AOU Classification Committee – North and Middle America

Proposal Set 2014-B

Split the Cuban Parrot (*Amazona leucocephala*) complex into multiple species

[***Note from Committee Chair:*** this is a revision of Proposal 2011-C-2, based on comments from the committee that suggested revising the proposal from the perspective of the biological species concept]

Background:

The Cuban Parrot (*Amazona leucocephala*) complex is composed of six extant populations (Cuba, Isla del la Juventud, Cayman Brac, Grand Cayman, Great Abaco, and Great Inagua) (Figure 1) with similar morphological features, including red throat and foreneck, white forehead and forecrown, red abdominal patch and pale bill (Forshaw 2006). The classification of the complex as species or subspecies has historically depended on qualitative plumage characteristics and geographic boundaries. However, significant morphological, behavioral, vocal and genetic differences have recently been identified between three of the six extant populations. Based on this new information, I recommend that the Cuban Parrot complex be reclassified as five biological species. In this proposal, I will outline the history of the classification of the Cuban Parrot complex and the new information on genetic, morphological, vocal and behavioral differences among the populations, which indicates that the classification is in need of being revisited.

History:

The Cuban Parrot complex has had a long history of name changes (Peters 1928). As early as 1731, Catesby documented the parrots in Cuba as *Psittacus paradisi*. On a trip to Grand Cayman in 1886, Cory documented *Chrysotis caymenensis* as a parrot distinct from the population in Cuba. Bryant (1867) grouped the parrot populations in the Bahamas with the Cuban population as *Psittacus collarus*, but recognized the Bahama birds as a distinct variety, *bahamensis*. Around the turn of the century, several records referred to the Bahama population as a distinct species either by the name *Chrysotis bahamensis* or *Amazona bahamensis* (Allen 1905, Bonhote 1903).

Peters (1928) examined the various populations of the Cuban Parrot complex and suggested a formal classification for the parrots in Cuba, the Cayman Islands and the Bahamas based on specimens in the Museum of Comparative Zoology (number of specimens unknown). He recognized four subspecies within a single species. This classification included *Amazona leucocephala leucocephala* on Cuba, *A. l. hesterna* on Cayman Brac and Little Cayman, *A. l. caymenensis* on Grand Cayman and *A. l. bahamensis* in the Bahamas. Peters did not indicate from which island the specimens of *bahamensis* were collected, but he excluded the Abaco population from the final description (Peters 1928).

Despite the extirpation of individual parrot populations on Little Cayman and Acklins Island in the Bahamas in the mid 1900’s, the distribution of the Cuban Parrot complex has remained relatively constant (Bond 1956 & Bond 1964). The range continues to encompass the Cayman Islands (Grand Cayman and Cayman Brac), Cuba (mainland Cuba and Isla de la Juventud), and the Bahamas (Great Abaco and Great Inagua Islands). The American Ornithologists' Union currently recognizes the six extant populations as *Amazona leucocephala* (AOU 1998). Until recently, five subspecies were described for *A. leucocephala*: *leucocephala* (Cuba), *palmarum* (Isla de la Juventud), *bahamensis* (Great Abaco and Great Inagua), *hesterna* (Cayman Brac), and *caymanensis* (Grand Cayman).

New information about these parrot populations has been obtained with more sophisticated methods than were available to Peters; thus, I suggest a new classification of the *Amazona leucocephala* complex.

New Information:

Morphology

Peters based his 1928 classification on morphological and plumage color traits. Reynolds and Hayes (2009) conducted a quantitative reassessment of morphological and color differences among the six extant populations and the extinct Acklins population using museum specimens. There were significant differences in all traits measured between islands including culmen, wing chord, tail, and foot. Additionally, they examined the amount and extent of white on the head, amount of red on the throat and belly, and color on the inner and outer eye (Table 1). No single characteristic could diagnose one population from another; however, when Reynolds and Hayes (2009) used two or more characteristics in a discriminant function analysis, individuals were assigned to correct populations an average of 81% of the time, with a 95% correct assignment of Cayman populations and an 89% correct assignment of Abaco populations when compared to all other populations. The authors also concluded that the three Bahama populations were as distinguishable as, if not more so than, other current populations in the complex. Comparison of neighboring populations showed that Abaco/Inagua populations can be differentiated 100% of the time. The population with the lowest degree of differentiation was the Cayman Brac population with 67% differentiation from the Cuba population. As a result of their investigations, Reynolds and Hayes (2009) proposed splitting *bahamensis* into three subspecies: *bahamensis* (extinct, formerly Acklins, Crooked, and Long Cay island group), *abacoensis* (Great Abaco), and *inaguaensis* (Great Inagua).

Behavior

Vocalizations

In parrots, vocalizations can be horizontally or vertically transmitted (Berg et al 2011); thus, specific calls and vocalizations are learned from other individuals in the population. The vocalizations can become population specific when learned in isolation from other populations. While vocalizations cannot necessarily be used as a single indicator of species differences as in songbirds, they may be indicators of the cultural structure of a population (Wright and Dorin 2001). Vocalizations in addition to variation in other characteristics (morphological, plumage, genetics) can create a clearer picture of social organization and differentiation.

A quantitative assessment of the flight calls of the six extant populations supported divergence of the individual island populations, with reduced differentiation between the two populations on Cuba (Reynolds et al. 2010). Abaco parrots are distinguishable from all other populations in the complex by their paired flight calls, which have a low fundamental frequency and few notes. Inagua parrot flight calls are also unique due to their high fundamental frequency and a frequency jump bifurcation. The Cayman Brac population is differentiated from other populations by long syllable duration and syllable interval length. The Cayman population is differentiated by having short syllables. The two Cuban populations are unique in their sharing of subharmonic features. However, sample sizes were small for these populations. Reynolds et al. (2010) did find distinct dialects among the Cuban populations.

Breeding

Species breeding segregation is not a diagnostic feature of different *Amazona* species. In fact, the introduction and subsequent interbreeding between different species of *Amazona* parrots is considered a major conservation threat to endemic/resident parrot species (Nichols 1980).

Nevertheless, a temporal segregation in breeding has developed in the Abaco population by initiating nesting at the end of May. The Inagua population initiates nesting two months earlier making breeding between populations unlikely.

Habitat use

The habitats on the different islands vary greatly. These differences may increase adaptation for those habitats and may underlie some of the genetic variation (see below). Local adaptation might be expected if traits for specific habitats are selected.

Abaco – The Abaco population is the only Amazon parrot to successfully nest in underground limestone solution cavities in the Caribbean pine forest (Snyder 1982). This population is also the latest nesting Amazon parrot population. The nesting season begins towards the end of May and ends mid-September (Gnam 1991). During the non-breeding season, this population migrates into hardwood forests on the island (Stahala 2008).

Inagua – The Great Inagua population uses a vast area of the dry and wet hardwood hammocks on the island. The Inagua parrot is only known to successfully nest in tree cavities, although ground cavities are available and are explored by Inagua parrots. Nesting occurs March through July (Stahala 2007).

Cuba – The Cuban populations inhabit areas with mature trees and snags including remote woodlands in mountains and lowlands. Palm groves are also used by parrots in savannas and wetland areas. Nesting occurs March through July, as in the Inagua parrot (Wiley et al 2004).

Cayman Islands – The Cayman populations use beach ridge scrubland, dry hardwood forests, black mangrove habitats and urban areas. Nesting occurs March through June (Wiley et al 2004).

Genetics

An in-depth genetic assessment of the Cuban Amazon complex shows divergence of the extant (and one extinct) *A. leucocephala* populations, with uncertainty remaining in the two Cuban and Cayman Brac populations (Russello et al 2010). Russello et al sampled the six extant populations and the recently extirpated Acklins Island population using mtDNA collected from field samples and museum specimens. The Bayesian mtDNA haplotype tree (Figure 2) indicates that the three Bahama populations (Abaco, Inagua, Acklins) and the Grand Cayman population all form monophyletic groups with high posterior probabilities (0.98-1.00), whereas the Cuban populations were paraphyletic with respect to the Cayman Brac population. Surprisingly, the two populations from the Cayman Islands are not sister taxa; both, however, are monophyletic.

Estimated sequence divergence between the various populations ranges from 1.2% to 4.8%. These divergences correspond well to those expected of full species (Johns and Avise 1998). The Grand Cayman and mainland Cuba populations show the largest divergence (4.8%), which is virtually the same (4.5%) as that between the Puerto Rican Parrot (*A. vittata*) and Hispaniolan Parrot (*A. ventralis*), which are recognized as species. Interestingly, the divergence between the Abaco and Inagua populations, which are currently considered one subspecies, is higher (2.8%) than that between the currently recognized subspecies of Cuba (*A.l. leucocephala* and *A.l. palmarum,* 1.2%). Moreover, the genetic differences between subspecies of *A. leucocephala* are higher than differences between recently recognized bird species in the Bahamas (0.7% - 1%; Table 3). The same part of the control region (CR1) was used in the Cuban Parrot study as was used in the Yellow-throated Warbler study (McKay et al. 2010) that elevated the Bahamas population to species status (American Ornithologists' Union 2010).

Russello et al (2010) also surveyed nine microsatellite loci for contemporary samples from Inagua and Abaco. They found high genotypic differentiation between individuals from these islands, as exemplified by a high proportion of private alleles (34% for Abaco and 62% for Inagua). A STRUCTURE analysis also revealed that individuals from the two islands formed distinct clusters.

Recommendation:

I propose, based on phenotypic differences and comparison of genotypic differences to those of other recently recognized biological species from the area (Table 3), that the Great Abaco, Great Inagua, and Grand Cayman populations be elevated to full species. The genetic differences in Russello et al. (2010) correspond remarkably well to the differences in morphology and vocalizations found by Reynolds and Hayes (2009) and Reynolds et al. (2010). Although the vocal, behavioral, and morphological characteristics may not be sufficient for species classification in these parrots, the congruent genetic evidence shows a strong underlying diversity among the populations proposed here to be distinct species (Alström et al. 2008, Johnson et al 1999). Additionally, the microsatellite studies of the Abaco and Inagua populations suggest divergence.

The data presented also suggests combining the two Cuban populations (Cuba and Isla del la Juventud) as a single subspecies (*Amazona leucocephala leucocephala*). Finally, the Cayman Brac population lacks data at this time; thus, I suggest no change to this population (Table 4; Figure 1). The proposed revisions follow the suggested divisions of Russello et al (2010).

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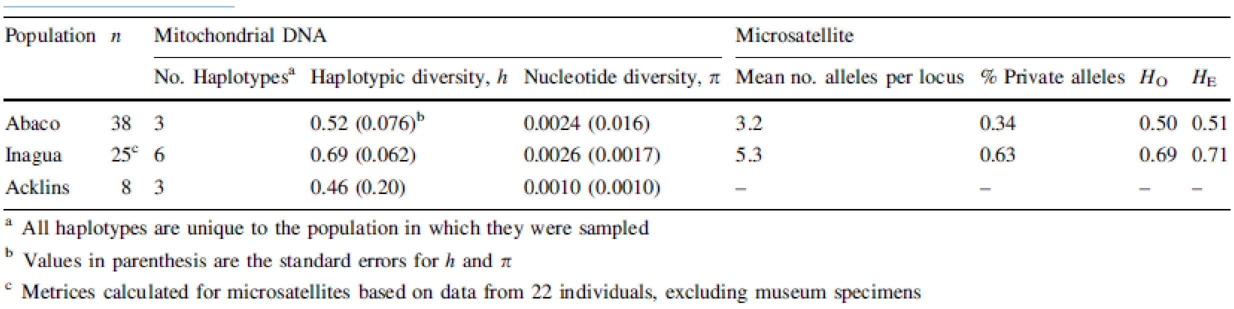
Table 1. Diagnostic characteristics

Bahama species descriptions are from Reynolds and Hayes (2009). Cuba and Cayman species descriptions are from Forshaw (2006) and Reynolds and Hayes (2009).

Amazona l. bahamensis (extinct – Acklins, etc.) Compared to all other *A. leucocephala* populations, specimens exhibit the largest average body size, more white on head and face, more rose on throat, less red on belly.
Amazona l. abacoensis (Great Abaco) Distinguished from *leucocephala*, *palmarum*, and *caymanensis* by larger size, more white on head and face, more rose on throat, and less red on the belly. Averages more red on belly and less red at orbit of eye than *bahamensis*. Averages more white on head and face and less red at orbit of eye than *inaguaensis*. Flight call typically consists of diagnostic paired syllables, unlike those of any other extant *A. leucocephala* population.
Amazona l. inaguaensis (Great Inagua) Distinguished from *leucocephala*, *palmarum*, and *caymanensis* by larger size, more white on head and face, more red on throat, and less red on the belly. Averages much less white in the head and face than *A. l. bahamensis*. Diagnostic flight call syllables have a high fundamental frequency and a severe frequency jump that, together, create a squeaky quality.
Amazona l. leucocephala (Cuba) Distinguished from *caymanensis* with more white on head and around eye and smaller in size. Less red on throat than *inaguaensis*. Shorter tail than *hesterna*.
Amazona l. palmarum (Isla de la Juventud) Falls between *A.l.leucocephala* and *A.l.hesterna* in amount of white on head however more red on throat and more white on inner white eye than these two.
Amazona leucocephala hesterna (Cayman Brac) Distinguished from *leucocephala* with more red around eye but more white around eye than *caymanensis*.
Amazona caymanensis (Grand Cayman) *Caymenensis* has the least amount of white on forehead and least amount of red on throat of any other population in the complex.

Table 2. Genetic variation within Bahama parrot populations (Russello 2010)



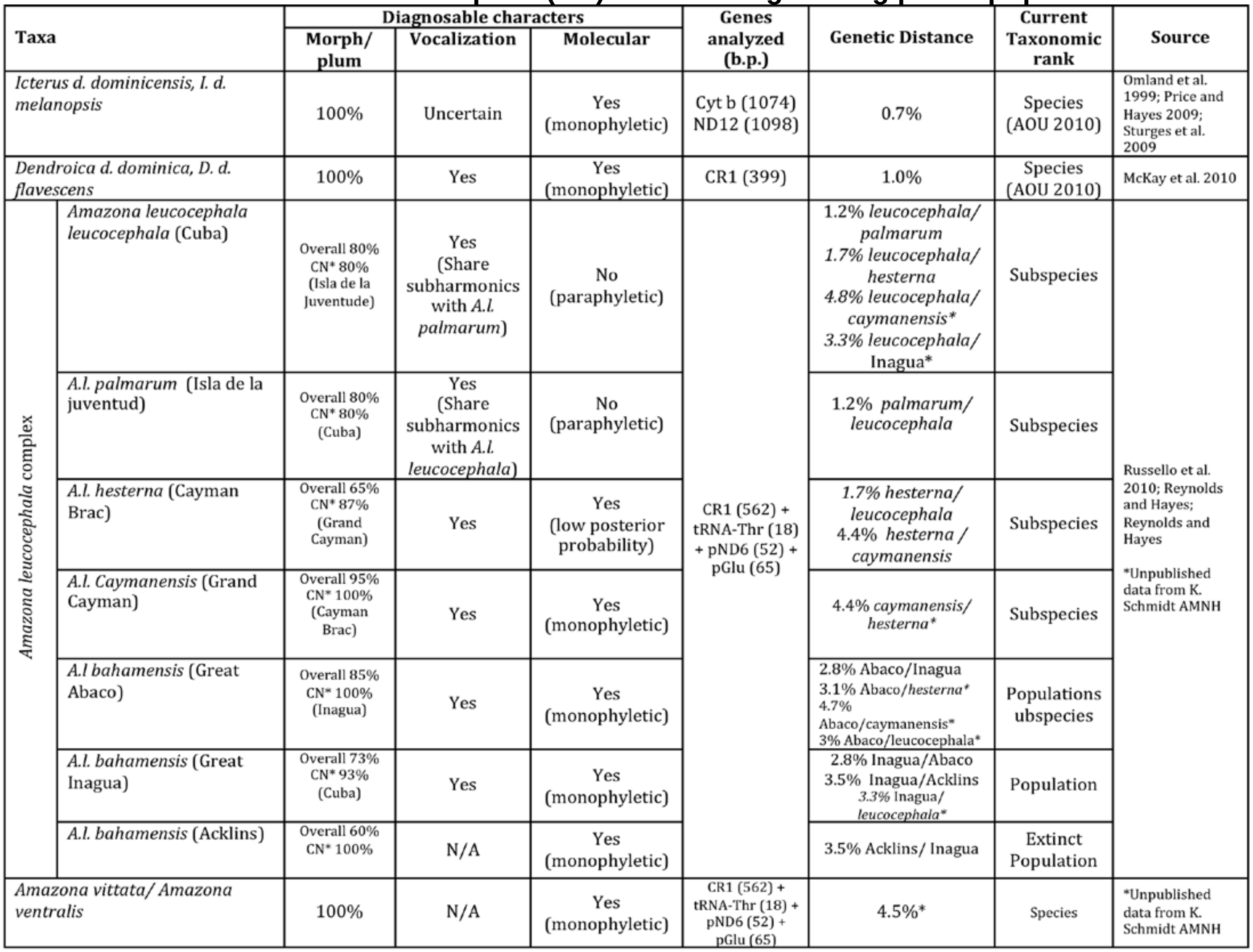
Population	n	Mitochondrial DNA			Microsatellite			
		No. Haplotypes[a]	Haplotypic diversity, h	Nucleotide diversity, π	Mean no. alleles per locus	% Private alleles	H_O	H_E
Abaco	38	3	0.52 (0.076)[b]	0.0024 (0.016)	3.2	0.34	0.50	0.51
Inagua	25[c]	6	0.69 (0.062)	0.0026 (0.0017)	5.3	0.63	0.69	0.71
Acklins	8	3	0.46 (0.20)	0.0010 (0.0010)	–	–	–	–

[a] All haplotypes are unique to the population in which they were sampled

[b] Values in parenthesis are the standard errors for h and π

[c] Metrices calculated for microsatellites based on data from 22 individuals, excluding museum specimens

Table 3. Comparison of criteria of recently reclassified species in the Caribbean to the Cuban Amazon complex. (CN) Closest neighboring parrot population.



Taxa		Diagnosable characters			Genes analyzed (b.p.)	Genetic Distance	Current Taxonomic rank	Source
		Morph/ plum	Vocalization	Molecular				
Icterus d. dominicensis, I. d. melanopsis		100%	Uncertain	Yes (monophyletic)	Cyt b (1074) ND12 (1098)	0.7%	Species (AOU 2010)	Omland et al. 1999; Price and Hayes 2009; Sturges et al. 2009
Dendroica d. dominica, D. d. flavescens		100%	Yes	Yes (monophyletic)	CR1 (399)	1.0%	Species (AOU 2010)	McKay et al. 2010
Amazona leucocephala complex	*Amazona leucocephala leucocephala* (Cuba)	Overall 80% CN* 80% (Isla de la Juventude)	Yes (Share subharmonics with *A.l. palmarum*)	No (paraphyletic)	CR1 (562) + tRNA-Thr (18) + pND6 (52) + pGlu (65)	1.2% *leucocephala/ palmarum* *1.7% leucocephala/ hesterna* *4.8% leucocephala/ caymanensis** *3.3% leucocephala/* Inagua*	Subspecies	Russello et al. 2010; Reynolds and Hayes; Reynolds and Hayes *Unpublished data from K. Schmidt AMNH
	A.l. palmarum (Isla de la juventud)	Overall 80% CN* 80% (Cuba)	Yes (Share subharmonics with *A.l. leucocephala*)	No (paraphyletic)		1.2% *palmarum/ leucocephala*	Subspecies	
	A.l. hesterna (Cayman Brac)	Overall 65% CN* 87% (Grand Cayman)	Yes	Yes (low posterior probability)		*1.7% hesterna/ leucocephala* 4.4% *hesterna / caymanensis*	Subspecies	
	A.l. Caymanensis (Grand Cayman)	Overall 95% CN* 100% (Cayman Brac)	Yes	Yes (monophyletic)		4.4% *caymanensis/ hesterna**	Subspecies	
	A.l bahamensis (Great Abaco)	Overall 85% CN* 100% (Inagua)	Yes	Yes (monophyletic)		2.8% Abaco/Inagua 3.1% Abaco/*hesterna** 4.7% Abaco/caymanensis* 3% Abaco/leucocephala*	Populations ubspecies	
	A.l. bahamensis (Great Inagua)	Overall 73% CN* 93% (Cuba)	Yes	Yes (monophyletic)		2.8% Inagua/Abaco 3.5% Inagua/Acklins *3.3%* Inagua/ *leucocephala**	Population	
	A.l. bahamensis (Acklins)	Overall 60% CN* 100%	N/A	Yes (monophyletic)		3.5% Acklins/ Inagua	Extinct Population	
Amazona vittata/ Amazona ventralis		100%	N/A	Yes (monophyletic)	CR1 (562) + tRNA-Thr (18) + pND6 (52) + pGlu (65)	4.5%*	Species	*Unpublished data from K. Schmidt AMNH

Table 4. Proposed Classification (based on diagnostic characteristics in Table 1)

Current Classification	Proposed Classification	Population locations
Amazona leucocephala leucocephala & A.l palmarum	Remains: *Amazona leucocephala* but combine to subsp. *leucocephala*	Mainland Cuba; Isla de la Juventude
A.l. hesterna	Remains: *Amazona leucocephala* subsp. *hesterna*	Cayman Brac
A.l. bahamensis	Proposed: *Amazona abacoensis*	Great Abaco, Bahamas
	Proposed: *Amazona inaguaensis*	Great Inagua, Bahamas
	Proposed: *Amazona bahamensis*	Acklins, Crooked, Long Cay Bahamas (extinct)
A.l. caymanensis	Proposed: *Amazona caymanensis*	Grand Cayman

Figure 1. Distribution map of Cuban Amazon complex with current and proposed classification.

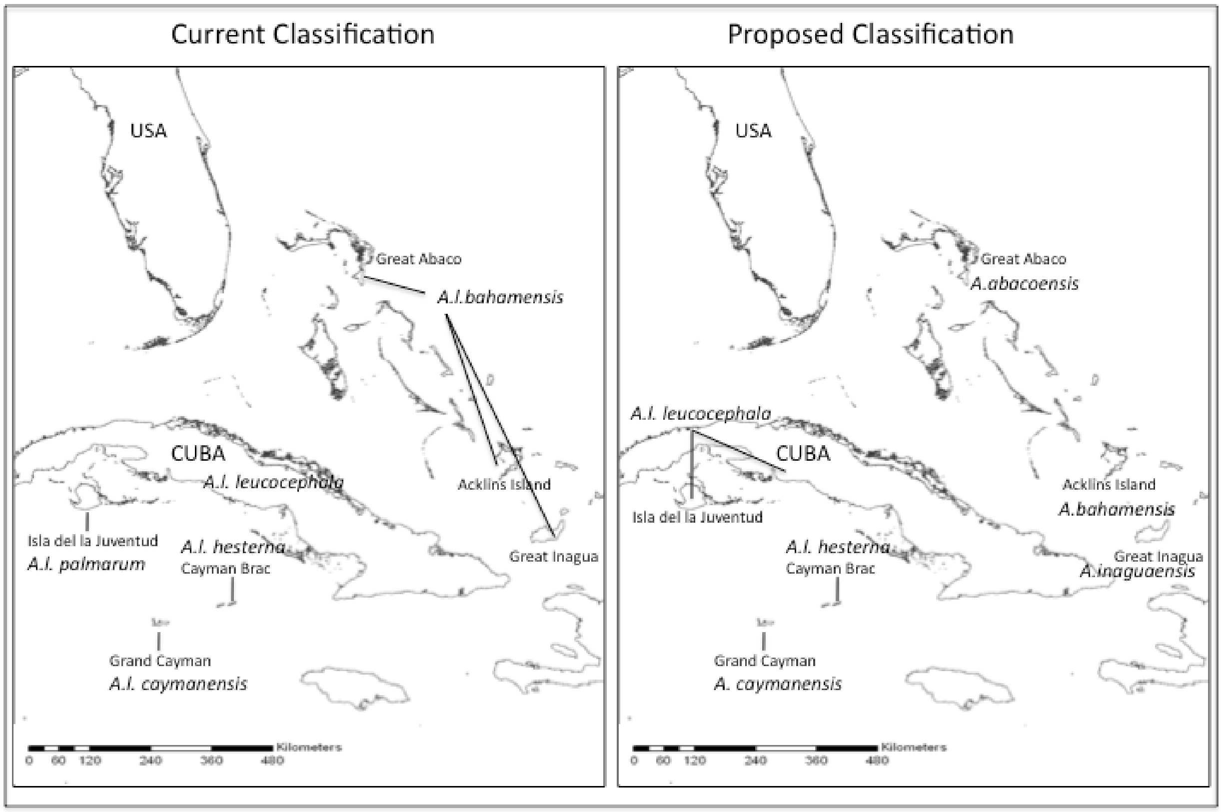
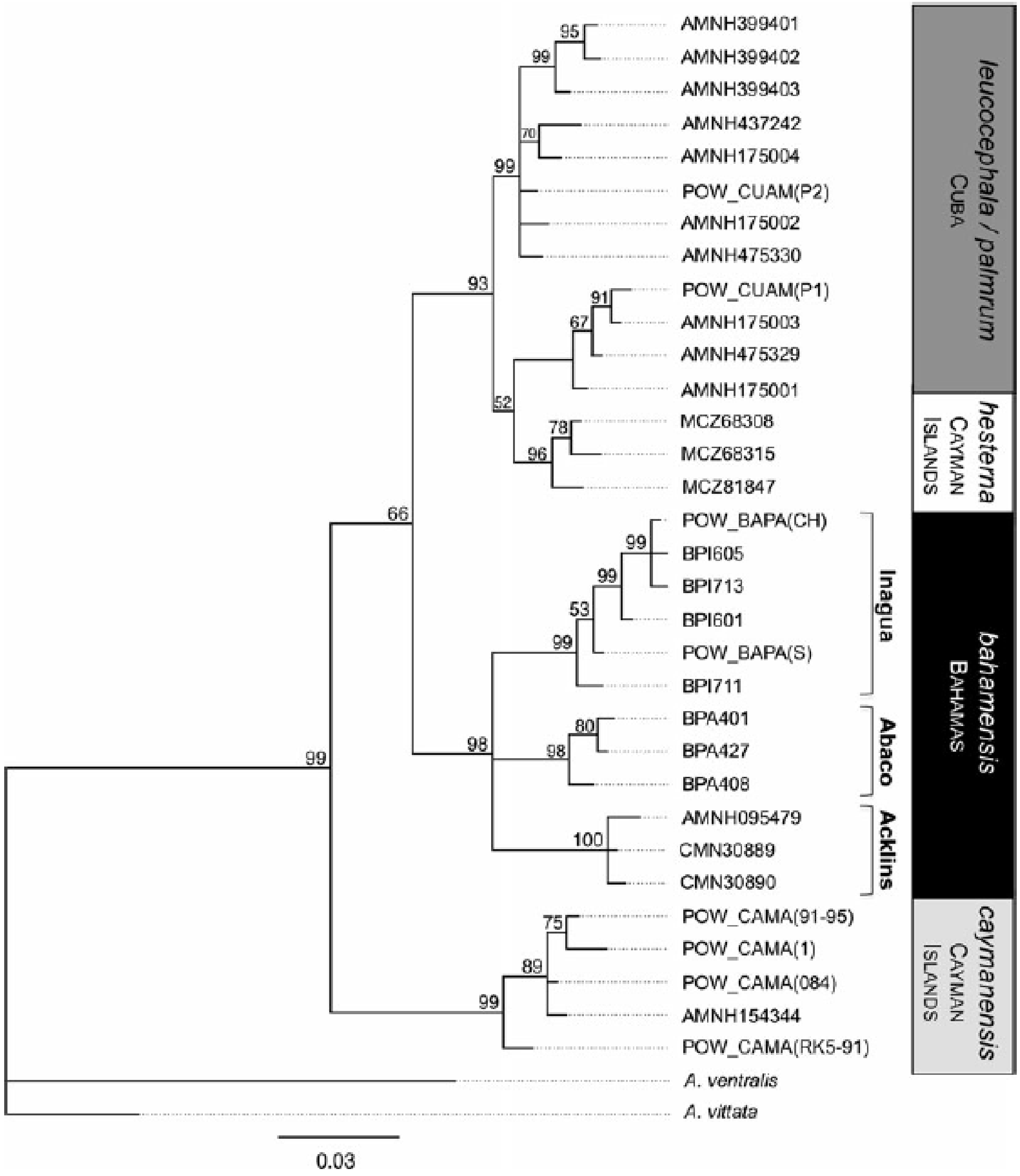


Figure 2. Bayesian haplotype tree based on mtDNA sequences (Russello et al 2010).



Add Maguari Stork *Ciconia maguari* to the main list

Background:

Species is not yet recorded in the AOU North America Checklist area.

New information:

The Scientific Committee of the Association of Ornithology of Costa Rica (CC-AOCR) received a report and photographs proposing to include the species in the Official List of the Birds of Costa Rica - Update 2013.

> **Report:** September 16, 2013. James Zook observed a single bird in the shrimp ponds next to the Gulf of Nicoya in Chomes, Puntarenas province. The ponds were only half full of water with a wide area of exposed mud around the edges. The bird was standing alone and occasional preening, flying to another pond and joining a large group of *Mycteria americana* (Wood Storks) and moving around more (foraging? – never saw it pick at anything but apparently searching). Other observers were Victor Leitón, Elizabeth Sánchez, Jason Vega and Karla Morera. Photos were taken by James Zook (MNCR-Z8168), Victor Leitón (MNCR-Z8169, Z8170) and Karla Morera (MNCR-Z8171, Z8172, Z8173). Below is MNCR-Z8171:

CC-AOCR decision: The proposal was accepted by unanimous decision by the Committee and the species was included in the Official List of the Birds of Costa Rica - Update 2013 as Accidental (Obando et al. 2013). All photos were archived and cataloged in the Department of Natural History, National Museum of Costa Rica (MNCR). Contact at MNCR: Armando Ruiz Boyer aruiz@museocostarica.go.cr

Recommendation: Add the species to the main list of the AOU Check-list.

Literature Cited:

Obando-Calderón, Gerardo., J. Chaves-Campos, R. Garrigues, M. Montoya, O. Ramirez y J. Zook. 2013. Lista Oficial de las Aves de Costa Rica – Actualización 2013. Comité Científico, Asociación Ornitológica de Costa Rica. Zeledonia 17-2. San José, Costa Rica. Free access http://avesdecostarica.org/biblioteca/17-2-004-lista.pdf

Submitted by:

On behalf of the CC-AOCR: James Zook – Observer and CC-AOCR member; Gerardo Obando Calderón – Coordinator, Official List of the Birds of Costa Rica, and CC-AOCR member.

Date of Proposal: 11 Dec 2013

Add Lined Seedeater *Sporophila lineola* to the main list

Background:

Species is not yet recorded in the AOU North America Checklist area.

New information:

The Scientific Committee of the Association of Ornithology of Costa Rica (CC-AOCR) received a Form and photographs proposing to include the species in the Official List of the Birds of Costa Rica - Update 2013.

> **Report:** October 5, 2013. Johan Chaves, accompanied by Roy Orozco, Karina Segura and Magaly Mendez, discovered a male in adult plumage perching on trees and foraging continuously throughout the day in a rice field located in the central Pacific region, playa El Rey, Quepos, Puntarenas province (9º22'45.15''N 84º03'32.10" W, elev. 5m). The bird was still on site on Oct. 6-7 and was confirmed by other observers, including James Zook of our Committee. It was sometimes associated with males and females of *S. torqueola* and *S. americana*. The individual showed a typical wild *Sporophila* behavior, arguing against the possibility that it was a caged bird that had escaped. Photos were taken by Roy Orozco (MNCR-Z8176, Z8177, Z8178) and Johan Chaves (MNCR-Z8179, Z8180, Z8181). Below is MNCR-Z8181:

CC-AOCR decision: The proposal was accepted by unanimous decision by the Committee and the species was included in the Official List of the Birds of Costa Rica - Update 2013 as Accidental (Obando et al. 2013). All photos were archived and cataloged in the Department of Natural History, National Museum of Costa Rica (MNCR). Contact at MNCR: Armando Ruiz Boyer aruiz@museocostarica.go.cr

Recommendation: Add the species to the main list of the AOU Check-list.

Literature cited

Obando-Calderón, Gerardo., J. Chaves-Campos, R. Garrigues, M. Montoya, O. Ramirez y J. Zook. 2013. Lista Oficial de las Aves de Costa Rica – Actualización 2013.

Comité Científico, Asociación Ornitológica de Costa Rica. Zeledonia 17-2. San José, Costa Rica. Free access http://avesdecostarica.org/biblioteca/17-2-004-lista.pdf

Submitted by:

On behalf of the CC-AOCR: Gerardo Obando Calderón – Coordinator, Official List of the Birds of Costa Rica.

Date of Proposal: 11 Dec 2013

Transfer Azure Gallinule *Porphyrio flavirostris* from the main list to the appendix

Background:

An Azure Gallinule (*Porphyrio flavirostris*) was found on Long Island, New York on 14 December 1986. The record was accepted by the American Birding Association (ABA) and the American Ornithological Union (AOU) circa 1988-1989. The ABA removed the record in 1999, when they determined there was enough evidence to conclude that it was an escaped captive bird. See Literature Cited for complete information.

New Information:

In recent years, the ABA and the AOU have changed their philosophy, agreeing to work together to prevent conflicts with each other's checklists. The Azure Gallinule record is still an anomaly. The ABA removed the record from their checklist; however, it is still retained by the AOU.

In the AOU Philosophy, there is reference to taking a conservative approach to changes. For a first record to the checklist, using the conservative philosophy, there should be irrefutable evidence of the validity of the record. This record does not meet the criteria. Some people were told it was an escaped bird, but the record was still maintained. Whether true or not, it is enough to remove the record and perhaps resubmit it at a later date if a second and validated Azure Gallinule sighting is ever documented in the AOU area.

As of now, no Azure Gallinules have ever been found outside of South America and only five have ever been found in extralimital locations within South America. The conservative approach should have been that there has been no evidence of migration or vagrancy within 2500 miles of New York. Until there are reports from Central America or southern North America, the assumption should be that it did not arrive naturally, particularly in light of the fact that there was a belief that the bird was an escapee. The belief was strong enough for the ABA to remove it from its checklist.

Recommendation: Transfer Azure Gallinule from the main list to the Appendix.

Literature Cited:

http://www.aba.org/checklist/ccr1988.pdf
https://www.aba.org/checklist/ccr1998.pdf
http://www.aba.org/birding/v39n4p22.pdf

Submitted by: Alex Borodayko (interested birder)

Date of proposal: 6 Feb 2014

Transfer Yellow-winged Cacique *Cacicus melanicterus* to *Cassiculus*

Background:

This taxon occurs in northwestern Mexico from Sonora south along the Pacific slope to Chiapas, extending inland along the Balsas drainage to southwestern Mexico, southern Guatemala and El Salvador. It was first described as follows: *Icterus melanicterus* Bonaparte, 1825, Journal of the Academy of Natural Sciences of Philadelphia, 4 (May), p. 385. (Mexico.)

It was given a different name in 1827: *Cassiculus coronatus* Swainson, 1827, The Philosophical Magazine or Annals of Chemistry, Mathematics, Astronomy, Natural History and General Science, new series,1, p. 436 (May). (Temasaltipec, Mexico).

In the same publication, Swainson established *Cassiculus* as a generic name: *Cassiculus* Swainson,1827, The Philosophical Magazine or Annals of Chemistry, Mathematics, Astronomy, Natural History and General Science, new series, 1, p. 436 (May). Type, by original designation, *Cassiculus coronatus* Swainson, 1827 = *Icterus melanicterus* Bonaparte, 1825.

A third name was given to the taxon: *Icterus diadematus* Temminck, 1829, Nouveau recueil de planches coloriées d'oiseaux, livr. 81 October), pl. 483. (Mexico.)

From Bonaparte 1850 to Griscom 1934, the species was almost universally cited as *Cassiculus melanicterus*. The one exception was Cassin 1867, who cited the name as *Cassicus (sic) melanicterus*. Hellmayr (1937:46) continued the use of *Cassiculus melanicterus*, but when we arrive at Blake (1968:148) we find it as *Cacicus melanicterus*. This was followed in the first edition of Howard & Moore (1980: 589), the second edition (1994:489), and Dickinson’s third edition (2003:700).

New Information:

With the publication of Fraga (2011: 751), one finds a return to *Cassiculus melanicterus*. In a note on the species, he says: “Often placed in the genus *Cacicus*, but preliminary mitochondrial DNA data suggest an ancestral position within the cacique-oropendola clade. Is a rather distinctive species, geographically isolated from other caciques, with habitat preferences different from those of the latter, and with nest-building closer to oropendolas. For all these reasons, placement in its own monotypic genus seems appropriate.”

Powell et al. (2014) produced a comprehensive and authoritative study of virtually all species in the family Icteridae. Their study offers new insights into the phylogeny of all four subfamilies: Sturnellinae (meadowlarks), Cacicinae (caciques and oropendolas), Icterinae (orioles), and Agelaiinae (blackbirds, cowbirds, and grackles).

To quote from their abstract: “Using mitochondrial gene sequences from all 108 currently recognized species and six additional distinct lineages, together with strategic sampling of four nuclear loci and whole mitochondrial genomes, we were able to resolve most relationships with high confidence. Our phylogeny is consistent with the strongly-supported results of past studies, but it also contains many novel inferences of relationship, including unexpected placement of some newly-sampled taxa, resolution of relationships among major clades within Icteridae, and resolution of genus-level relationships within the largest of those clades, the grackles and allies. We suggest taxonomic revisions based on our results, including restoration of *Cacicus melanicterus* to the monotypic *Cassiculus*, merging the monotypic *Ocyalus* and *Clypicterus* into *Cacicus*, restoration of *Dives atroviolaceus* to the monotypic *Ptiloxena*, and naming *Curaeus forbesi* to a new genus, *Anumara*. Our hypothesis of blackbird phylogeny provides a foundation for ongoing and future evolutionary analyses of the group.”

The relevant part of Figure 4 from Powell et.al. (2014: 106) is reproduced below. From this, it is clear that *melanicterus* is sister to the clade consisting of the remaining caciques (*Cacicus* spp. plus *Ocyalus latirostris* and *Clypicterus oseryi*) + oropendolas (*Psarocolius* spp.).

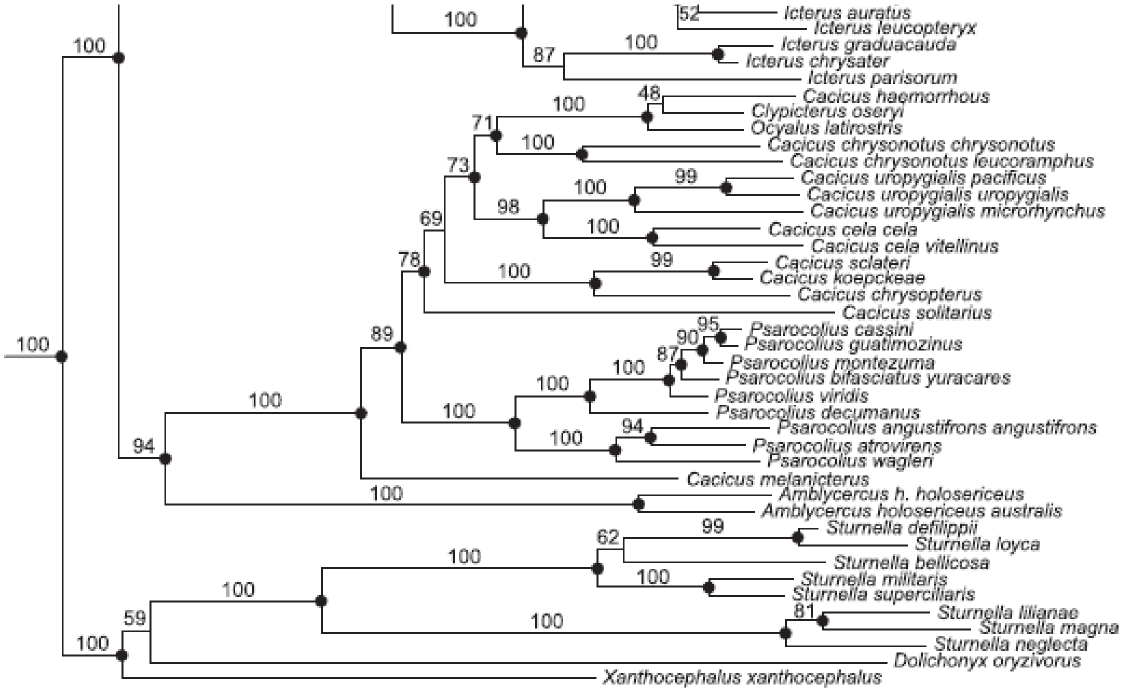


Fig. 4. Phylogeny of the New World blackbirds (Icteridae) inferred from mitochondrial and nuclear DNA sequences of 118 taxa (outgroups not shown). The topology shown here is the single best tree (−ln*L* = 127652.47) found under maximum likelihood (ML). Nonparametric bootstrap percentages from ML analysis appear immediately above or below branches. Filled circles indicate nodes with estimated posterior probabilities of ⩾0.95 in Bayesian analyses of the same concatenated dataset.

Recommendation:

Clearly the genetic evidence justifies absolutely the reallocation of *melanicterus* to *Cassiculus*. In the linear sequence, it should be placed after *Amblycercus*, and before all other oropendolas and caciques.

Literature Cited:

Blake, E. R. (1968) Family Icteridae, American Orioles and Blackbirds. In Paynter (ed.), Checklist of Birds of the World, vol. 14, pp. 128-241. Museum of Comparative Zoology, Cambridge, Mass.

Dickinson, E. (ed.) (2003) The Howard and Moore Complete Checklist of the Birds of the World, 3rd Edition, London: Christopher Helm.

Fraga R. M. (2011) Family Icteridae, pp. 684-907, in del Hoyo J., Elliott, A. & Christie, D. (eds). Handbook of the Birds of the World, vol. 16: Tanagers to New World Blackbirds, Lynx Edicions, Barcelona.

Hellmayr, C. E. (1937) Catalogue of Birds of the Americas and Adjacent Islands, Part X, Icteridae. Field Museum of Natural History, Zoological Series, Volume XIII.

Howard, R, & Moore, A. (1980). A Complete Checklist of the Birds of the World, Oxford, Oxford U.P.

Howard, R, & Moore, A. (1980). A Complete Checklist of the Birds of the World, 2nd edn, London, Academic Press.

Powell, A. F.L.A., Barker, F. K., Lanyon, S. M., Burns, K. J., Klicka, J., and Lovette, I. J. (2014) A comprehensive species-level molecular phylogeny of the New World blackbirds (Icteridae). *Molecular Phylogenetics and Evolution* 71: 94-112

Submitted by: Dr John Penhallurick

Date of proposal: 21 Feb 2014

Split *Gymnopithys leucaspis* into two species

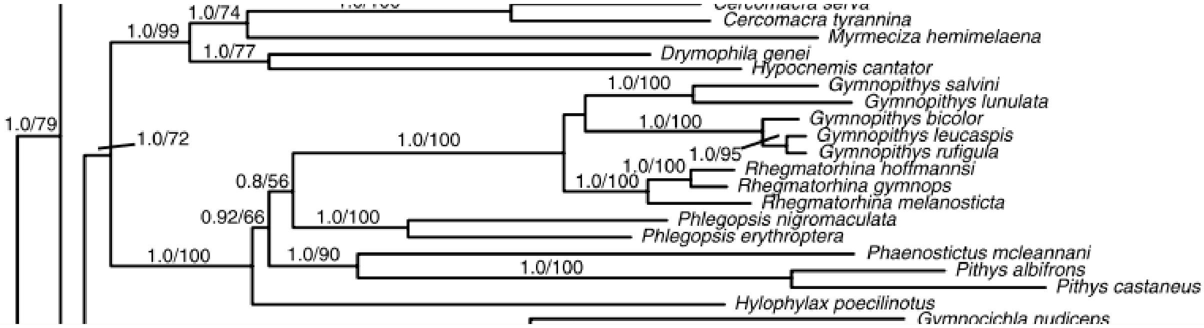
This proposal, if passed, would split *Gymnopithys leucaspis* into two species, trans-Andean *G. bicolor* and cis-Andean *G. leucaspis*. The name of the species in our area would become *Gymnopithys bicolor*, and the Distribution and Notes in the account for this species would also change.

Background:

Gymnopithys bicolor is a humid lowland antbird distributed both east and west of the Andes. Nine subspecies are currently recognized: five in Central America and western Colombia/Ecuador (the *bicolor* group, hereafter *bicolor*) and four in the northwest Amazon basin (the *leucaspis* group, hereafter *leucaspis*). The status quo classification followed by SACC (tagged as “proposal badly needed”) lumped *bicolor* and *leucaspis*, following the rationale outlined by Zimmer (1937a). However, various authors have followed the alternate treatment of considering *bicolor* and *leucaspis* as separate species (Willis 1967, Hilty & Brown 1986, Sibley & Monroe 1990). There is now sufficient data describing patterns of genetic, vocal, and plumage variation within this complex for SACC to vote on these alternatives. This proposal has now been passed by SACC.

New Information:

Genetic data: Hackett (1993) found significant (~5%) allozyme divergence between trans-Andean *bicolor* and Amazonian *leucaspis*, but refrained from making a taxonomic recommendation and suggested analyzing these populations with more sensitive molecular markers. More recently, Brumfield et. al (2007) included samples of both *leucaspis* and *bicolor* (as well as samples of the other three recognized *Gymnopithys* species) in a broader phylogeny of ant-following antbirds. This study used both mitochondrial and nuclear markers, and found strong support for a sister relationship between *leucaspis* and *G. rufigula*, a congeneric species with an allopatric Amazonian distribution (*G. rufigula* is a Guianan Shield species, whereas *leucaspis* is present in northwest Amazonia), with trans-Andean *bicolor* sister to the combined *leucaspis* + *rufigula* group (see snapshot of their tree below).



Snapshot of the relevant portion of the maximum-likelihood tree presented by Brumfield et al (2007). Bayesian (before slash) and bootstrap (after slash) support values are given.

Vocal data: Differences in antbird vocalizations have been used to justify splitting of antbird species. However, there is no published analysis of vocalizations within *G. leucaspis* (as currently defined, including *bicolor*). The species account in *Handbook of Birds of the World* (Zimmer and Isler 2003) provides a detailed verbal description of *leucaspis* and *bicolor* loudsongs, stating that *bicolor* song "starts with long, upslurred whistles that shorten rapidly and gain in intensity, followed by shorter notes that drop in pitch and intensity before becoming harsh" while that of *leucaspis* "begins with upslurred whistles at an even pitch that shorten into rather abrupt notes dropping in frequency and intensity, then lengthen and increase again in intensity, finally decreasing in intensity and becoming harsh." Additionally, the loudsong of *bicolor* is reported to be ten notes, compared to 20 for *leucaspis*, although the HBW account (Zimmer and Isler 2003) also notes that loudsongs are "quite variable in length".

Plumage data: For antbirds, plumage is rather divergent within *Gymnopithys*: *G. rufigula* is entirely brown with patches of cinnamon, and *G. salvini* and *lunulata* are sexually dichromatic, with gray males and brown females. In contrast, plumage variation in *bicolor* and *leucaspis* is relatively slight, with subspecific plumage variation in head/side coloration and overall darkness. Nevertheless, there appear to be diagnostic plumage differences between these two groups: the *bicolor* group has two plumage traits – a black subocular area and blue-gray plumage behind the eye – that the *leucaspis* group lacks.

Recommendation:

There are two possible treatments at this time.

(1) Maintain the status quo, leaving all taxa within both *bicolor* and *leucaspis* groups in a broadly-defined *G. leucaspis*.
(2) Split *G. bicolor* from *G. leucaspis*.

I suggest that current evidence supports splitting *bicolor* from *leucaspis*. The strongest data supporting this split is Brumfield et al.'s (2007) finding that the Amazonian *leucaspis* is sister to the Amazonian *G. rufigula* and not trans-Andean *bicolor*. This relationship was strongly recovered in both mitochondrial and nuclear markers. As the species status of *G. rufigula* has not been questioned, these genetic relationships strongly argue *bicolor* and *leucaspis* should be treated as different species.

Vocal and plumage data supporting this split are less conclusive. Loudsongs may differ (Zimmer and Isler 2003), but have not yet been subjected to quantitative analysis or behavioral playback experiments. Plumage is likewise similar between *bicolor* and *leucaspis*, although there are diagnostic differences in multiple plumage patches, providing weak support for the proposed split.

In sum, genetic evidence of divergence and especially the sister relationship of *leucaspis* with *G. rufigula* supports splitting *bicolor* from *leucaspis*. This split is additionally weakly supported by vocal and plumage divergence. This proposed treatment is also supported by biogeography, as cis-Andean and trans-Andean populations of widely-distributed lowland forest taxa are commonly found to be sufficiently divergent to merit species status.

Vernacular Names:

If passed, this proposal would require new English names for *bicolor* and *leucaspis*. Ridgely and Greenfield (2001) suggested “White-cheeked Antbird” for *leucaspis* and retaining “*Bicolor*ed Antbird” for *bicolor*. This treatment emphasizes the most prominent plumage difference between the two taxa – the white “cheek” of *leucaspis* – and therefore seems like an appropriate suggestion for English names.

Literature Cited:

Brumfield, R. T., J. *G.* Tello, Z. Cheviron, M. D. Carling, N. Crochet, and K. V. Rosenber*G.* 2007. Phylogenetic conservatism and antiquity of a tropical specialization: army-ant-following in the typical antbirds (Thamnophilidae). Molecular Phylogenetics and Evolution 45:1-13.

Hackett, S. J. 1993. Phylogenetic and biogeographic relationships in the Neotropical genus Gymnopithys (Formicariidae). The Wilson Bulletin 105:301-315.

Zimmer, K. and M. Isler. 2003. Family Thamnophilidae (typical antbirds). Pages 448-681 *in* J. del Hoyo, A. Elliot, and D. A. Christie, editors. Handbook of the Birds of the World. Vol. 8. Broadbills to Tapaculos. Lynx Edicions, Barcelona.

Other papers are cited in the SACC bibliography online.

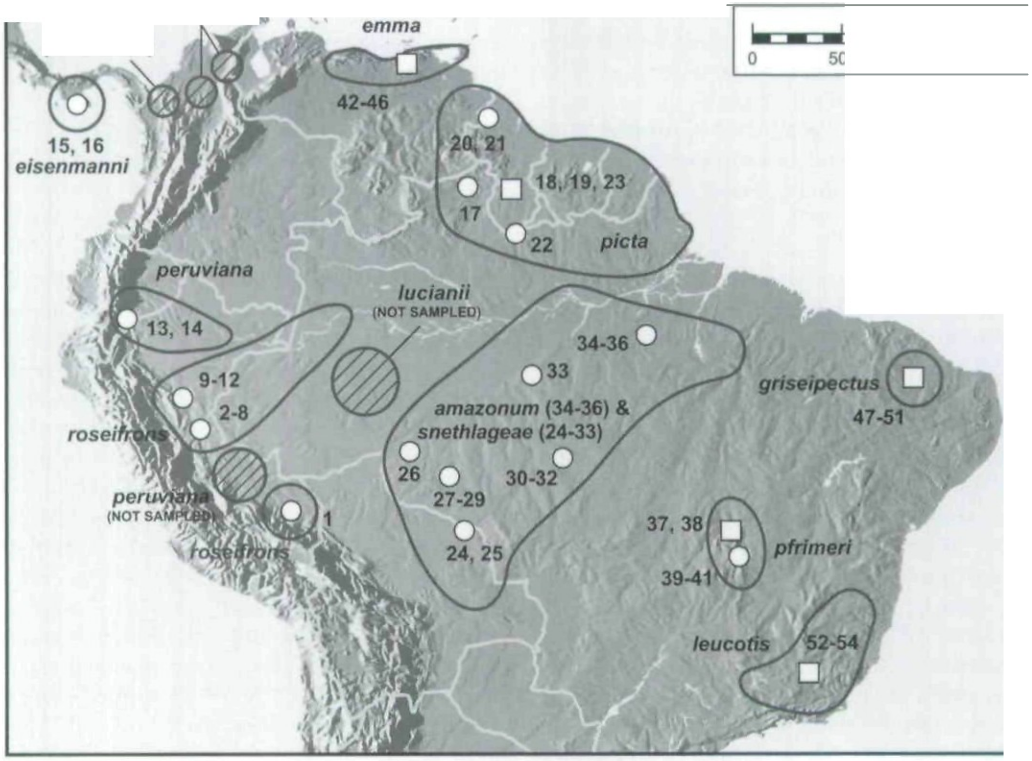
Submitted by: Ben Freeman, Cornell University

Date of proposal: 18 Sep 2013

Split *Pyrrhura roseifrons, lucianii,* and *amazonum* from *P. picta*

Background:

The highly polytypic *Pyrrhura picta* was found to be non-monophyletic with respect to *P. leucotis*, on the basis of an mtDNA tree (Ribas et al. 2006) and morphological analyses (Joseph 2002 and others). They were therefore recommended for treatment as several species in SACC proposals #306 http://www.museum.lsu.edu/~Remsen/SACCprop306.html and #403 http://www.museum.lsu.edu/~Remsen/SACCprop403.html). There were many possible options among South American taxa and insufficient information was available to judge the most appropriate status of some of them. Given that the options are succinctly described in the SACC proposals, there seems no reason to restate everything. In the treatment that was adopted with near-unanimity (after one reversal, SACC #403), the former two species *picta* (*s.l.*) and *leucotis* are now considered to be six species. Of these, only *picta* (*s.s.*), the species that includes Panamanian *eisenmanni*, occurs in the NACC region.



Although in Ribas et al.'s (2006) mtDNA tree (Fig. 2, below), *eisenmanni* is fairly deeply diverged from other *picta* (Guianan Shield) plus *emma* (the NC Venezuelan form), the geographically intervening taxa *subandina* and *caeruleiceps*, plus *pantchenkoi* (NE Colombia and NW Venezuela, recognized in IOC) were not included in the analysis. SACC voted to keep *eisenmanni* (and *emma*, *subandina*, and *caeruleiceps*) in *picta*.

(Note that *emma* had previously been considered part of *leucotis*.) I am not aware of subsequent studies that would give us reason to reconsider the possibility that was raised (and rejected by SACC) of splitting *eisenmanni* with or without *subandina* and/or *caeruleiceps* from *picta* at this time.

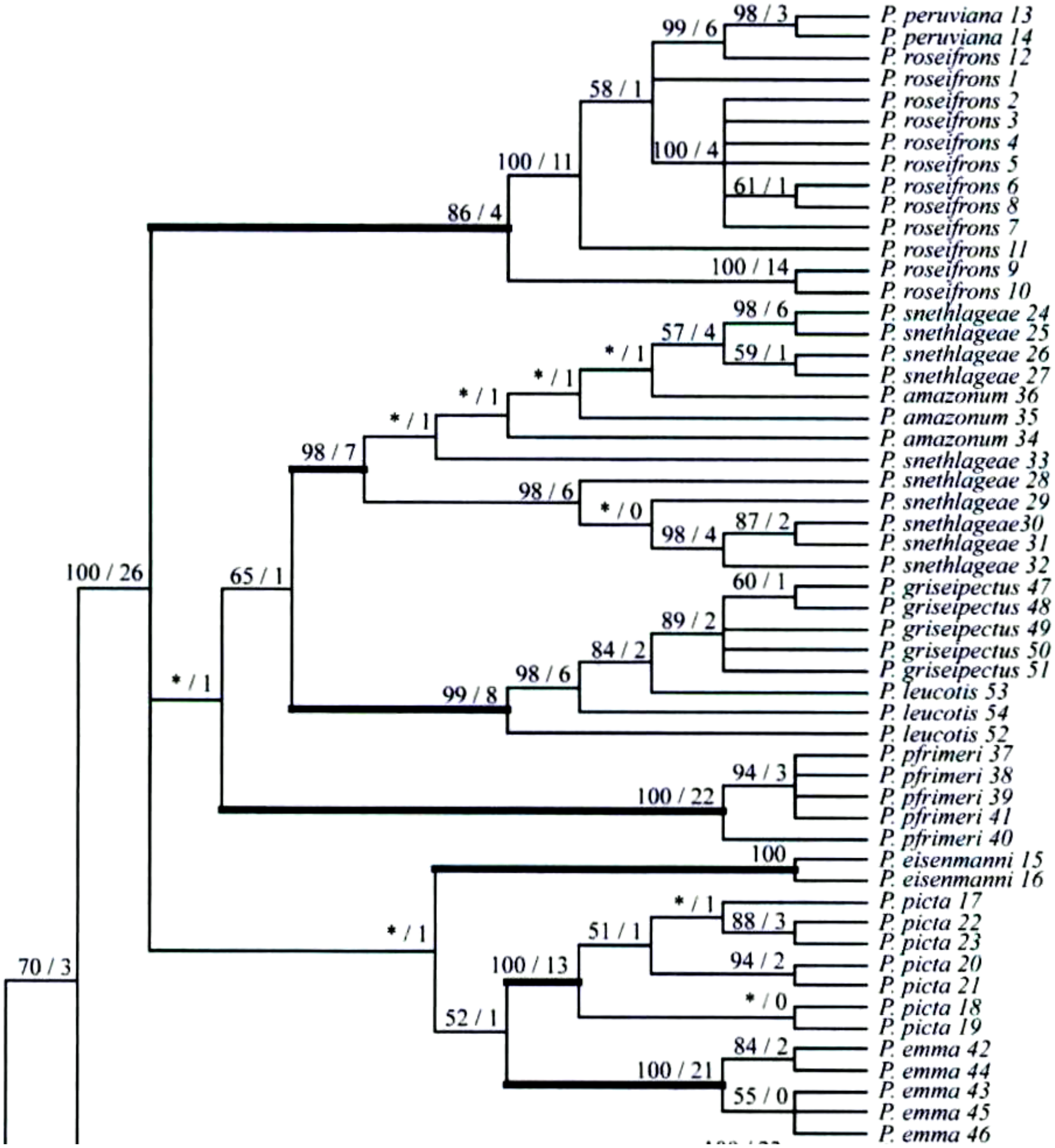


Fig. 2 from Ribas et al. (2006).

New information:

None subsequent to Ribas et al. (2006) and the SACC proposals 306 and 403, to my knowledge.

Recommendation: I recommend that we follow SACC's (306, with the modification of 403) lead on this and vote YES to treat *griseipectus, leucotis, amazonum, roseifrons*, and *lucianii* as separate species. SACC's recommended treatment is now widely followed. If we accept (as SACC did) that *griseipectus, leucotis, amazonum, roseifrons,* and *lucianii* should each be considered separate species from *picta*, I have suggested modifications to the Distribution and Notes sections in the Check-list.

> **Distribution**.—*Resident* in western Panama (Azuero Peninsula); and patchily in northern South America from northern Colombia through the Guianan Shield.
>
> **Notes**.—The subspecies *eisenmanni* in Panama is sister to a clade containing Guianan Shield *picta* and NC Venezuelan *emma* (but not *P. leucotis*) in an mt-DNA phylogeny (Ribas et al. 2006), however, intervening N South American populations were not sampled. *Pyrrhula picta* (*s.l.*) has been split into *P. amazonum*, *P. roseifrons*, and *P. lucianii* (Joseph 2002, Ribas et al. 2006).

Literature Cited:

Joseph, L. 2002. Geographical variation, taxonomy and distribution of some Amazonian *Pyrrhura* parakeets. Ornitología Neotropical 13:337-363.

Ribas, C. C., L. Joseph, and C. R. Miyaki. 2006. Molecular systematics and patterns of diversification in *Pyrrhura* (Psittacidae) with special reference to the *picta-leucotis* complex. Auk 123:660-680.

Submitted by: Pam Rasmussen, Michigan State University

Date of proposal: 22 February 2014

Revise the linear sequence of species in the genus *Saltator*

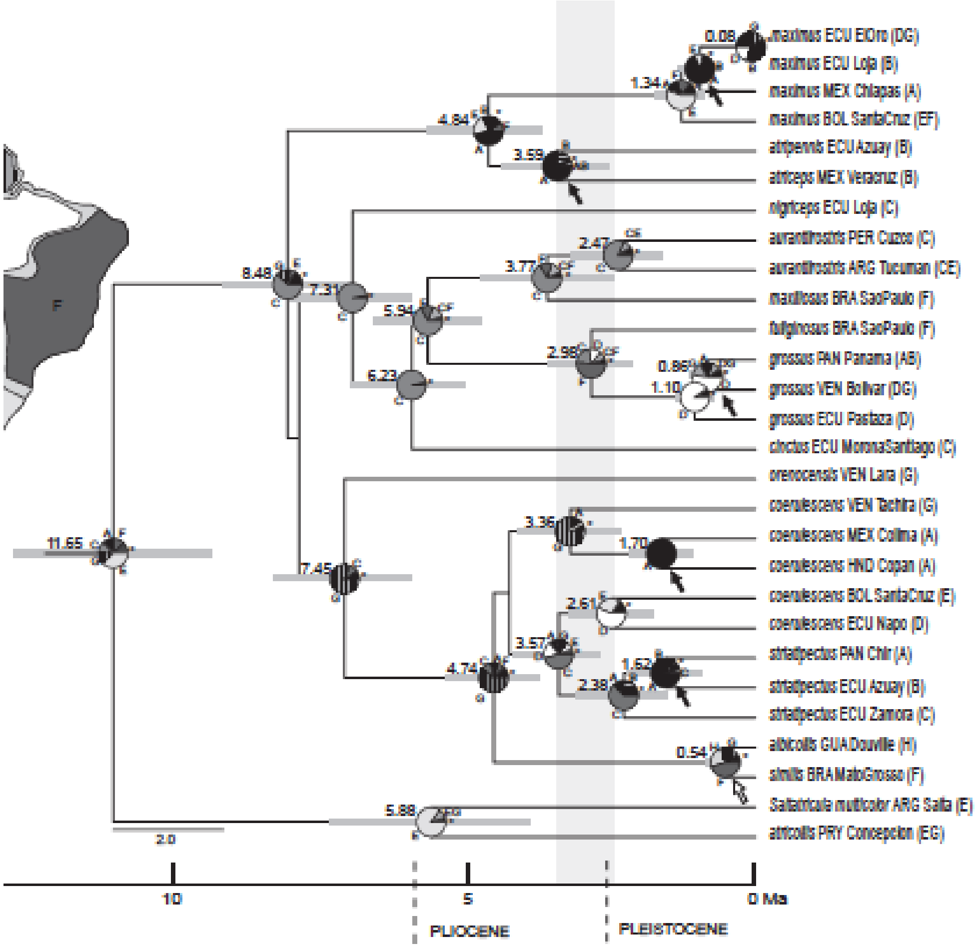
This proposal would revise the linear sequence of species. It is modified from a proposal that passed SACC unanimously.

Background:

Our current linear sequence is based largely on historical momentum and perceptions of relationships by various authors, including the study of phenotypic characters by Hellack and Schnell (1977). *Saltator grossus* was formerly separated in the genus *Pitylus* and is thus placed at the end of our sequence.

New Information:

Chaves et al. (2013) produced a phylogeny of all species recognized in the genus using mtDNA (ND2, cyt-b; missing ND2 for *S. maxillosus*). A poor screen shot of their results is pasted in below, although the major tree is too large to have any resolution here; let me know if you need a pdf of the original.



These results largely support the traditional view of relationships with the following two exceptions: (a) (extralimital) *S. nigriceps* is not the sister to (extralimital) *S. aurantiirostris* + *S. maxillosus* but rather is the sister to those two plus *S. grossus* + *S. fuliginosus*; (b); *S. striatipectus* is part of the *S. coerulescens* group, as originally treated by Paynter and others; (c) and (extralimital) *Saltatricula multicolor* is the sister to (extralimital) *Saltator atricollis*. (They also found that inclusion of Middle American *grandis* in *S. coerulescens* makes that a paraphyletic species. I worry that this might be a gene tree/species tree problem, but Hilty [2003] already split *grandis* based on voice; regardless, this would require a separate proposal.)

To incorporate these results into our classification requires a change in the linear sequence of species.

Our current linear sequence is as follows:

Saltator albicollis Lesser Antillean Saltator
Saltator striatipectus Streaked Saltator
Saltator coerulescens Grayish Saltator
Saltator maximus Buff-throated Saltator
Saltator atriceps Black-headed Saltator
Saltator grossus Slate-colored Grosbeak

As long as the sequence has to be modified to show the proper relationships of *S. grossus*, I think we should overhaul the sequence to reflect the tree produced by Chaves et al. using our conventions (least-diverse branch first, and so on; for sister species or allospecies in superspecies, northwestern-most listed first). The following is the proposed sequence – please check for better alternatives:

Saltator atriceps Black-headed Saltator
Saltator maximus Buff-throated Saltator
Saltator grossus Slate-colored Grosbeak
Saltator albicollis Lesser Antillean Saltator
Saltator coerulescens Grayish Saltator
Saltator striatipectus Streaked Saltator

Recommendation:

The proposed new sequence reflects the findings of Chaves et al. (2013) and, barring additional tweaks, removes previous misconceptions on relationships in the genus.

Although I'm usually opposed to changing traditional English names, I think it's time to consider changing Slate-colored Grosbeak to Slate-colored Saltator. Although "grosbeak" carries no phylogenetic significance, "saltator" does, and so this minor change would restrict the English name to that genus and prevent confusion on the species' true relationships. I think I will propose this to SACC, which has not only this species but also the other ex-*Pitylus*, *S. fuliginosus*.

Literature Cited:

Chaves, J. C., J. R. Hidalgo, and J. Klicka. 2013. Biogeography and evolutionary history of the Neotropical genus *Saltator* (Aves: Thraupini). Journal of Biogeography 40: 2180–2190.
Hellack, J. J., and G. D. Schnell. 1977. Phenetic analysis of the subfamily Cardinalinae using external and skeletal characteristics. Wilson Bulletin 89: 130-148.
Hilty, S. L. 2003. Birds of Venezuela. Princeton University Press, Princeton, New Jersey.

Submitted by: Van Remsen, Louisiana State University

Date of proposal: Feb 2014

Revise the linear sequence of species in the genus *Dendrocincla*

This would make a very minor change in the species sequence in *Dendrocincla* to reflect recent research and to follow sequencing conventions. It is a modification of a slightly expanded proposal to SACC, which passed unanimously.

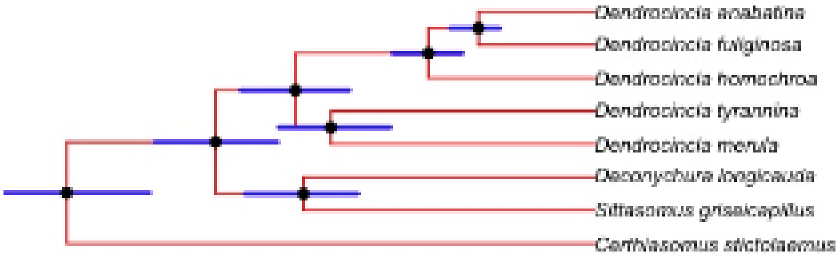
Background:

Our current sequence, a traditional one, is as follows:

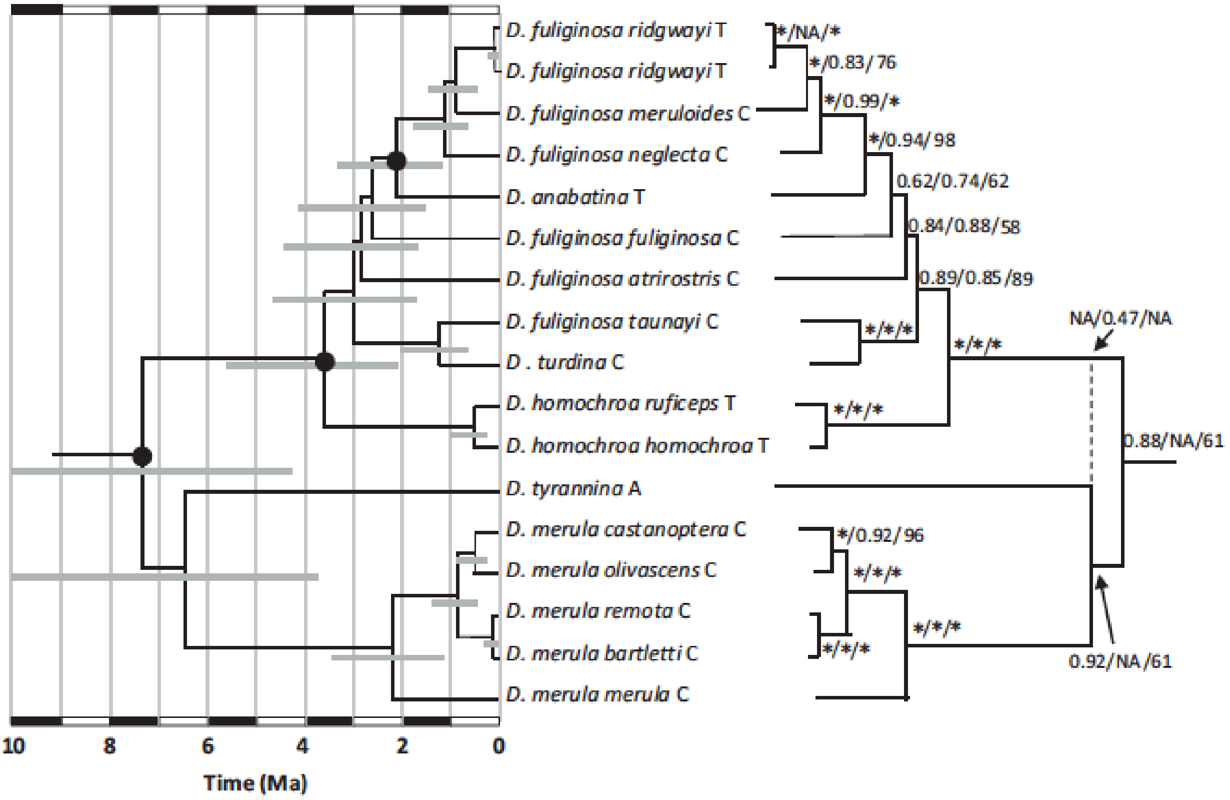
Dendrocincla fuliginosa Plain-brown Woodcreeper
Dendrocincla anabatina Tawny-winged Woodcreeper
Dendrocincla homochroa Ruddy Woodcreeper

New information:

Derryberry et al. (2011) sampled several mitochondrial and nuclear loci and 285 of 293 species in the Furnariidae to produce a comprehensive phylogeny. The portion of the tree that contains *Dendrocincla* is pasted in below:



Weir & Price (2011) independently studied relationships in the genus with multiple mitochondrial and nuclear genes, and many additional subspecies taxa. They produced the following tree, which was essentially congruent with that of Derryberry et al. (2011) except that their sampling of subspecies currently in *D. fuliginosa* was much greater, revealing potential paraphyly with *D. anabatina*:



The monophyly of the genus was confirmed, but relationships within the genus differed from traditional views. That extralimital *D. merula* and extralimital *D. tyrannina* were sister species was especially surprising to me, although seemingly anomalous biogeographical results are not new in this family – e.g., the sister relationship of *Drymornis* of the Chaco and *Drymotoxeres* of the humid N. Andes. Using the convention of least-diverse branch first, and NW to SE arrangement of sister taxa or allospecies in a superspecies, a revised sequence would be:

Dendrocincla homochroa Ruddy Woodcreeper
Dendrocincla anabatina Tawny-winged Woodcreeper
Dendrocincla fuliginosa Plain-brown Woodcreeper

Assuming the trees of Derryberry et al. (2011) and Weir & Price reflect the true phylogeny, then this is the only linear sequence that mirrors those findings.

Recommendation:

This is a tiny adjustment to accommodate recent findings, and I see no reason not to vote YES. It would also make NACC and SACC sequences the same.

Literature Cited:

Derryberry, E., S. Claramunt, G. Derryberry, R. T. Chesser, J. Cracraft, A. Aleixo, J. Pérez-éman, J. V. Remsen, Jr., and R. T. Brumfield. 2011. Lineage diversification and morphological evolution in a large-scale continental radiation: the Neotropical ovenbirds and woodcreepers (Aves: Furnariidae). Evolution 65: 2973–2986.

Weir, j. T., and m. Price. 2011. Andean uplift promotes lowland speciation through vicariance and dispersal in *Dendrocincla* woodcreepers. Molecular Ecology 21: 4550-4563.

Submitted by: Van Remsen, Louisiana State University

Date of proposal: Feb 2014

2014-B-10 N&MA Classification Committee pp. 350-353

Revise the classification of *Automolus* and relatives

This proposal would transfer *Hyloctistes subulatus* to *Automolus*, *Automolus rubiginosus* to *Clibanornis*, and place *Thripadectes* between these two genera. This is a spinoff of a larger proposal approved unanimously by SACC.

Background:

Our current classification largely follows traditional boundaries.

Hyloctistes subulatus Striped Woodhaunter
Automolus ochrolaemus Buff-throated Foliage-gleaner
Automolus rubiginosus Ruddy Foliage-gleaner
Thripadectes rufobrunneus Streak-breasted Treehunter

New Information:

Derryberry et al. (2011) showed that the limits of the genera *Automolus*, (extralimital) *Clibanornis*, *Hyloctistes*, and (extralimital) *Hylocryptus* were problematic. Specifically, (a) *Hyloctistes* was embedded in *Automolus*, (b) *Automolus rubiginosus* and *A. rufipectus* were not members of *Automolus* but instead closest to *Hylocryptus erythrocephalus*; and (c) *Hylocryptus rectirostris* was sister to *Clibanornis dendrocolaptoides.* Rather than make taxonomic changes within that paper, a subset of the same author group deferred a revision of the group to a subsequent paper; see Claramunt et al. (2013) for all the details, including an expanded tree from Derryberry et al. (2011) in terms of taxon and population sampling (all critical nodes strongly supported) and an important discussion of how to define limits of genera combining morphology and phylogeny.

A summary tree of the results and recommended classification is as follows:

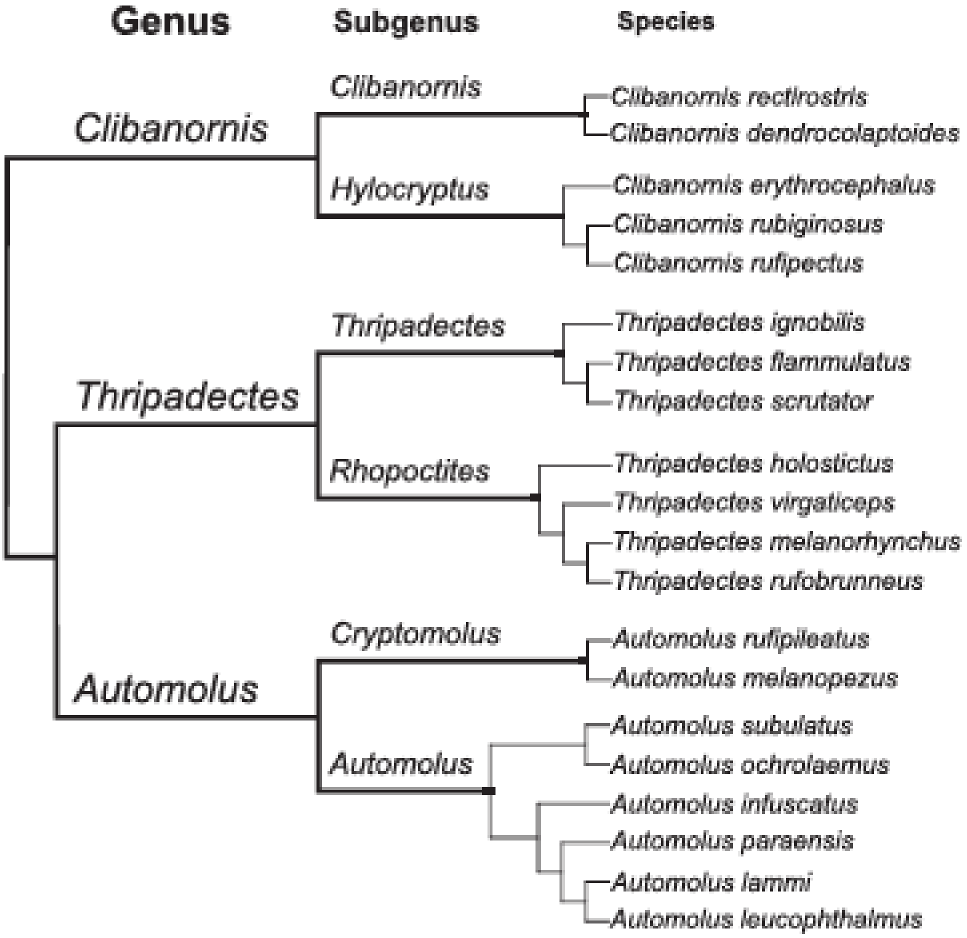


FIGURE 4. Phylogenetic tree with new classification of *Automolus* and allies.

They collapsed 5 genera into 3 (and used the taxonomic category of subgenus to mark additional nodes in the tree). Note also that *Clibanornis* is sister to *Automolus* + *Thripadectes*, which affects our linear sequence. The new classification for species in NACC area, using the standard sequencing conventions, would be:

Clibanornis rubiginosus Ruddy Foliage-gleaner
Thripadectes rufobrunneus Streak-breasted Treehunter
Automolus ochrolaemus Buff-throated Foliage-gleaner
Automolus subulatus Striped Woodhaunter

Recommendation:

The data behind this phylogeny are extensive in terms of loci and populations sampled, and all the important nodes are strongly supported. The analysis of generic boundaries is careful and sensible. In hindsight, the results make good ecological and biogeographic sense, e.g., Atlantic forest region *rectirostris* and *dendrocolaptoides* are sisters, and the more terrestrial foraging behavior of the species in *Clibanornis*. The one result that I initially had a problem with was the sister relationship between *Hyloctistes subulatus* and *Automolus ochrolaemus*. However, when I compared the skins of *H. subulatus* and the most strongly pattern subspecies of *A*. *ochrolaemus*, I was surprised at how similar they were in plumage and morphology.

I recommend a YES.

Literature Cited:

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Submitted by: Van Remsen, Louisiana State University

Date of proposal: Feb 2014

Split Siberian Stonechat *Saxicola maurus* from Common Stonechat *S. torquatus*

Background:

The Common Stonechat *Saxicola torquatus* (*s.l.*) is highly polytypic over most of the Paleotropics (except Australasia) from the British Isles and Africa through East Asia. Although treated as a single species for many years, this has been a contentious issue for decades, and much has been written on the subject of their taxonomy and identification, especially because of the frequent appearance of vagrant "Siberian" Stonechats of the *maurus* group in western Europe. Sibley and Monroe (1990) briefly split *maurus* from *torquatus* (including West European taxa), but then soon thereafter retracted this treatment (Sibley and Monroe 1993).

Although all taxa traditionally included in *torquatus* are allopatric in breeding distribution, as far as is known, in South Asia the very similar marsh specialist White-tailed Stonechat *S. leucurus* occurs sympatrically with *S. torquatus indicus* throughout its much narrower range in the Indus-Ganges-Brahmaputra-Irrawaddy valleys from Pakistan to Myanmar, segregated largely by habitat. Both occur in the same sites, where they choose different microhabitats, and they do not appear to intergrade (Rasmussen and Anderton 2012). The fact that *leucurus* (which looks very like *indicus* except for its tail) is undeniably a good biological species is one very good reason to doubt that all other stonechats (which show a lot of morphological variation; HBW illustrated 8 taxa) are best considered conspecific.

New information:

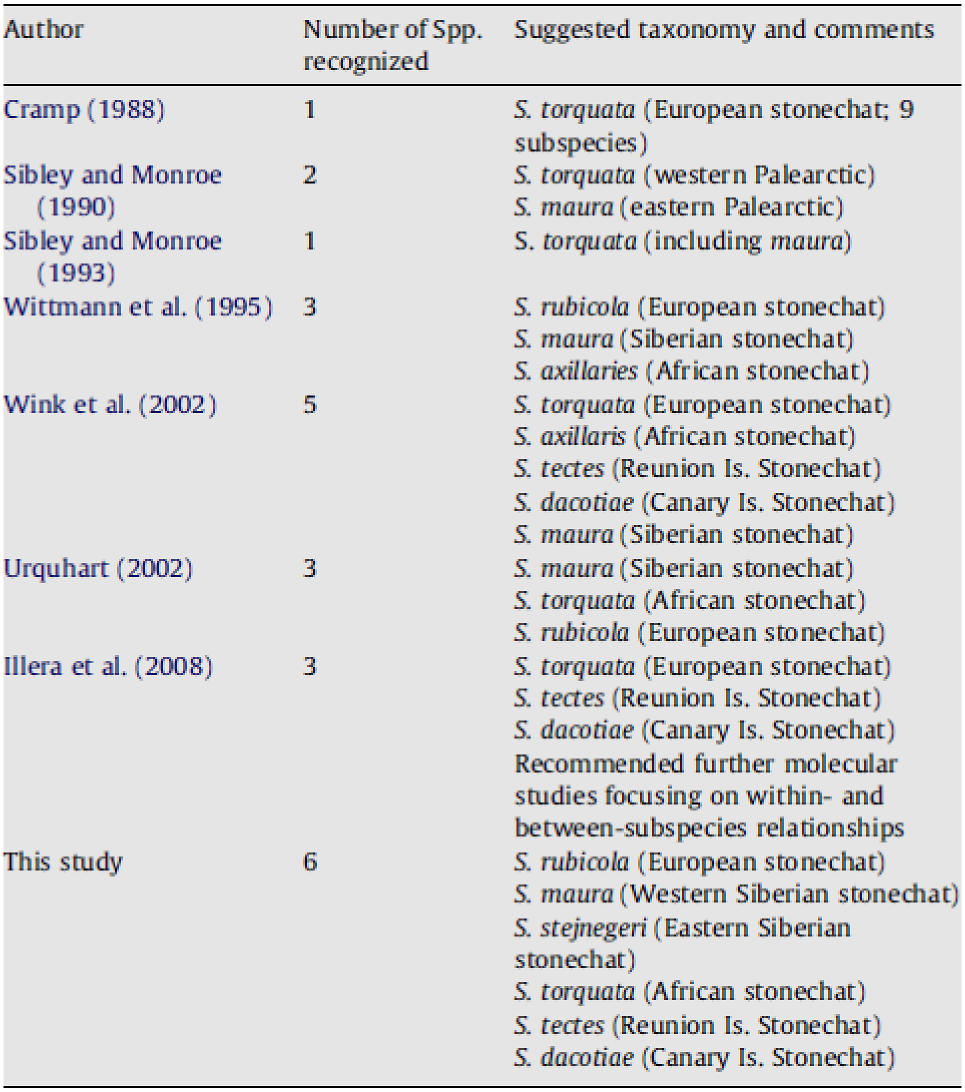
Within the past few years, several mtDNA analyses of the stonechat complex have been published (Illera et al. 2008, Woog et al. 2008, Zink et al. 2009), to add to the less complete earlier ones (Wittmann et al. 1995, Wink et al. 2002a,b). Each of these focuses on a particular section of the huge range of the species complex. For example, Illera et al. (2008) is especially concerned with the Iberian population, while Woog et al. (2008) is focused on the Madagascan, Reunion (Indian Ocean), and African populations. Zink et al. (2009) sequenced several samples from East Asian *stejnegeri* (Parrot, 1908) but none from the South Asian taxa *indicus* (Blyth, 1847) or Sino-Tibetan *przewalskii* (Pleske, 1889); the latter has not yet been included in any study [and a Nepal "*indicus*" specimen (see below for circumstances) in Illera et al. (2008) oddly enough clustered with some Iberian birds, which are far distant from most other Iberian birds].

Illera et al. (2008) obtained 958 bp sequences of cyt-b from 11 of the 12 recognized species of *Saxicola* and 15 of the 45 described subspecies, of which "14 morphologically diverse and/or geographically disjunct populations (nine subspecies) were analysed" within *torquata*. Woog et al. (2008) obtained 915 and 1041 bp sequences of cyt-b and ND2 of nine taxa of *Saxicola*, five of them normally treated within *S. torquata*. Both Illera et al. (2008) and Woog et al. (2008) evidently used mostly blood samples, although exactly how many seems unclear. Zink et al. (2009) used ND2 from 171 specimens of the *S. torquata* complex, 27 from Eurasian and 3 from African sites. I did not find a statement of sequence length in Zink et al. (2009).

The only one of these studies to include the White-tailed Stonechat *S. leucurus* is Illera et al. (2008), and that was a blood sample of a single individual taken by "Bird Conservation Nepal", according to the Acknowledgments. The same source is responsible for the only (blood) sample of putative *indicus* in any of the studies. Given that no indication is provided as to how they were identified, or what sex/age they were came from (relevant because female *leucurus* are not especially distinctive), and that the *leucurus* and *indicus* cluster close together on the tree in Illera et al. (2008), further corroboration using better documented samples is needed. However, what their tree putatively shows is that *leucurus* is very closely related to some taxa of *torquatus* (not surprisingly, given their morphological and vocal similarity).

All of the most recent studies included the insular *S. tectes* and *S. dacotiae*, and it is clear that the former (not surprisingly, based on geography) is sister to the African clade(s), whereas the latter is sister to the Western Palearctic clade (again, not surprising geographically). Although this could be taken to show that *tectes* and *dacotiae* should be lumped within an inclusive *torquatus*, the same cannot be said for the sympatric *leucurus*.

Below is Table 1 from Zink et al. (2009), which summarizes influential recent treatments of *Saxicola torquatus*. Note that *tectes, dacotiae*, and *leucurus* are not included within *torquatus* by any author listed here. This table does not mention Woog et al. (2008), which focuses on Afro-Malagasy taxa, although no explanation is given in Zink et al. (2009) as to why, and the paper is cited therein.



Author	Number of Spp. recognized	Suggested taxonomy and comments
Cramp (1988)	1	*S. torquata* (European stonechat; 9 subspecies)
Sibley and Monroe (1990)	2	*S. torquata* (western Palearctic) *S. maura* (eastern Palearctic)
Sibley and Monroe (1993)	1	S. *torquata* (including *maura*)
Wittmann et al. (1995)	3	*S. rubicola* (European stonechat) *S. maura* (Siberian stonechat) *S. axillaries* (African stonechat)
Wink et al. (2002)	5	*S. torquata* (European stonechat) *S. axillaris* (African stonechat) *S. tectes* (Reunion Is. Stonechat) *S. dacotiae* (Canary Is. Stonechat) *S. maura* (Siberian stonechat)
Urquhart (2002)	3	*S. maura* (Siberian stonechat) *S. torquata* (African stonechat) *S. rubicola* (European stonechat)
Illera et al. (2008)	3	*S. torquata* (European stonechat) *S. tectes* (Reunion Is. Stonechat) *S. dacotiae* (Canary Is. Stonechat) Recommended further molecular studies focusing on within- and between-subspecies relationships
This study	6	*S. rubicola* (European stonechat) *S. maura* (Western Siberian stonechat) *S. stejnegeri* (Eastern Siberian stonechat) *S. torquata* (African stonechat) *S. tectes* (Reunion Is. Stonechat) *S. dacotiae* (Canary Is. Stonechat)

Taken together, these studies (see figs. below) show that *S. torquatus* (*s.l.*) is paraphyletic with respect to the distinctive-appearing taxa long considered to be separate species, the Canary Islands or Fuerteventura Stonechat *S. dacotiae*, the Reunion Stonechat *S. tectes*, and the sympatric White-tailed Stonechat *S. leucurus.* They also confirm the existence of the following distinct clades: the West European *rubicola* group, the mainly Central Asian *maurus* group, the African *torquatus* group, the Malagasy *sibilla* group, and the NE Asian *stejnegeri*, which is especially genetically distinct and sister to all the others (according to Zink et al. 2009, the only study to sample *stejnegeri*). However, this latter finding is difficult to interpret without knowledge of where *przewalskii* fits in.

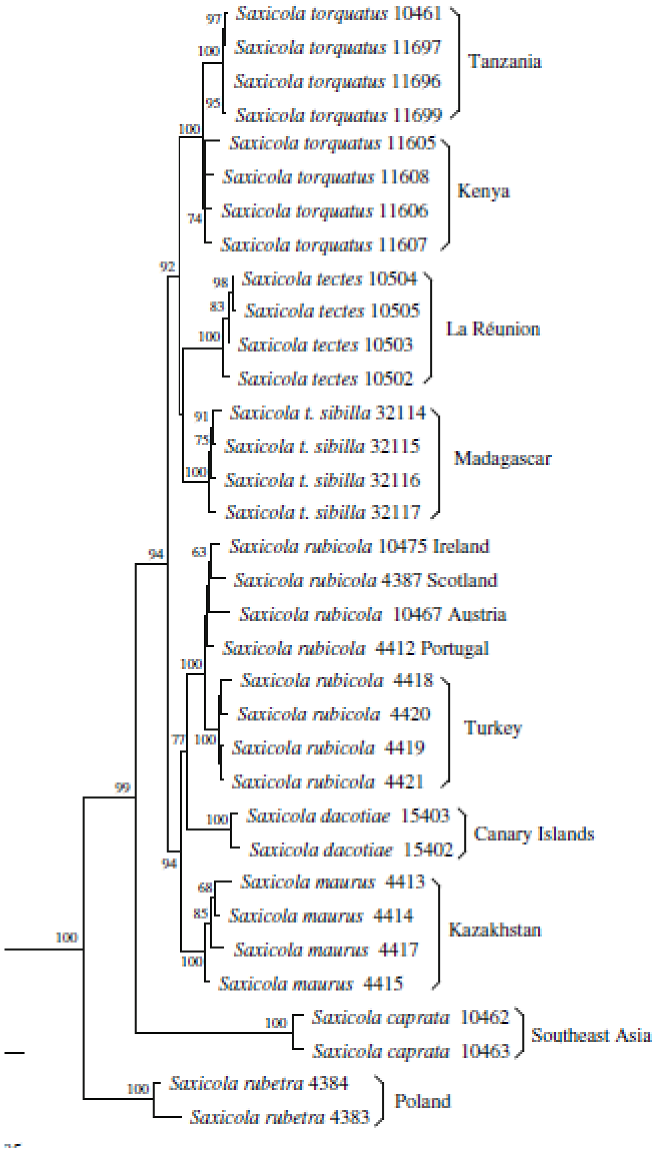


Fig. 2. Woog et al. (2008).

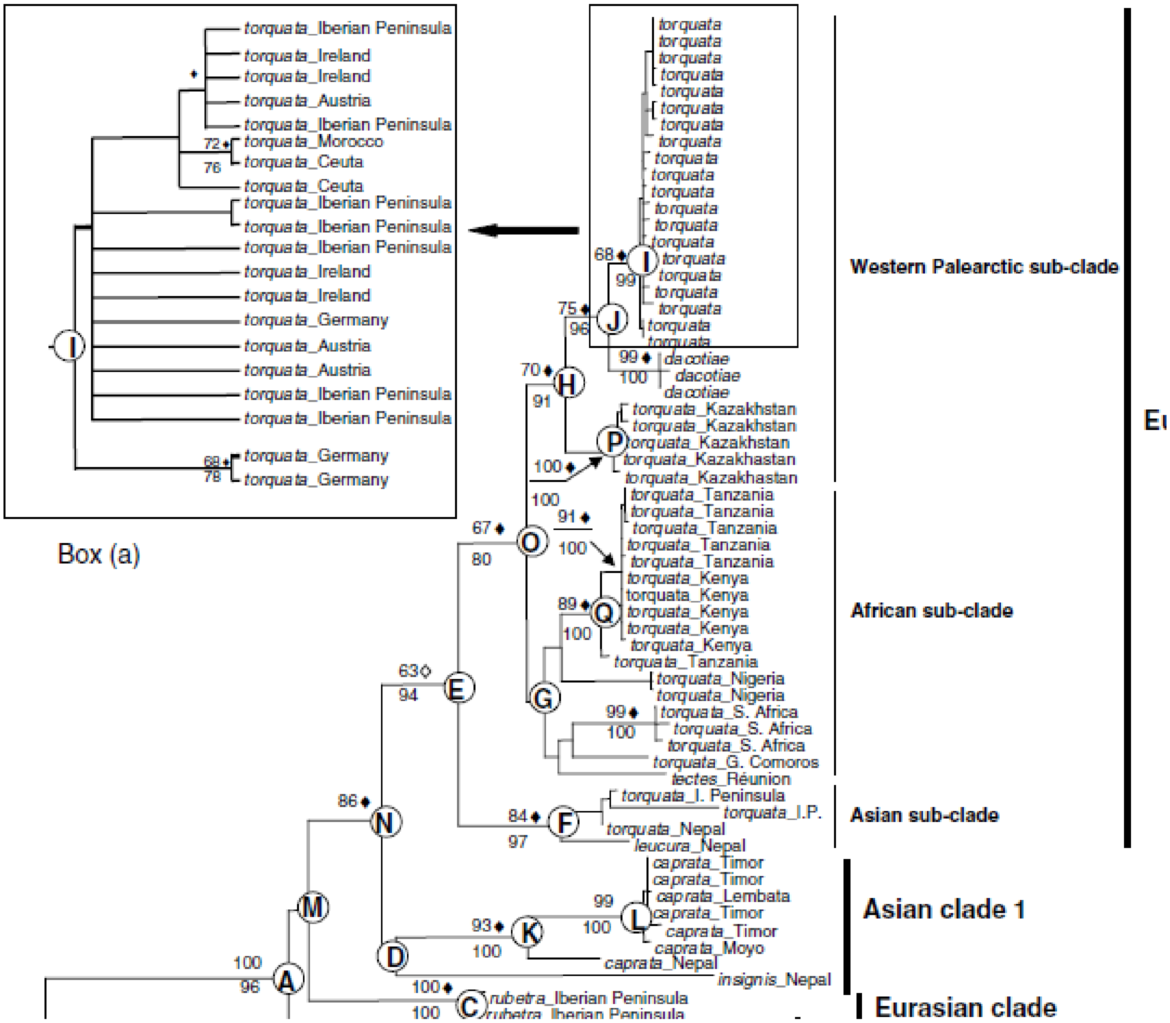


Fig. 1. Illera et al. (2008).

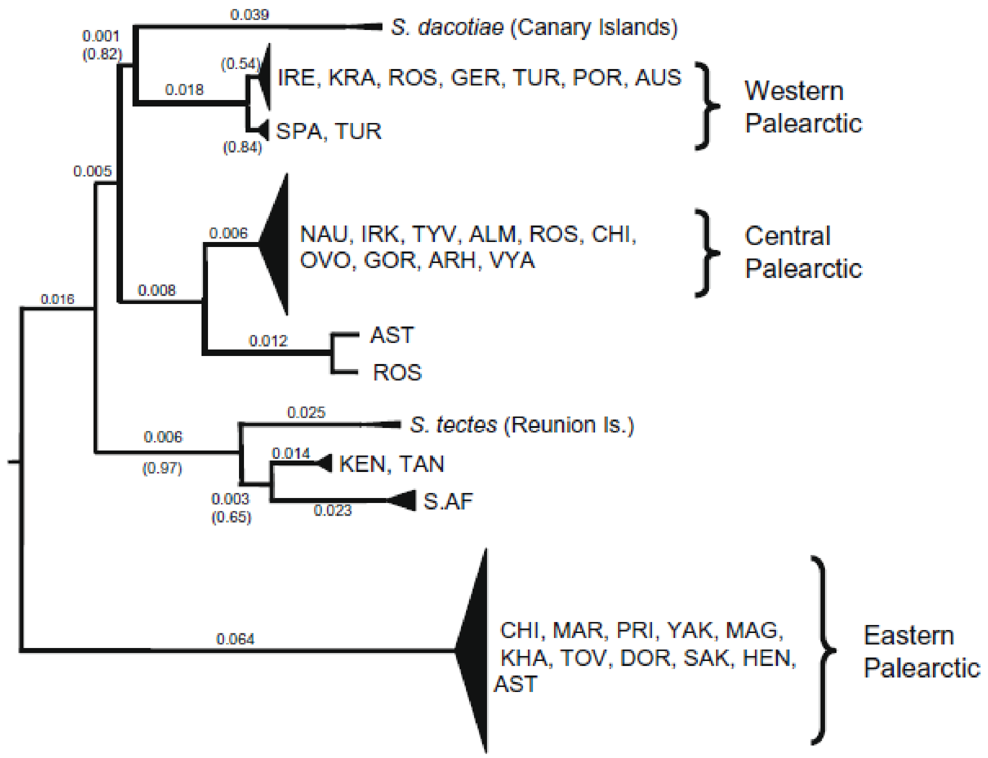


Fig. 2. Zink et al. (2009)

Subsequent Treatments:

HBW (Collar 2005, and http://www.hbw.com/species/common-stonechat-saxicola-torquatus) and BirdLife International (http://www.birdlife.org/datazone/speciesfactsheet.php?id=6682) have refrained thus far from adopting any split of *torquatus* (*s.l.*).

In Sangster et al. (2011), *maurus* was split from the nominate and *rubicola*, but *stejnegeri* was maintained under *maurus* despite the deep divergence in Zink et al. (2009), because that paper did not include the key taxon *przewalskii*, which is morphologically quite distinct from both *indicus* and *stejnegeri* (which have a moderate level of morphological divergence between them; Rasmussen and Anderton 2012). Hence, splitting *stejnegeri* without knowing the placement of *przewalskii* is risky because *przewalskii* would have priority over *stejnegeri*, if they are united, and *indicus* over both. Rasmussen and Anderton (2012) followed the BOU on this matter.

IOC 4.1 (http://www.worldbirdnames.org/chats-revised/) basically follows Zink et al. (2009) by recognizing *rubicola*, *torquatus*, *maurus*, and *stejnegeri* as full species, and in addition follows Woog et al. (2008) in treating the Malagasy birds as a full species. They also adopt the taxonomic recommendations of Svensson et al. (2012) concerning nomenclature of central Asian *maurus*.

Recommendation:

Stonechats of any taxon are very rare vagrants in the AOU area. The first North American record documented photographically was of a female in New Brunswick in 1 Oct 1983 (Wilson 1986). One slightly fuzzy photograph was published (http://sora.unm.edu/sites/default/files/journals/nab/v040n01/p00016-p00017.pdf) and, as identified in the original article, it fits the eastern taxon *stejnegeri*, although it could also be the Central Asian *maurus s.s.* (Wilson 1986). Because *maurus* is a frequent vagrant to Western Europe, it seems perhaps more likely to be that rather than a Siberian *stejnegeri* having made its way all across Alaska and Canada, but it may never be possible to determine this. The Western European *rubicola* group is not highly migratory so is less likely to occur in North America.

The first North American specimen of a stonechat (UAM 5301, a frozen bird found in the spring in a Bank Swallow burrow in Galena, Alaska) was identified as *stejnegeri*, the north-east Asian breeding taxon (Osborne and Osborne 1987). As this form is highly migratory, it is not surprising that it turns up as a vagrant occasionally in Alaska, with several records from St. Lawrence I. and a few others in Alaska, and one from San Clemente I., California (http://www.wfopublications.org/Rare_Birds/Stonechat/Stonechat.html).

As far as I've been able to determine, all North American stonechat records have been identified as, or at least assumed to be, *stejnegeri* or *maurus*. Thus, splitting stonechats will lead to a name change in the Check-list and a revised account. If we vote to split deeper, removing *stejnegeri* from *maurus*, at least the New Brunswick and perhaps other records will likely be indeterminable (not that this should influence anyone's decision in the slightest).

There are numerous possibilities, and I've attempted to keep it as simple as possible:

1) No change, leave as *Saxicola torquatus* (emendation to specific epithet already accepted on the basis of David and Gosselin 2002). This would mean that, to avoid paraphyly, the species would need to be expanded to include some taxa traditionally considered separate species, the Canary Islands Stonechat *S. dacotiae*, the Reunion Stonechat *S. tectes*, and the White-tailed Stonechat *S. leucurus* (that is, if extralimital authorities were to agree with this treatment, which seems unlikely given that many have already followed one or another of the various splitting options). Of course, no change could also mean a preference to await more conclusive evidence regarding how to enact the splits before proceeding.

2) A three-way split between the *maurus* group (including all Central Asian races, *indicus*, *przewalskii*, and *stejnegeri*), the W European *rubicola* group, and the African *torquatus* group. This would be a conservative approach given the issue with *przewalskii* not being included in any molecular analysis thus far and having priority over *stejnegeri* if lumped. It would also mean that all North American

records fit within this single species. It would also be affirmative of the interim approach taken by BOC (Sangster et al. 2011). However, it has the disadvantage of not reflecting the deep divergence between *stejnegeri* and all other stonechat taxa as recovered in Zink et al. (2009).

Option 2a would be to also split the Madagascan taxa (oldest name *sibilla*, Linnaeus, 1766), which was supported by Woog et al. (2008).

3) A four-way split between the *maurus* group (Central and South Asian races only), *stejnegeri*, the *rubicola* group, and the *torquatus* group. This, as noted above, ignores *przewalskii* and may lead to further revision when that taxon is included in a future study. Nevertheless, given the deep divergence between *stejnegeri* and other taxa demonstrated in Zink et al. (2009), this would be a reasonable course of action, if perhaps premature. This result has not yet been corroborated by any other study, but it is based on a fairly large sample size.
   Option 3a would be to also split the Madagascan taxa (oldest name *sibilla*, Linnaeus, 1766), as suggested by Woog et al. (2008).

I recommend (for the reasons and with the reservations expressed above) voting YES on Option 2.

As regards Option 2a, I recommend voting NO. Although Woog et al. (2008) show that there is a distinct clade of Malagasy birds, their (and all the other) analyses are missing some key African taxa, like the distinctively pied Ethiopian highlands race *albofasciatus*, and there is significant structure within African taxa. Even Woog et al. (2008) presented their results tentatively and stated that further study was needed. It's not, however, a priority issue, as with *przewalskii*. Sangster et al. (2011) do not clearly state their views on species status of *sibilla* (even though they cite Woog et al. 2008) but in their decision it falls implicitly within the African *torquatus* group. Thus, again, voting against 2a would be a vote for conformity with BOU on the matter of an extralimital taxon.

Note that the English name "Siberian Stonechat" has become widely associated with *maurus*, whether in the restricted sense of Option 3 or the broader sense of Option 2. If Option 3 is adopted, this name is a bit unfortunate since most of Siberia is occupied by what is called in IOC 4.1 Stejneger's Stonechat *S. stejnegeri*, rather than Siberian Stonechat *S. maurus*.

PS: There is a typo in the Check-list on p. 498: it should say "Winters: [*torquata*] group" rather than "*torguata*". This may be irrelevant if we accept either Options 2 or 3, however, as I assume that text would disappear.

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Submitted by: Pamela C. Rasmussen, Michigan State University

Date of proposal: 23 Feb 2014

Revise the generic assignments of several introduced estrildids

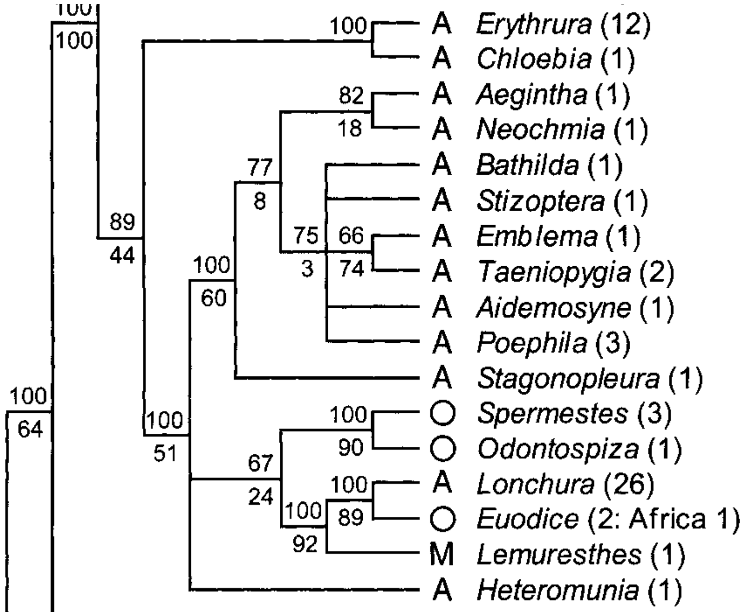
Background:

Generic relationships of munias and mannikins have long been based on morphology, song, and displays (e.g., Goodwin 1982, Baptista et al. 1999), often as deduced from studies of cage birds. The songs are notoriously soft and the birds are hard to study in field conditions, but most species are amenable to captivity. The Java Sparrow *Padda oryzivora* (as in AOU 1998) has long been treated together with another Indonesian species, the Timor Sparrow *Padda fuscata*, as the only two members of the genus *Padda* Reichenbach, 1850. Both species are distinctive-looking large munias; however, the justification for maintaining the genus *Padda* for them as distinct from other Asian *Lonchura* Sykes, 1832, has been called into question by numerous authors (e.g., Restall 1996).

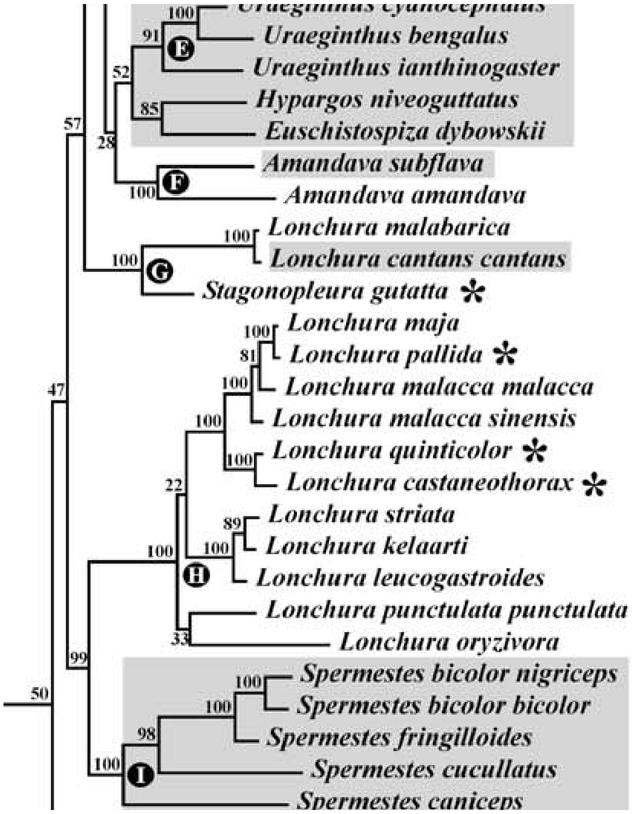
The generic placement of two other taxa frequently treated within *Lonchura* (as in AOU 1998), the African Silverbill *Lonchura cantans* and the Indian Silverbill *L. malabarica* (treated as conspecific in AOU 1998 but split by AOU 2000), also needs reassessment. These two species have often been considered the only members of the genus *Euodice* Reichenbach 1863. They are clearly closely related to each other, and occur sympatrically in the southern Arabian peninsula, but their relationships with other munias and mannikins is not obvious. A third group of mannikins treated in AOU 1998 within *Lonchura* includes the African species Bronze Mannikin *Lonchura cucullata*, which has often been placed with other similar African species in *Spermestes* Swainson, 1837.

All of these taxa are introduced to small tropical areas of the AOU area, specifically Hawaii (*oryzivora, cantans*) or Puerto Rico (*oryzivora, malabarica, cucullata*).

New information: Two recent molecular phylogenies for the Estrildidae provide new data on relationships within the family. Neither are ideal for this purpose; Sorenson et al. (2004) is primarily focused on mapping host-parasite evolution, and lumps species together within the genera of interest to us without specifically showing each on the phylogeny (because they are not brood-parasite hosts), and Arnaiz-Villena et al. (2009) is poorly edited. In addition, there is a lack of concordance between these studies on the exact position of *Euodice*. Arnaiz-Villena et al.'s (2009) study used cyt-b of 61 species, apparently mostly from blood samples. Sorenson et al.'s (2004) study used about 1650 bp of two mtDNA regions for 74 estrildid species. However, both phylogenies recover a core *Lonchura* that includes *oryzivora* but not *Spermestes* and *Euodice*. In Sorenson et al. (2004), *cantans* and *malabarica* (*Euodice*) are fairly close sisters to *Lonchura*, but in Arnaiz-Villena et al. (2009) they are not. In both, *Spermestes* (plus the other "silverbill", *Odontospiza caniceps*) is a clearly distinct clade sister to *Lonchura* (plus *Euodice* in Sorenson et al. 2004).



Relevant portion of Fig. 1 from Sorenson et al. (2004).



Relevant portion of Fig. 1 of Arnaiz-Villena et al. (2009).

Subsequent treatments:

Several recent treatments have placed *oryzivora* within *Lonchura* and/or resurrected *Euodice* and *Spermestes* (e.g. Restall 1996, Payne 2010; e-bird Version 1.54, http://help.ebird.org/customer/portal/articles/1006825-the-ebird-taxonomy?b_id=1928&t=401132; SACC, http://www.museum.lsu.edu/~Remsen/SACCBaseline11.htm; IOC Version 4.1, http://www.worldbirdnames.org/n-weavers.html).

Recommendation:

Elements of this proposal, if accepted, would remove one genus (*Padda*) from the Check-list and would add two others (*Euodice* and *Spermestes*). The species would therefore be treated as *Lonchura oryzivora, Euodice malabarica*, *Euodice cantans,* and *Spermestes cucullata*. Based on the phylogenies of Sorenson et al. (2004 and in prep.) and Arnaiz-Villena et al. (2009), the linear sequence for taxa in these genera would become:

- *Spermestes cucullata*
- *Euodice malabarica*
  - *E. cantans*
- *Lonchura oryzivora*
  - *L. punctulata*
  - *L. malacca*
  - *L. atricapilla*

I recommend YES on transferring *oryzivora* to *Lonchura*, YES on transferring *cantans* and *malabarica* to *Euodice*, and YES on transferring *cucullata* to *Spermestes*.

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Submitted by:: Pamela C. Rasmussen, Michigan State University

Date of proposal: 23 Feb 2014

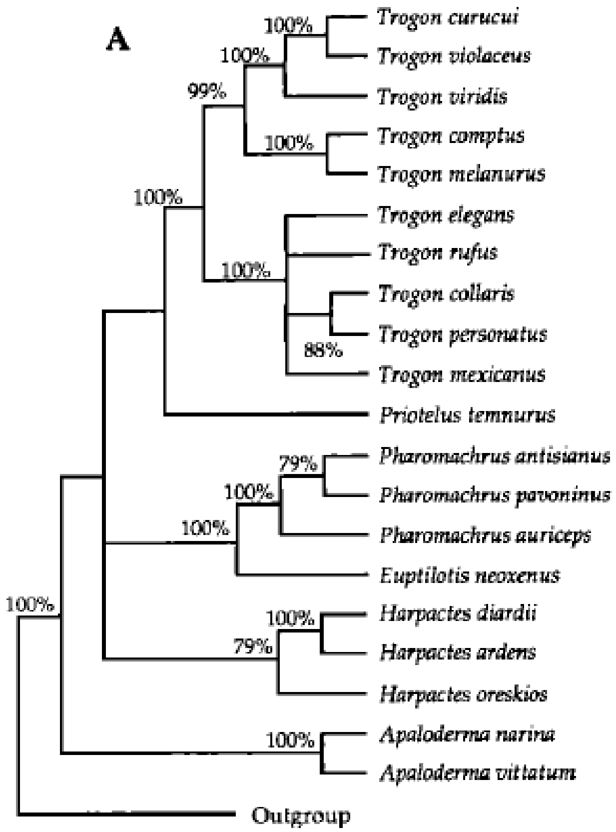
Eliminate Trogoninae (New World Trogons) as a subfamily of the Trogonidae

Background:

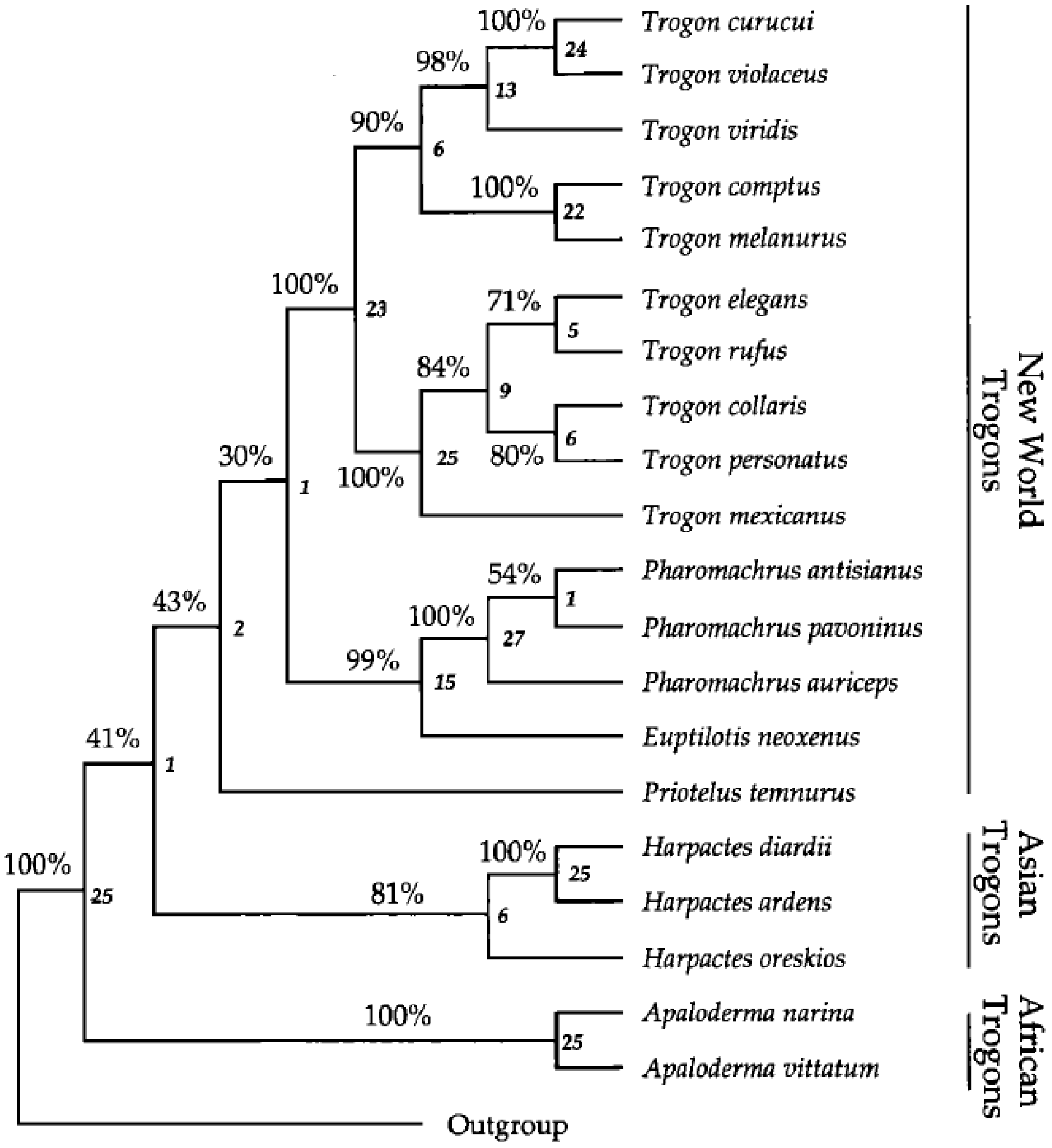
We currently recognize the Trogoninae (New World Trogons) as a subfamily of the Trogonidae. All New World trogons and quetzals are included in this subfamily. Presumably this is a remnant of a geographical subfamily structure that consisted of the Trogoninae, the Aplodermatinae (African taxa), and the Harpactinae (Asian taxa). I am aware of no morphological studies of relationships within the Trogonidae, although numerous studies have assessed the relationships of trogons to other birds.

New Information:

The first molecular study to include a reasonable sampling of trogons and quetzals was that of Espinosa de los Monteros (1998), who sequenced two mitochondrial genes, cyt-b and 12S, for 20 species. His higher-level results were equivocal: five clades were identified with reasonably strong (79-100%) bootstrap support (1. African trogons *Apaloderma* spp.; 2. Asian trogons *Harpactes* spp.; 3. Caribbean trogons *Prioteles* spp., although only one species was sampled; 4. quetzals *Pharomachrus* and *Euptilotis* spp.; and 5. the other New World trogons *Trogon* spp.), but relationships among these clades were poorly resolved (bootstraps < 50%) regardless of the type of analysis (e.g., equal weighting of all characters or downweighting or elimination of third positions). This is his tree using equal weighting of all positions:

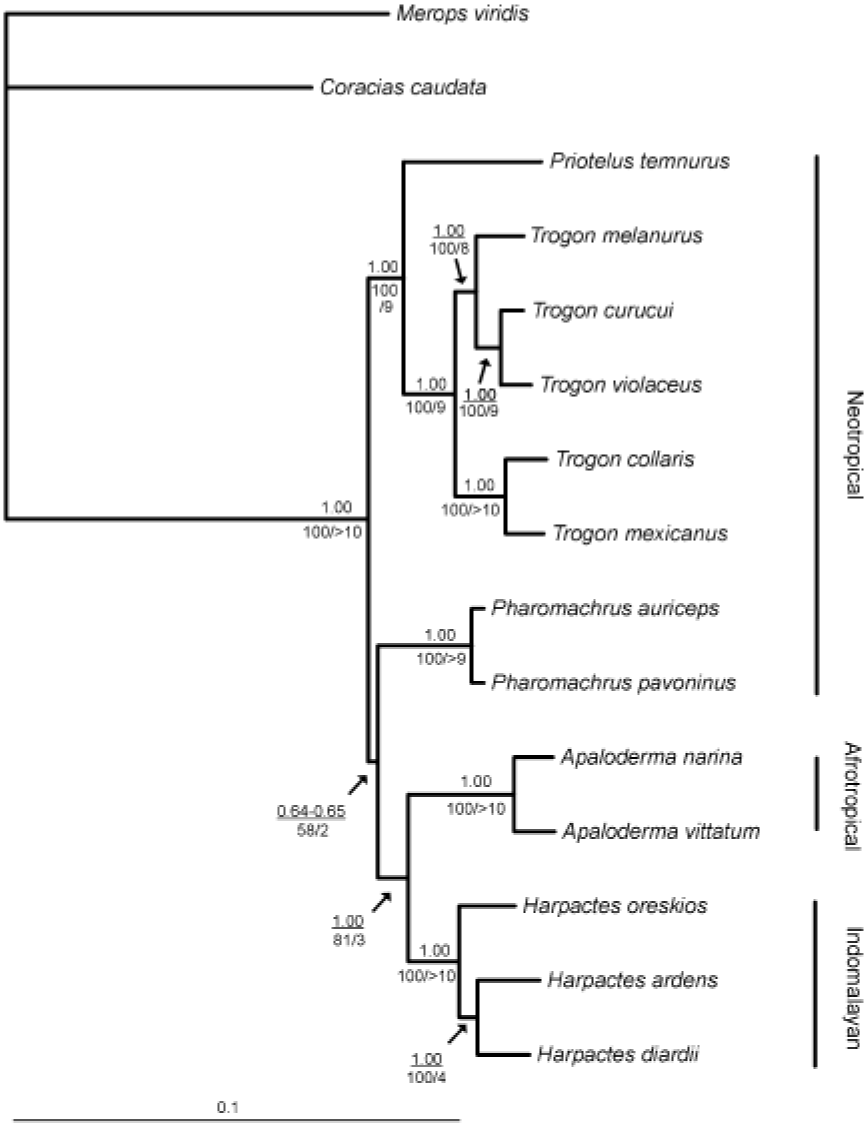


and his tree with third positions excluded from the analysis:



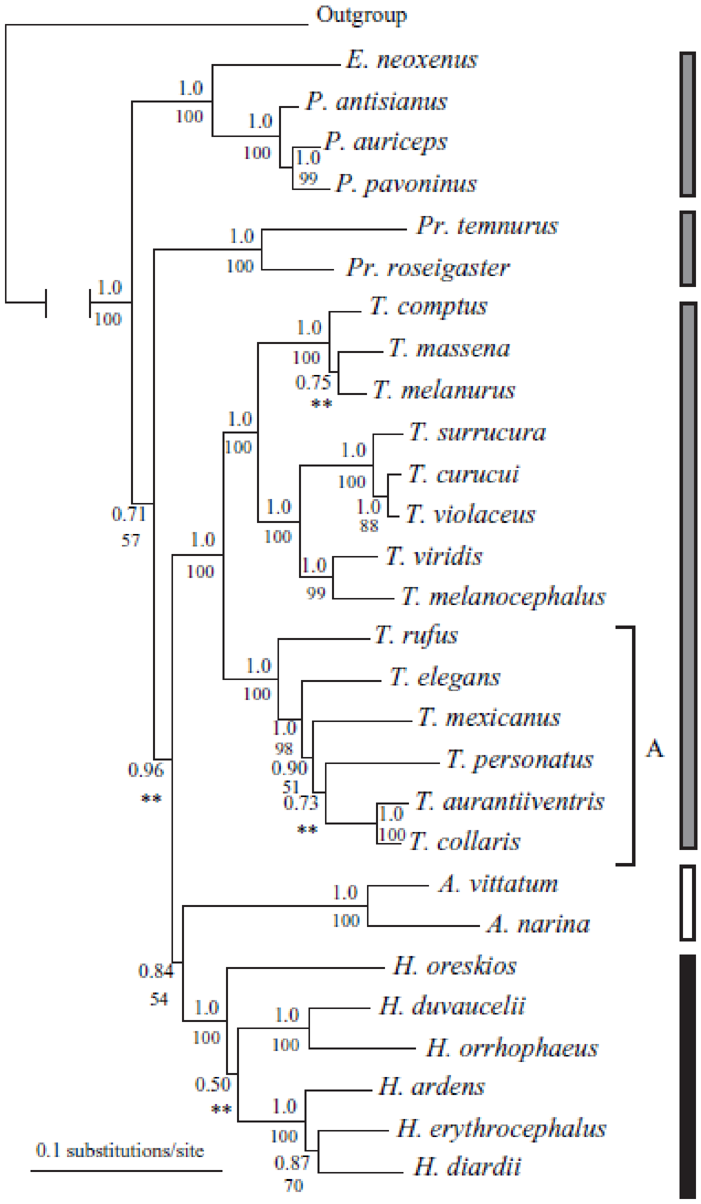
This tree, with third positions excluded, was his preferred tree, but bootstrap values for relationships among groups were poor, and these relationships differed when different methods of analysis were used. In addition, as pointed out by Moyle (2005), the two mitochondrial genes were incongruent: one (cyt-b) supported the basal position of the African trogons, as above, whereas the other (12S) supported quetzals as the basal taxon, in agreement with Moyle's own study (see below).

A second major study was that of Johansson and Ericson (2004), who sampled 13 species for three nuclear introns (myoglobin intron 2, beta-fibrinogen intron 7, and G3PDH intron 11) for the express purpose of re-evaluating basal relationships among the Trogonidae. Their results indicated that the African and Asian trogons were sister groups (1.0 pp, 81% bootstrap), that the quetzals were sister to this clade (0.65 pp, 58% bootstrap), and that *Prioteles* and *Trogon* spp. formed a strongly supported clade (1.0 pp, 100% bootstrap) that was sister to the African-Asian-quetzal clade. Thus, the New World species did not form a clade. This is their nuclear tree:



Johansson and Ericson (2004) also conducted analyses that combined their nuclear data with the mitochondrial sequences of Espinosa de los Monteros (1998). In these analyses, the quetzals became sister to the *Prioteles-Trogon* clade (0.72 pp, 62% bootstrap), making the New World taxa monophyletic, and the Asian and African trogons became successive sisters to the New World clade, rather than forming an African-Asian clade. Johansson and Ericson (2004) concluded that “it is not possible to discriminate between the different hypotheses of basal phylogenetic relationships” in the Trogonidae.

The most recent and best sampled study was that of Moyle (2005), who sequenced 28 species for the mitochondrial gene ND2 and the nuclear exon RAG-1. His results indicated that the African and Asian trogons were sister groups (0.84 pp, 54% bootstrap), that *Trogon* spp. were sister to the African-Asian clade (0.96 pp, <50% bootstrap), that *Prioteles* spp. were sister to this large clade (0.71 pp, 57% bootstrap), and that the quetzals were sister to the rest of the family. Thus, the New World taxa formed three separate clades that were not sister groups. This is his tree (“*P.*’ here is *Pharomachrus*):



Moyle (2005) noted that both of the genes sequenced for his study supported this topology (although with generally mediocre support), as did one of the genes (12S) sequenced by Espinosa de los Monteros (1998).

In summary, the monophyly of each of the five groups identified by Espinosa de los Monteros (1998) is well supported, but relationships among them remain poorly resolved, despite more recent studies that addressed their relationships using a variety of nuclear genes. The various phylogenetic trees are characterized by starkly different results and instability at the base of the tree, which may result from rooting issues associated with the distant relationships of the Trogonidae with other birds.

Recommendation:

There is no strong evidence indicating that the New World trogons form a monophyletic group, but also no strong evidence that they do not. As I see it, we have two options. First, we could maintain the status quo of acknowledging the subfamily Trogoninae, although recognizing that it has no strong support. The argument for this is that we should change our current classification only when the data strongly support it, and in this case there is no strong support for changing our current classification. Alternatively, we could eliminate the subfamily structure from our classification and simply group all species under the family Trogonidae. The argument for this is that our classification should reflect well supported groupings except when we are forced to make a determination based on poor data, which in this case we are not – we could simply eliminate the subfamily structure in this family, taking a neutral position on intrafamilial systematics in the group pending further data. Both arguments seem reasonable, but I would recommend a YES vote on the proposal to eliminate the subfamily structure from our classification. Although there is no consistent support for any substructure among New World trogons, our current classification suggests that these taxa do form a clade, which at this point seems misleading.

Addendum: After submitting this proposal, I learned that Joel Cracraft and colleagues have been looking into this problem and have sequenced a number of additional nuclear genes in an attempt to provide better resolution at the base of the trogon tree. Their unpublished results indicate that New World trogons are monophyletic – the bootstrap support for this is 77% (JLC, in litt.), which isn't great but is quite a bit better than the support in any of the published studies. Given this, we may wish to keep the status quo (recognizing Trogoninae) a bit longer, until these data are published and can be evaluated.

Literature Cited:

Espinosa de los Monteros, A. 1998. Phylogenetic relationships among the trogons. *Auk* 115: 937–954.

Johansson, U. S., and P. G. P. Ericson. 2004. A re-evaluation of basal phylogenetic relationships within trogons (Aves: Trogonidae) based on nuclear DNA sequences. *Journal of Zoological Systematics and Evolutionary Research* 43: 166–173.

Moyle, R. G. 2005. Phylogeny and biogeographical history of Trogoniformes, a pantropical bird order. *Biological Journal of the Linnean Society* 84: 725–738.

Submitted by: Terry Chesser, Smithsonian Institution

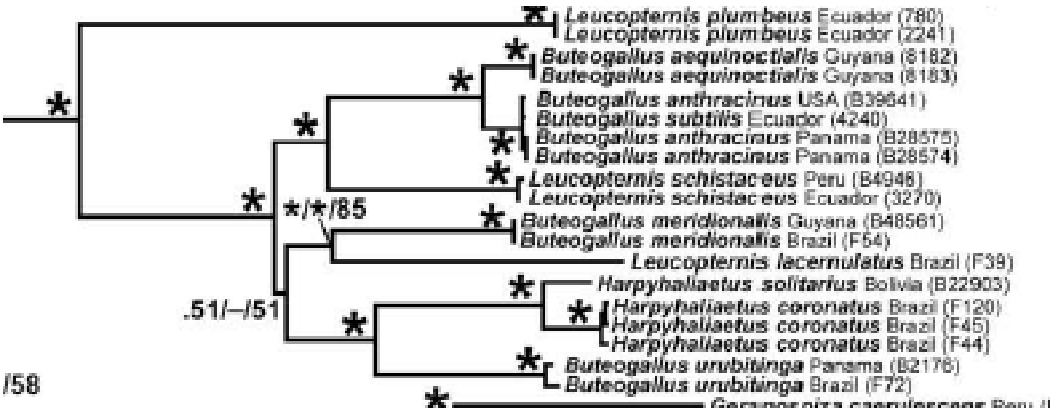
Date of proposal: 28 Feb 2014

2014-B-14 N&MA Classification Committee pp. 97-98

Remove hyphens from English names of the “Black-Hawks"

This is a spinoff of a SACC proposal (#515) from several years ago that passed unanimously that I neglected to then send to NACC. AOU policy is that hyphenation of group names indicates that the group is monophyletic.

Raposo do Amaral et al. (2009; Molecular Phylogenetics & Evolution 53: 703-715; 6000 bp, mtDNA and nDNA) showed conclusively that “Common Black-Hawk” and “Great Black-Hawk” do not form a monophyletic group within *Buteogallus*. Below is a screen grab from their Fig. 1; if anyone needs a pdf, just let me know.



Great Black-Hawk and Common Black-Hawk are not even close to being sisters. Therefore, the hyphen “Black-Hawk”, now misleading, should be removed from their English names, as well as the one from Cuban Black-Hawk, *B. gundlachii*.

Submitted by: Van Remsen

Date of proposal: 4 Mar 2014