are conflicting treatments in the toucans regarding similar cases with weak to no vocal distinctions, disjunct distributions and soft part differences. Given that, in my view, this comes down to whether the committee feels strongly enough about the current treatment to remain at odds with most other treatments, in particular the North American committee. Based on this, recognizing a weak argument for any treatment, I favor splitting *ambiguus* and *ambiguus* to be consistent with most other literature (except for HBW by Short and Horne).

“If we don’t split *swainsoni* from *ambiguus*, I think we will need to change the common name of the broad *ambiguus*. Yellow-throated Toucan has been suggested. Doesn’t dazzle me, but I don’t have a better option, and it has been in the literature for a while.”

Comments from Zimmer: “YES. I agree that evidence for either course is weak, and given that, it seems better to stick with the more widespread status quo, rather than our current treatment. It seems as if the color differences in bare parts may serve as an isolating mechanism in the case of contact, but who knows?”

Comments from Stiles: “A tentative YES. The problem here has been that the maroon-mandibled *swainsonii* and the blackish-mandibled *abbreviatus* do intergrade around the upper Magdalena valley, as pointed out by Haffer – but in the past, *abbreviatus* was lumped into the black-mandibled, but cis-Andean, *ambiguus* based upon mandible color. The rather slight size difference, very different bare facial color, a mostly subtle difference in vocalizations and distribution would in my opinion rather strongly tip the balance towards considering *abbreviatus* a subspecies of *swainsonii* rather than of *ambiguus* (unless one decides to lump all three under *ambiguus*, which is the other alternative). The lack of genetic data for *abbreviatus* complicates things a bit, but when available, if this form falls out with *ambiguus* this would strongly favor lumping all three; were it to prove closer to *swainsonii* (which I suspect will be the case) this would be rather weaker evidence favoring the split as detailed here. In any case, the two-species treatment seems to be the prevalent one in most recent literature.”

Comments from Pacheco: “YES. Um “sim” tentativo, especialmente a partir das colocações de Gary.”

Comments from Nores: “YES, aunque con poco convencimiento. Es evidente que no hay demasiados elementos como para inclinarse hacia una u otra opción, pero el color del pico y de la cara me parece que es de peso. Además, reconocer *swainsoni* equivale a ponerse de acuerdo con la mayoría de las publicaciones más importantes que han aparecido en los últimos tiempos. Lo que no me parece que apoya la separación de *swainsoni* es el comentario que hay en la propuesta “A rationale for treating *swainsonii* as separate from *ambiguus* would be based on allopatric distributions”. La distribución alopátrica es más característica de subespecies que de especies, ya que todas las subespecies tienen distribución alopátrica o a lo sumo parapátrica.”

Comments from Remsen: “NO. The proposal correctly pointed out that the SACC starting point was Dickinson (2003), which split them, but the problem, not unique to this case, is that changes were made in galley proof stage in Dickinson (2003) that made the version we used differ from the final printed version. Nonetheless, I think that Donegan et al. (2010) have sufficiently summarized the facts to favor retaining the broadly defined species, to the point that if this were a proposal to lump the taxa, I’d vote YES.

“Let’s examine one-by-one the categories of evidence presented by Donegan et al.:

“1. ‘allopatric distributions’ = irrelevant to species limits under any species concept.

2. ‘diagnostic differences in bare skin and bill coloration’ = to assess the importance of these characters in toucans would require a comparative analysis of parapatric populations of *Ramphastos* taxa. Subspecies within most *Ramphastos* species differ more in bill coloration than do the taxa in question, and definitely more in bill pattern, so without further analyses, I suspect that this is not relevant. As for facial skin color, the differences between intergrading *R. v. culminatus* and *R. v. ariel* are much more dramatic, so as long as these are treated as subspecies, facial skin color alone cannot be used. [If *ariel* would be ranked as a species, then I suspect facial color differences would be concordant with species limits in *Ramphastos*.]

3. ‘moderate mtDNA variation’ = in itself irrelevant to species limits, unless one adheres to some sort of naive bar-coder approach to species limits. Even as is, the mtDNA difference falls below the one typically used for ‘species differences’ by bar-coders. One cannot determine species vs. subspecies rank based solely on genetic distance (otherwise, for example, there would only be about 4 species of Galapagos finches). What genetic differences can tell you is, provided the samples are taken close to contact zones, whether there is gene flow between the populations in question.

4. ‘average differences in biometrics’ = utterly irrelevant to species limits. See, for example, recent paper on elevational differences in biometrics in *Glyphorhynchus spurius* populations continuously distributed in Ecuador.

5. ‘possibly song speed’ = suggestive, but even with the small N examined so far, overlap is suggested and diagnosability not evident.

“Add to this the points made by Gary on intergradation and *abbreviatus*, and I think the burden-of-proof falls on those who would rank them as separate species.

“I also want to sound off on a couple of themes brought out by this proposal. First, there is an implication that outliers in classification must be wrong because they are outliers ... as if taxonomy was some sort of voting procedure. The tone is clearly that SACC is somehow out of touch on this particular issue (despite the clear absence of solid data to address the question one way or another). Given how much blind-faith copying goes on and how few independent assessments are taken by the various sources cited, I find this attitude simplistic at best. What counts are the details and facts, not how many other classifications piggyback on a particular stance. Second, the proposal also implies that the number of differences between two taxa somehow adds up to favoring species rank for the two. This theme is also repeated to a degree in the Helbig et al. paper on determining species limits and even more so in the more recent

Tobias paper on the same topic. In an attempt to make more objective the assignment of species rank, they engage in a form of numerical or phenetic taxonomy, as if all characters have equal weight. But if we adhere to a species definition that focuses on gene flow or its absence, potential or actual, then only those data relevant to assessing gene flow are relevant, not various other characters that vary among subspecies known to intergrade.”

Comments from Jaramillo: “NO. The evidence is weak for this split, particularly given that there is known hybridization. There is not much here that really suggests two biological species are involved.”

Additional comments from Zimmer: “I would like to change my vote to a NO. There is precious little real evidence one way or another, but in mulling it over, I am persuaded by Van’s arguments on this one. And, sticking with the single-species treatment would certainly be more consistent with the way we (and others) have treated other pairs of toucan taxa that differ primarily in bill color/pattern or facial skin color.”

Additional comments from Donegan: “One follow-up point: the issue of hybridisation or intermediates appears to have been misinterpreted in some of the later comments by committee members. The taxa *abbreviatus* and *swainsonii* are basically points on a cline or step cline from the lowlands of the Magdalena valley of Colombia north through to Central America. However, following Stiles et al (1999), these two taxa are both in *R. swainsonii* group. There is no known hybridisation or intergradation between the *swainsonii* and *ambiguus* groups, as defined in this proposal, as a result of their allopatric distributions. I note this proposal has failed. That is probably the correct outcome in light of the vocal, plumage and biometric similarities between the two groups applying BSC. Our maintenance of the split of these birds in the Colombian checklist and field guide was based on these being species under various concepts, including phylogenetic species concepts; the difficulties in applying BSC to allopatric populations; and the reluctance of many persons - and especially certain SACC committee members - to changing existing treatments. However, if one ignores the weight of taxonomic history and just applies BSC comparatively based on the actual data available, then Van Remsen's arguments and preferred lumped treatment have a lot of sense to them.”