AOS Classification Committee – North and Middle America

Proposal Set 2018-C

1 March 2018

Adopt (a) a revised linear sequence and (b) a subfamily classification for the Accipitridae

Background:

Our current linear sequence of the Accipitridae, which places all the kites at the beginning, followed by the harpy and sea eagles, accipiters and harriers, buteonines, and finally the booted eagles, follows the revised Peters classification of the group (Stresemann and Amadon 1979). This classification was based largely on feeding ecology and morphology and included no higher-level subdivisions:

Leptodon cayanensis	Gray-headed Kite
Chondrohierax uncinatus	Hook-billed Kite
Elanoides forficatus	Swallow-tailed Kite
Gampsonyx swainsonii	Pearl Kite
Elanus leucurus	White-tailed Kite
Rostrhamus sociabilis	Snail Kite
Helicolestes hamatus	Slender-billed Kite
Harpagus bidentatus	Double-toothed Kite
Ictinia mississippiensis	Mississippi Kite
Ictinia plumbea	Plumbeous Kite
Milvus migrans	Black Kite
Haliaeetus leucocephalus	Bald Eagle
Haliaeetus albicilla	White-tailed Eagle
Haliaeetus pelagicus	Steller's Sea-Eagle
Busarellus nigricollis	Black-collared Hawk
Circus hudsonius	Northern Harrier
Circus buffoni	Long-winged Harrier
Circus aeruginosus	Western Marsh Harrier
Accipiter poliogaster	Gray-bellied Hawk
Accipiter soloensis	Chinese Sparrowhawk
Accipiter superciliosus	Tiny Hawk
Accipiter striatus	Sharp-shinned Hawk
Accipiter cooperii	Cooper's Hawk
Accipiter gundlachi	Gundlach's Hawk
Accipiter bicolor	Bicolored Hawk
Accipiter gentilis	Northern Goshawk
Geranospiza caerulescens	Crane Hawk
Cryptoleucopteryx plumbea	Plumbeous Hawk
Buteogallus anthracinus	Common Black Hawk
Buteogallus gundlachii	Cuban Black Hawk
Buteogallus meridionalis	Savanna Hawk
Buteogallus urubitinga	Great Black Hawk

Buteogallus solitarius	Solitary Eagle
Morphnarchus princeps	Barred Hawk
Rupornis magnirostris	Roadside Hawk
Parabuteo unicinctus	Harris's Hawk
Geranoaetus albicaudatus	White-tailed Hawk
Pseudastur albicollis	White Hawk
Leucopternis semiplumbeus	Semiplumbeous Hawk
Buteo plagiatus	Gray Hawk
Buteo nitidus	Gray-lined Hawk
Buteo lineatus	Red-shouldered Hawk
Buteo ridgwayi	Ridgway's Hawk
Buteo platypterus	Broad-winged Hawk
Buteo solitarius	Hawaiian Hawk
Buteo brachyurus	Short-tailed Hawk
Buteo swainsoni	Swainson's Hawk
Buteo albonotatus	Zone-tailed Hawk
Buteo jamaicensis	Red-tailed Hawk
Buteo lagopus	Rough-legged Hawk
Buteo regalis	Ferruginous Hawk
Morphnus guianensis	Crested Eagle
Harpia harpyja	Harpy Eagle
Aquila chrysaetos	Golden Eagle
Spizaetus tyrannus	Black Hawk-Eagle
Spizaetus ornatus	Ornate Hawk-Eagle
Spizaetus melanoleucus	Black-and-white Hawk-Eagle

New Information:

The phylogeny of the Accipitridae received a flurry of focused attention during the period 2005-2009 (Lerner and Mindell 2005, Lerner et al. 2008, Griffiths et al. 2008, Raposo do Amaral et al. 2009). However, other than a revision of the generic classification and linear sequence of the buteonine hawks (Chesser et al. 2015), the results of these studies have yet to be reflected in our classification of the family.

The studies with the best broad-based sampling of the Accipitridae (Lerner and Mindell 2005, Griffiths et al. 2008) produced very similar phylogenies (see Fig. 1 and Fig. 2 below). Sister to all other groups were the elanine kites, which include our Pearl Kite *Gampsonyx swainsonii* and White-tailed Kite *Elanus leucurus*. Sister to the remaining groups was a clade consisting of the pernine kites and part of the Old World vultures. Of groups that occur in our area, the next successive sisters were the harpy eagles and booted eagles. The final clade consisted of the Double-toothed Kite *Harpagus bidentatus* (not sampled by Lerner and Mindell); the harriers and accipiters; the milvine kites, atypical hawks, and sea eagles; and the buteonines. Relationships within this clade were not as well-resolved or consistent as in the other groups, but Raposo do Amaral et al. (2009; Fig. 3 below) provided somewhat better resolution. Relationships within groups were often sketchy due to limited taxon sampling, although sampling within the buteonines (Raposo do Amaral et al. 2009) was excellent.

Lerner and Mindell (2005) proposed a higher-level classification of the Accipitridae consisting of 14 subfamilies, whereas Griffiths et al. (2008) proposed a 3-subfamily classification; the latter has been adopted by SACC (Proposal 553 from 2012), Dickinson and Remsen (2013), and del Hoyo and Collar (2014).

Revising our classification according to these phylogenies and the 3-subfamily arrangement would result in the following new sequence:

Family ACCIPITRIDAE

Subfamily ELANINAE

Gampsonyx swainsonii	Pearl Kite
Elanus leucurus	White-tailed Kite

Subfamily GYPAETINAE

Chondrohierax uncinatus	Hook-billed Kite
Leptodon cayanensis	Gray-headed Kite
Elanoides forficatus	Swallow-tailed Kite

Subfamily ACCIPITRINAE

Morphnus guianensis	Crested Eagle
Harpia harpyja	Harpy Eagle
Aquila chrysaetos	Golden Eagle
Spizaetus tyrannus	Black Hawk-Eagle
Spizaetus melanoleucus	Black-and-white Hawk-Eagle
Spizaetus ornatus	Ornate Hawk-Eagle
Harpagus bidentatus	Double-toothed Kite
Circus hudsonius	Northern Harrier
Circus buffoni	Long-winged Harrier
Circus aeruginosus	Western Marsh Harrier
Accipiter poliogaster	Gray-bellied Hawk
Accipiter soloensis	Chinese Sparrowhawk
Accipiter superciliosus	Tiny Hawk
Accipiter striatus	Sharp-shinned Hawk
Accipiter cooperii	Cooper's Hawk
Accipiter gundlachi	Gundlach's Hawk
Accipiter bicolor	Bicolored Hawk
Accipiter gentilis	Northern Goshawk
Milvus migrans	Black Kite
Haliaeetus leucocephalus	Bald Eagle
Haliaeetus albicilla	White-tailed Eagle
Haliaeetus pelagicus	Steller's Sea-Eagle

Ictinia mississippiensis	Mississippi Kite
Ictinia plumbea	Plumbeous Kite
Busarellus nigricollis	Black-collared Hawk
Geranospiza caerulescens	Crane Hawk
Rostrhamus sociabilis	Snail Kite
Helicolestes hamatus	Slender-billed Kite
Cryptoleucopteryx plumbea	Plumbeous Hawk
Buteogallus anthracinus	Common Black Hawk
Buteogallus gundlachii	Cuban Black Hawk
Buteogallus meridionalis	Savanna Hawk
Buteogallus urubitinga	Great Black Hawk
Buteogallus solitarius	Solitary Eagle
Morphnarchus princeps	Barred Hawk
Rupornis magnirostris	Roadside Hawk
Parabuteo unicinctus	Harris's Hawk
Geranoaetus albicaudatus	White-tailed Hawk
Pseudastur albicollis	White Hawk
Leucopternis semiplumbeus	Semiplumbeous Hawk
Buteo plagiatus	Gray Hawk
Buteo nitidus	Gray-lined Hawk
Buteo lineatus	Red-shouldered Hawk
Buteo ridgwayi	Ridgway's Hawk
Buteo platypterus	Broad-winged Hawk
Buteo solitarius	Hawaiian Hawk
Buteo brachyurus	Short-tailed Hawk
Buteo swainsoni	Swainson's Hawk
Buteo albonotatus	Zone-tailed Hawk
Buteo jamaicensis	Red-tailed Hawk
Buteo lagopus	Rough-legged Hawk
Buteo regalis	Ferruginous Hawk

Recommendation:

Although not the last word in the classification of the Accipitridae (problems with apparently paraphyly and uncertain relationships must await better species-level sampling), this sequence based on Lerner and Mindell (2005), Griffiths et al. (2008), and Raposo do Amaral (2009) is vastly superior to our current sequence. I recommend that we adopt both (a) the new linear sequence and (b) the subfamily classification.

Literature Cited:

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Raposo do Amaral, F., F. H. Sheldon, A. Gamauf, E. Haring, M. Riesing, L. F. Silveira, and A. Wajntal. 2009. Patterns and processes of diversification in a widespread and ecologically diverse avian group, the buteonine hawks (Aves, Accipitridae). Molecular Phylogenetics and Evolution 53: 703–715.

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Submitted by: Terry Chesser

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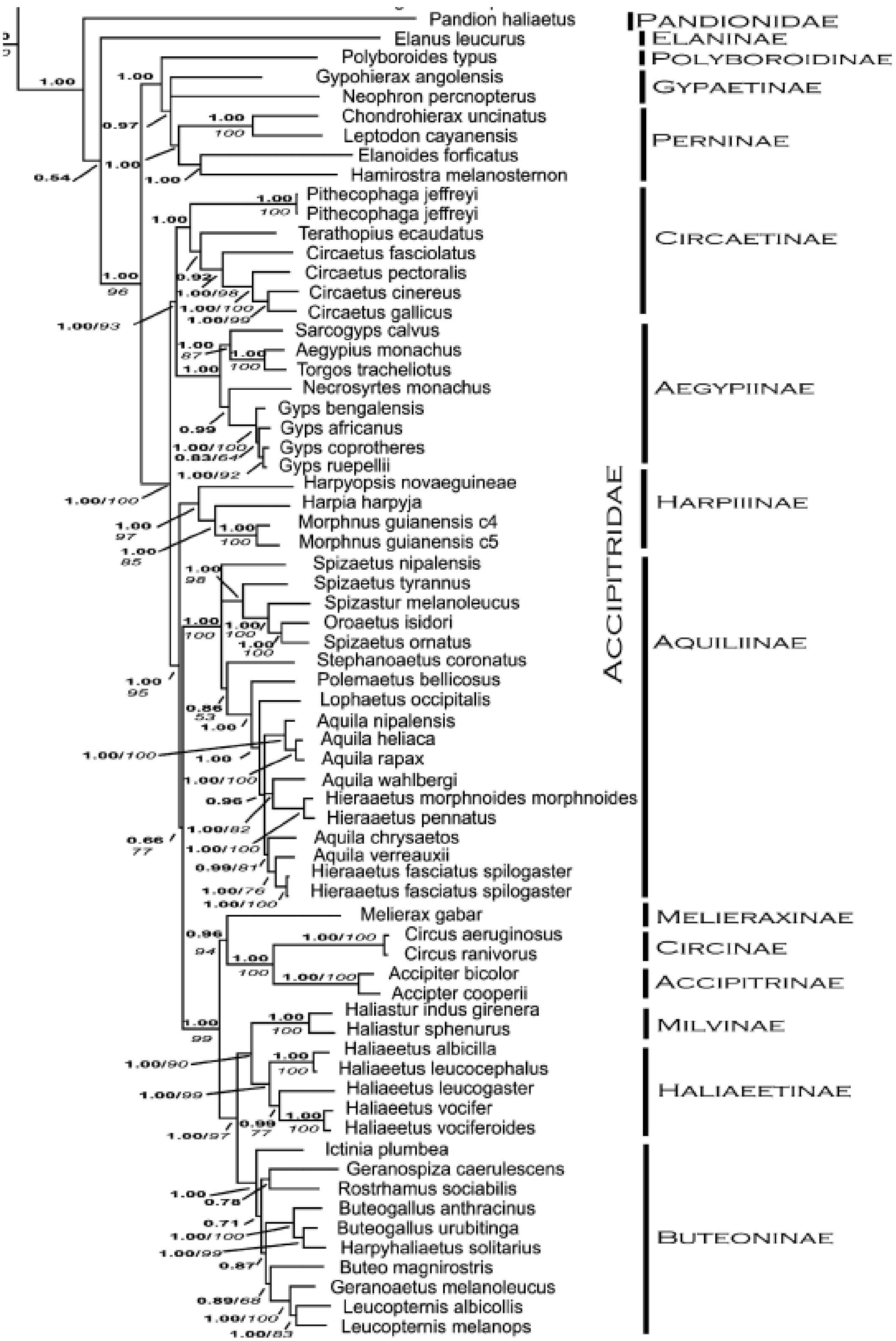

Figure 1. Bayesian phylogeny of the Accipitridae based on mitochondrial and nuclear DNA sequences (Lerner and Mindell 2005).

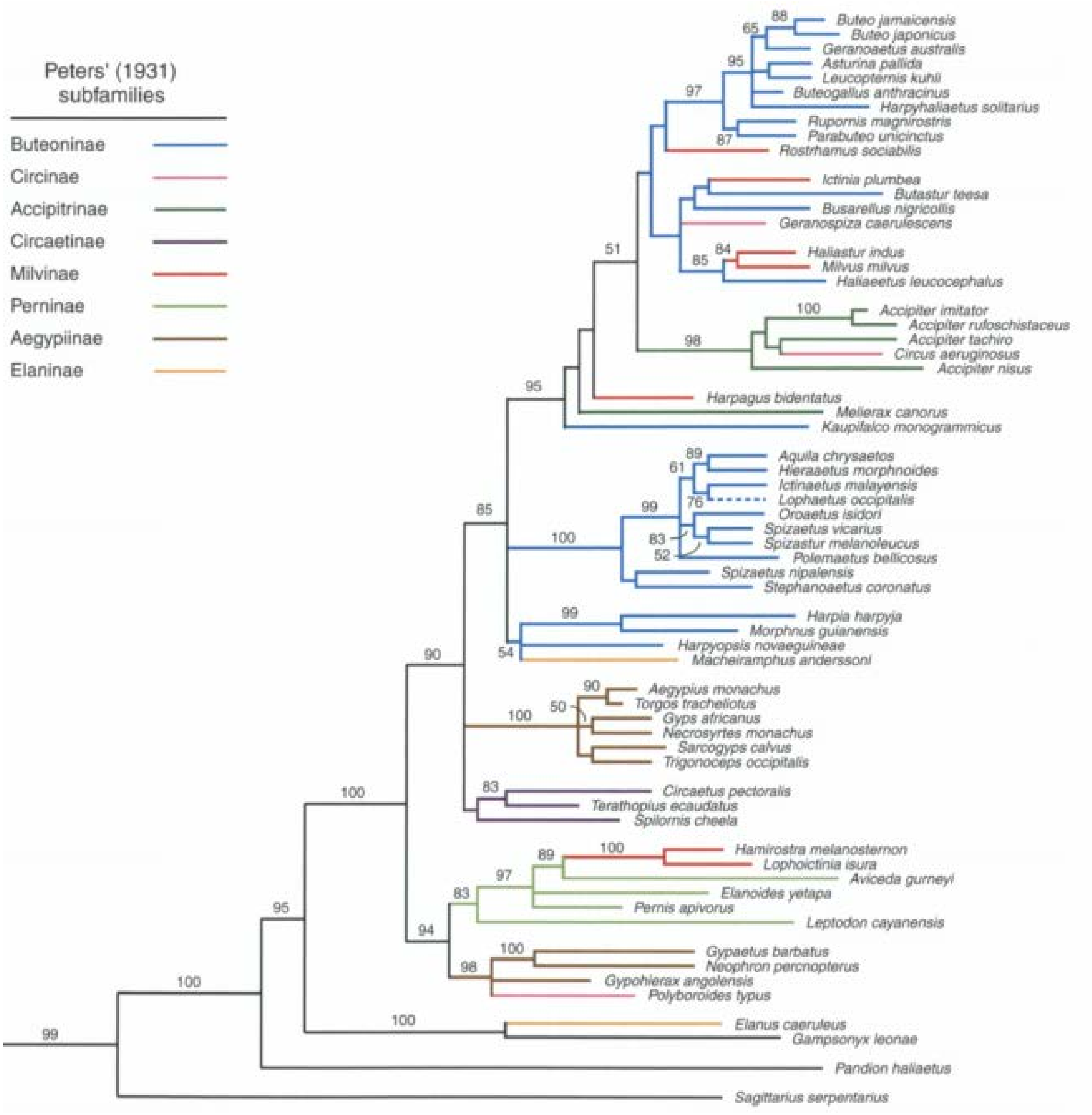

Figure 2. Maximum-likelihood phylogeny of the Accipitridae based on sequences of the nuclear gene RAG-1 (Griffiths et al. 2008).

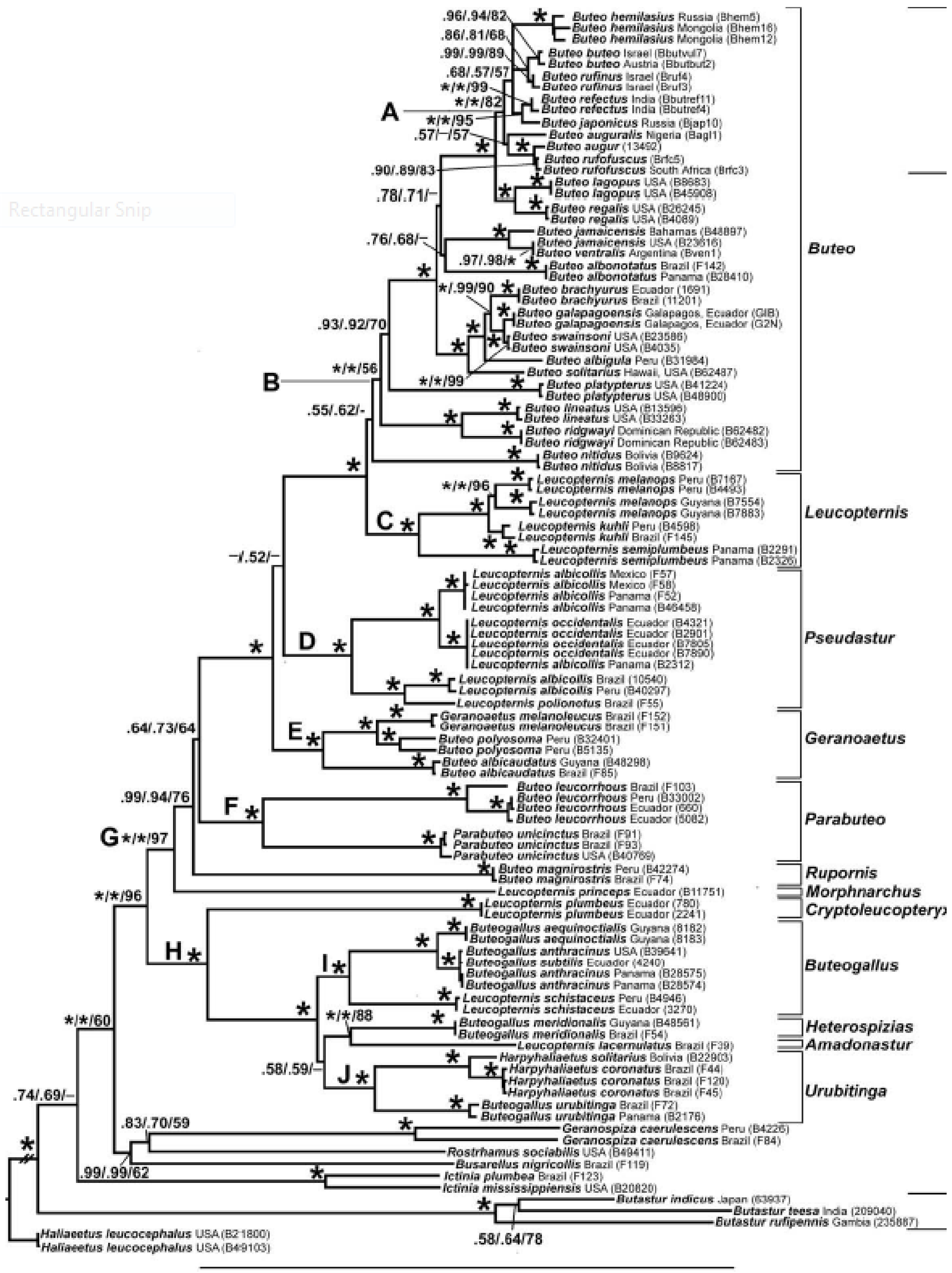

Figure 3. Maximum-likelihood phylogeny of the buteonines and closely related outgroups based on sequences of mitochondrial and nuclear DNA (Raposo do Amaral et al. 2009).

Split Yellow Warbler (*Setophaga petechia*) into two species

Background:

Hellmayr (1935), cited the plumage of birds from Martinique as good evidence to consider *Dendroica* (now *Setophaga*) *petechia*, the often chestnut-capped Caribbean birds, and *D. erithachorides*, the chestnut-hooded birds of mainland mangroves, as conspecifics. Aldrich (1942), who stated he was not convinced by Hellmayr's taxonomic conclusion, provided evidence on plumage coloration, wing shape, and measurements and concluded that the northern migratory *aestiva* and *petechia* from the West Indies were conspecific. AOU (1944), citing Hellmayr (1935), considered *erithachorides* and *petechia* to be conspecific, and AOU (1945), citing Aldrich (1942), treated *aestiva* and *petechia* as conspecific. Only one species of Yellow Warbler was recognized in the 5th edition of the Check-list (AOU 1957).

Klein and Brown (1994) reported a deep split in mtDNA between *aestiva* and their tropical group (members of the *petechia* and *erithachorides* groups), but noted that a Baja population, phenotypically similar to the *erithachorides* group, clustered with *aestiva*. They found two distinct subclades in the southern tropical group (*petechia* and *erithachorides* groups), but no geographic coherence between the clades; thus, the authors did not recognize taxonomic divisions. Klein and Brown (1994) also reported that West Indian birds (*petechia* group) are not monophyletic, nor are birds in the *erithachorides* group from Middle America and northern Venezuela, and the authors concluded that all populations represent one species. AOU (1998) recognized one species consisting of the northern migrant *aestiva* group, the sedentary *petechia* group from tropical Florida, insular Caribbean and coastal Venezuela, and the sedentary *erithachorides* group from coastal Mexico to the Galapagos Islands and coastal Colombia and western Venezuela.

Klein and Brown (1994) are cited by AOU (1998) as having "clarified relationships among populations in this complex." The 7th edition of the Check-list (AOU 1998) did not mention that some authors (e.g., Olson 1980, Wiedenfeld 1991, Browning 1994), although perhaps following the status quo, were aware that some Yellow Warblers are dissimilar to others and that the relationships of the complex were not fully clarified. Lowther et al. (1999), also cited Klein and Brown (1994) and stated, "Details of species limits are not certain, however, and more study is needed before taxonomic decisions can be made."

Klein and Brown's (1994) study showed at least two geographic clades, one clade including the *aestiva* group and the other including the *petechia* and *erithachorides* groups, but Klein and Brown (1994) stopped short of recognizing the *aestiva* group as a species distinct from the tropical birds. They wrote: "Although migratory populations that nest in North America have at times been considered a separate species (*D. aestiva*) (Hellmayr 1935) and should perhaps still be so classified (Ridgely 1976), substantial variation in intraspecific divergence is found even among haplotypes sampled only from sedentary tropical populations (0.14-2.22%).” Ridgely and Greenfield (2001) considered the information in Klein and Brown (1994) as reason to split northern *aestiva* from resident *petechia*. The IOC list (Gill and Donsker 2017) recognizes a northern migratory species (*aestiva*) and a tropical species (*erithachorides* and *petechia* groups).

Despite the AOU’s (1998) comment that there is clarification on the systematics of Yellow Warbler (*sensu lato*), controversy remains. A good example is proposal number 62 to the South American Checklist Committee from Van Remsen, dated October 2003, titled “Split *Dendroica petechia* into 2+ species.” Six of seven members of the Committee voted no (to maintain the status quo), although their comments indicated controversy about the taxonomy of the complex. The latest quantitative data referred to in proposal number 62 was Klein and Brown (1994). Later information from citations (e.g., Hilty 2003, Dunn and Garrett 2003) in the proposal was qualitative. More recent studies (e.g., Mennill 2001, Navarro-Siguenza and Peterson 2004, Browne et al. 2008, Salgado-Ortiz et al. 2008, Chaves et al. 2012, MacKinnon-Haskins and Dzib-Chay 2017, Curson 2017) call for or contribute to greater clarification of the taxonomic relationships of Yellow Warblers.

New information:

Breeding Ranges

A consideration of species limits between the *aestiva* group and the other groups of Yellow Warbler is their breeding ranges. The taxon *gundlachi*, a member of the *petechia* group, is a resident breeder in mangroves of southern Florida, where it is in contact only with migrant subspecies of the *aestiva* group (Stevenson and Anderson 1994, Prather and Cruz 1995). Recent surveys (Lloyd and Slater 2014) revealed that Florida *gundlachi* is confined to non-mainland mangroves. The taxon *oraria*, a member of the *erithachorides* group, breeds in mangroves of extreme southern Texas (Brush 2008). Members of the *aestiva* group no longer breed in Texas (Dunn and Garrett 1997, *contra* Lowther 1999), with no confirmed nesting in the state since 1956 (Lockwood and Freeman 2014). Accidental occurrences by individuals in the *erithachorides* group at San Diego, the southern end of Salton Sea, and central Arizona (Banfield et al. 2009) are likely representatives of the subspecies *castaneiceps* of southern Baja California Sur or *rhizophorae* of the northwestern coast of mainland Mexico or both (Dunn and Alderfer 2017). Members of the *aestiva* group do not breed near the ranges of the taxa of *erithachorides*. Breeding populations of the *aestiva*, *petechia*, and *erithachorides* groups are allopatric (AOU 1998, Dunn and Alderfer 2017).

Habitat

Taxa in the *aestiva* and *petechia* groups prefer variable breeding habitats (Lowther et al. 1999), with representatives in the *aestiva* group occurring from coastal mangroves to dry scrub, riparian and humid forests (Dunn and Garrett 1997). Members of the *erithachorides* group are confined to coastal mangroves (Dunn and Garrett 1997). However, *gundlachi* (in the *petechia* group) is confined to mangroves in Florida (Prather and Cruz 1995). Representatives of the *aestiva* group (migrating/wintering) are observed in upland habitats and not associated with resident members of *petechia* group (*bartholemica*) of mangroves on St. Kitts (Steadman et al. 1997), but members of the *aestiva* group are known (Dunn and Garrett 1997) to occur in mangroves to upland habitat. Yellow Warblers from the Galapagos and Cocos Island are more widely found and occur in dry forest to wet cloud forest (Chaves et al 2012).

Morphology – Color and Pattern

Based on plumage color and pattern, there are 43 subspecies (Browning 1994, Dunn and Garrett 1997) of Yellow Warbler. Males of the northern migratory subspecies (*aestiva* group) essentially lack chestnut on their heads, whereas the sedentary *petechia* group have chestnut caps and the sedentary *erithachorides* group have chestnut hoods. However, according to Lowther (1999), the subspecies *dugesi*, breeding in interior Mexico and in the *aestiva* group, is not migratory (Lowther 1999, Curson 2017). This is not confirmed because current information about movements is lacking. Migrant northern subspecies of Yellow Warbler are rare and annual winter visitors to southern California (Unitt 2004), and it is reasonable that some *dugesi* might overwinter within their breeding range.

The chestnut-hooded subspecies *ruficapilla* (from Martinique) is adjacent to members of the *petechia* group, and the Martinique taxon and *cienagae* (coastal Venezuela) are more similar in head color and pattern to members of the *erithachorides* group than to members of the *petechia* group (Lowther et al. 1999). Subspecies *aureola* from the Cocos and Galapagos islands, often placed in the *erithachorides* group (e.g. Browning 1994), is similar in color to members of the *petechia* group (Olson 1980), but is similar to the *erithachorides* group in size (Lowther et al. 1999) and in mtDNA (Chaves et al. 2008).

The non-migratory taxon *dugesi* is clearly a member of the *aestiva* group (Lowther et al. 1999). Martinique's *ruficapilla* is morphologically and phenotypically a member of the *erithachorides* group (Lowther et al. 1999, Chaves et al. 2012). Morphologically and phylogenetically, *ruficapilla* and *cienagae* belong to the *petechia* group, and *aureola* belongs to the *erithachorides* group (Lowther et al. 1999, Chaves et al. 2012).

Morton (1976) reported that first winter dull olive birds (*rubiginosa* and *amnicola*) from the *aestiva* group avoid competition with brighter and more yellow adults, are not territorial, join mixed flocks of birds, and wander during winter.

Territorial male Yellow Warblers exhibited more aggression toward males having greater amounts of chestnut breast streaks (Studd and Robertson 1985). Yezerinac and Weatherhead (1997) wrote, “Larger male yellow warblers [*aestiva* group from Canada] had higher within-pair parentage and males with more streaking on their breast plumage had higher extra-pair mating success.” They also wrote, “This is the second species for which there is genetic evidence that a plumage trait is related to extra-pair success...” Although chestnut streaking in the Yellow Warbler complex is geographically variable and not diagnostic in identifying members of the three groups (Browning 1994), the amount of chestnut on the head likely plays a role in the birds identifying themselves.

Morphology – Measurements

Size and plumages convinced Aldrich (1942) to consider northern migrants (*aestiva* group) and Antillean birds (*petechia* group) to be conspecific. He noted that most wings of *sonorana* and *dugesi,* southern members of the *aestiva* group, indicate "all manner of intergradation" between the alleged pointed-winged *aestiva* group from more northern localities and the rounded-winged *petechia* group. Pyle (1997) represented wing shape in a wing formula, with all taxa in the *aestiva* group having p9 = p8 = p7 > p6 and the formula for *oraria* in the *erithachorides* group and *gundlachi* in the *petechia* group as p9 < p8 = p7 = p6. Although Wiedenfeld (1991) found that northern birds (*aestiva*) have pointed wings, the shape of the wing tended to be more round with decreasing latitude, thereby supporting Aldrich (1942).

Measurements reported by Wiedenfeld (1991) are summarized statistics, not means and ranges. His results indicate a sharp break in tarsus length between the *petechia* and *aestiva groups.* Tarsus length from specimens (Browning 1994) of *gundlachi (petechia* group), including those from Florida, average longer than those of the *aestiva* group from other southeastern Atlantic states (Ridgway 1902). Luther and Greenberg (2014) did not cite Wiedenfeld (1991), but both sources agree that members of the *aestiva* group have shorter tarsi than taxa breeding in mangroves. Means for tarsi, which were used in combination with other measurements by Luther and Greenberg (2014), are inexplicably smaller than means from other sources (e.g., Ridgway 1902, Wetmore 1984, Browning 1994:38, Curson et al. 1994). Differences in mean between other sources and Luther and Greenberg (2014) involve less than 5 mm, but such an amount might, but not always, might be significant when comparing such small birds. Nevertheless, members of the *aestiva* group have shorter tarsi than tarsi of most members of the *petechia* and *erithachorides* groups (Ridgway 1902, Wetmore et al. 1984, Wiedenfeld 1991, Luther and Greenberg 2014).

According to Luther and Greenberg (2014), bills of male and female Yellow Warblers living in mangroves have greater surface area and are longer, wider, and deeper than those occupying other habitats. The authors also observed sexual dimorphism in bill measurements of birds from non-mangrove habitats, but not in birds from other habitats. Unfortunately, Luther and Greenberg (2014) included *dugesi,* an interior subspecies of the *aestiva* group) with taxa occupying mangroves. The trend (Luther and Greenberg 2014) of sexual dimorphism in bills was reversed in the southwestern form (*sonorana*), where females reportedly have bills smaller than males compared to northern and eastern samples of females, with bills averaging larger than males. Luther and Greenberg (2014) reported that sexual dimorphism of the non-mangrove taxa ranged from -3 to 6% and found no sexual dimorphism in birds representing the *petechia* and *erithachorides* groups.

Molt

Curson et al. (1994) stated that *aestiva* group juveniles have a post juvenile molt (June to Aug) and a partial pre-breeding molt (Feb to Apr); in the *erithachorides* group, juveniles molt "directly into an adult-type plumage." Curson et al. (1994) stated that adult female *petechia* lack ventral streaking, that *aestiva* females are streaked, and does not remark about streaks in females of the *erithachorides* group. However, streaking occurs in adult females of the *erithachorides* and *petechia* groups (Browning 1994, Dunn and Garrett 1997). There is little to no helpful information concerning molt of taxa in the *petechia* and *erithachorides* groups.

Vocalizations

Ficken and Ficken (1965:370-371) mentioned qualitative vocal differences between members of the three taxonomic groups of Yellow Warbler. Curson (2017) stated that the tropical taxa are vocally more similar to each other than to the northern migrant *aestiva* group. Northern *aestiva* sing an accented ending song and an unaccented ending song, whereas, according to Morse (1966), two taxa of Mangrove Warbler (*bryanti* and *xanthotera*) and one taxa of Golden Warbler (*rufivertex*) sing only unaccented ending songs. Morse (1966) concluded: “The apparent ability of some North American Yellow Warblers to obtain mates without singing Accented Ending Songs suggests that song itself would not be a completely effective isolation mechanism between these individuals and the tropical ones, should the breeding ranges of the populations ever come together. Thus, the absence of the species-distinct song in this case could not be considered an adequate reason in itself for splitting these forms.” Spector (*in* Lowther et al. 1999) considered that “preliminary data suggests Golden [*petechia* group] and Mangrove [*erithachorides* group] warbler songs are similar to those of migrant Yellow Warblers [*aestiva*], although the song types are quite different [emphasis mine].” The song of birds from Costa Rica and Belize (*erithachorides* group) were stated (Lowther et al. 1999) as “recognizable as this species [Yellow Warbler *sensu* AOU 1998], but subjectively different from North American populations (NKK)” and songs of some Mangrove Warblers are longer and lower in frequency. Mennill (2001), using univariate and multivariate analyses, confirmed that song of northeastern birds representing the *aestiva* group and *bryanti* of S Mexico representing the *erithachorides* group differ quantitatively, that the song of Mangrove Warblers is in a lower frequency than songs of *aestiva*, and that the “length, frequency and syllabic characteristics, and principal components analysis separates their [*bryanti* and nominate *aestiva*] songs entirely.” Songs of mangrove warblers of subspecies *bryanti* contain significantly more syllables and more types of syllables than migrant *aestiva* from northeastern samples (Mennill 2001). Mennill (2001) wrote “Mangrove Warbler songs are significantly longer, have a longer terminal syllable, and the point of maximum amplitude comes significantly later in the song.” Also discussed (Mennill 2001 and references therein) is the fact that Mangrove Warblers sing all year and that both males and females defend their territory whereas migrant *aestiva* do not sing during winter and females do not take part in territorial defense.

Chestnut-sided Warblers (*Setophaga pensylvanica)* are reported (Dunn and Garrett 1997) countersinging with territorial northern (*aestiva* group) Yellow Warblers. Qualitatively, some field ornithologists confuse songs of *S. pensylvanica* and northern Yellow Warblers (Kroodsma et al. 1983). Probably the birds “subjectively” know what they are hearing (MRB).

Call notes are used by Yellow Warblers for winter territorial defense (Neudorf and Tarof 1998). Mangroves Warblers have a soft *chup* note whereas migrant *aestiva* have a *chip* note (Morton and Stutchbury 2012).

Behavior – territoriality, breeding duration

Defense of wintering *aestiva* territories includes aggressively chasing several species of warblers (especially Magnolia), flycatchers and vireos in Mexico (Greenberg and Ortiz 1994) and Guatemala (Greenberg et al. 1996). A Golden Warbler chased a migrant Yellow Warbler from its territory in Barbados (McNair et al. 1999). Resident *castaneiceps* of the *erithachorides* group from eastern Baja California Sur responded in spring and fall positively toward "generic" Yellow Warbler song (Whitmore et al. 2000).

Members of the *petechia* and *erithachorides* groups build nests in mangroves and place nests 2 to 12 feet above the water, whereas members of the *aestiva* group build in a variety of foliage and place nests 3 to 6 feet above the ground (Dunn and Garrett 1997). Compared to migrant *aestiva*, Mangrove Warblers have "longer breeding seasons, smaller clutch sizes, longer incubation and nestling periods, lower nesting success, higher rates of nest depredation, higher annual adult survival rates" (Salgado-Ortiz et al. 2008, Salgado-Ortiz et al. 2009). Small clutch sizes and long incubation periods are listed in Table 5 of Salgado-Ortiz et al. (2008), including those for representatives of the *petechia* group (e.g., from Key Largo and Puerto Rico) and the *erithachorides* group (e.g., from Galapagos). Larger clutch size and short incubation periods are listed (Salgado-Ortiz et al. 2008) for several populations of the temperate *aestiva* group. These differences for representatives in the *aestiva* group and the tropical groups (*petechia* and *erithachorides* groups) do not appear to be related to latitude. Duration of incubation and size of clutch for *gundlachi* (*petechia* group), also documented in Florida by Prather and Cruz (1995) but not listed by Salgado-Ortiz et al. (2008), are similar to those reported elsewhere for the *petechia* and *erithachorides* groups. Traits of life histories of Mangrove Warblers are more similar to those of tropical species than to those of migrant Yellow Warblers (Salgado-Ortiz et al. 2008). Although northern *aestiva* normally have one brood (Lowther et al. 1999), two broods occur in southern California (Unitt 2004) and, owing to the length of the nesting period, more than one brood is suggested for warblers from Arizona (Wise-Gervais in Corman and Wise-Gervais 2005). Note that the taxon breeding in Arizona is *sonorana*, whereas individuals in southern California belong to taxa not included in the alleged (Boulet and Gibbs 2006) southern lineage (see below under genetics).

Competitive interactions on the breeding grounds between different species of parulids are not uncommon (Martin and Martin 2001).

When parasitized by Brown-headed Cowbirds (*Molothrus ater*), northern warblers belonging to the *aestiva* group reject cowbird eggs by either burying them in their nests or abandoning their nests (e.g., Guigueno and Sealy 2010). Parasitized members of the *petechia* group reject eggs of Shiny Cowbirds (*M. bonariensis*) in Puerto Rico and St. Lucia (Post et al. 1990, Wiley 2012). Martinique, home to the chestnut-hooded *ruficapilla* that resembles members in the *erithachorides* group, is mentioned by Post et al (1990) as having populations of cowbirds and warblers, but they do not explicitly state there was actual parasitism. They wrote: “The Yellow Warbler, which made up 18% of this population [on Martinique], was the only species that is frequently reported parasitized by the Shiny Cowbird.” Reading somewhat between the lines, it is possible that Yellow Warblers were parasitized on Martinique, but additional data is not provided. Members of the *erithachorides* group are parasitized (Salgado-Ortiz et al. 2008) by *M. bonariensi*s. Egg burial in the *erithachorides* group is not reported.

Genetics

Klein and Brown (1994) performed a phylogenetic analysis using mtDNA of all named taxa within the *S. petechia* complex and reported that a major split divides the migratory *aestiva* group from the remaining taxa. Their migratory *aestiva* group from North America did contain a single sample of one member (*castaneiceps* from Baja California) belonging to the sedentary *erithachorides* group. Klein and Brown (1994) wrote: “It is also surprising that NA-G [=Baja California sample, aka subspecies *castaneiceps* of *erithachorides* group] is placed in the middle of the North American group, making the migratory populations paraphyletic. However, because monophyly of the haplotypes from migratory populations (with NA-G as the sister taxon to them) requires only one extra step, support for this paraphyletic arrangement is not strong.” Klein and Brown (1994:1923), noting that some authors recognize the migratory group as a species, posited that the group “should perhaps still be so classified...” Lovette and Bermingham's (1999:1631) Fig. 1 of phylogenetic relations of 24 *Setophaga* indicated divergences within the Yellow Warbler that are greater or as great as shown for several non-controversial species in the genus. They reported mtDNA divergence of the three groups of Yellow Warbler ranged from 0.9 to 2.4% and, concerning the *Setophaga* species *townsendi*, *occidentalis*, *virens*, *nigrescens* and *graciae,* Lovette and Bermington (1999:1634) wrote: “interspecific distances within these shallow clades (range 0.9-1.7%) are consistent with speciation in the Middle Pleistocene era under the assumption of a 2%Myr^{-1} rate of divergence.” Klein et al. (2004) also demonstrated mtDNA divergences between samples of Yellow Warbler from Michigan and the Dominican Republic that are similar to those found between other species of warbler.

Milot et al. (2001) sequenced eastern and western lineages in the *aestiva* group and reported deep mtDNA differences between the *aestiva* group and clustered members in the *petechia* and *erithachorides* groups. Boulet and Gibbs (2006) reported three lineages representing the *aestiva* group including overlapping eastern and western lineages, which clustered together and apart from a southern lineage that included southwestern members of the *aestiva* group and resident individuals in the *petechia* (four samples) and *erithachorides* (eight samples) groups. Basal haplotypes from residents from Mexico, Venezuela and Puerto Rico “tended to be nested with the southern haplotypes (Fig. 1)” and there was no support for taxonomically recognizing the *petechia* and *erithachorides* groups as species (Boulet and Gibbs 2006).

A third lineage, the southern lineage, was reported by Boulet and Gibbs (2006). The authors found migrant eastern and western lineages of the *aestiva* group (Boulet and Gibbs 2006) to be more similar to each other, but to differ from the southern lineage.

Although not so stated by Boulet and Gibbs (2006), their southern lineage seems possibly analogous to a similar lineage reported by Klein and Brown (1994). Boulet and Gibbs (2006) did not sample birds from Baja California and did not cite Klein and Brown (1994). A Bayesian tree (Boulet and Gibbs 2006) demonstrated 50 to 75% support in posterior probabilities between the southwestern sample and their sample of Mangrove Warblers. Although the southern lineage included samples from resident Yellow Warblers in Boulet and Gibbs (2006), Boulet et al. (2006) did not include resident birds in the southern lineage in their study of migration. Boulet et al. (2006:32-33) stated that the southern birds they sampled "probably belong to *D. p. sonorana*," a more rounded-winged bird that may perform a leap-frog migration. The southern lineage (Boulet et al. 2006) included samples from southwestern states (NV, UT, NM, AZ), but *sonorana* does not breed in Utah (Browning 1994). Birds representing *sonorana* in the Lower Colorado River Valley are rare and regular winter residents (Rosenberg et al. 1991). More germane to this proposal, Boulet et al. (2006) recognized that migrant birds from the *aestiva* group are genetically and morphologically distinct from the two resident tropical groups.

Additional genetic studies have focused on tropical taxa, especially birds from the Galapagos Islands. These studies also impact the systematics of the Yellow Warbler complex. For example, North American birds (eastern and western Canada), according to Browne et al. (2008) have a mean sequence divergence of 6.7% from the Galápagos populations (subspecies *aureala*). Note, however, that Browne et al. (2008) use of the sample from Pennsylvania is problematic: the Pennsylvania birds even differ considerably in percent mtDNA sequence divergence from samples from eastern and western Canada. Further, the Browne et al. (2008) study did not cite Boulet and Gibbs (2006) or Boulet et al. (2006), studies that used larger samples with few to no samples from Pennsylvania. Nonetheless, Browne et al. (2010:12) summarized: "The mtDNA data (Browne et al. 2008) indicated significant genetic divergence between Galapagos *D*. *petechia* and populations from the American continents. The rusty crown of Galapagos *D. p. aureola* clearly separates it from other *D. petechia* populations. Our results show that Galapagos *D. p. aureola* are also significantly larger than at least some North American populations in culmen length, culmen width and body mass."

Chaves et al. (2012) demonstrated genetic separation of *aureola* of the Galapagos from the older *aestiva* group and closer relationship between members of the *petechia* and *erithachorides* groups. A Bayesian phylogeny (Chaves et al. 2012; see tree below) based on mtDNA sequences grouped *aureola* with *xanthotera* from Costa Rica and *erithachorides* from Panama, both of which belong to the *erithachorides* group. Chaves et al. (2012) wrote: "Analyses also strongly supported the monophyly and sister relationship between '*aestiva*' from North America and '*erithachorides*' + '*petechia*', but the phylogenetic relationship between these last two groups was not supported (Fig. 1)."

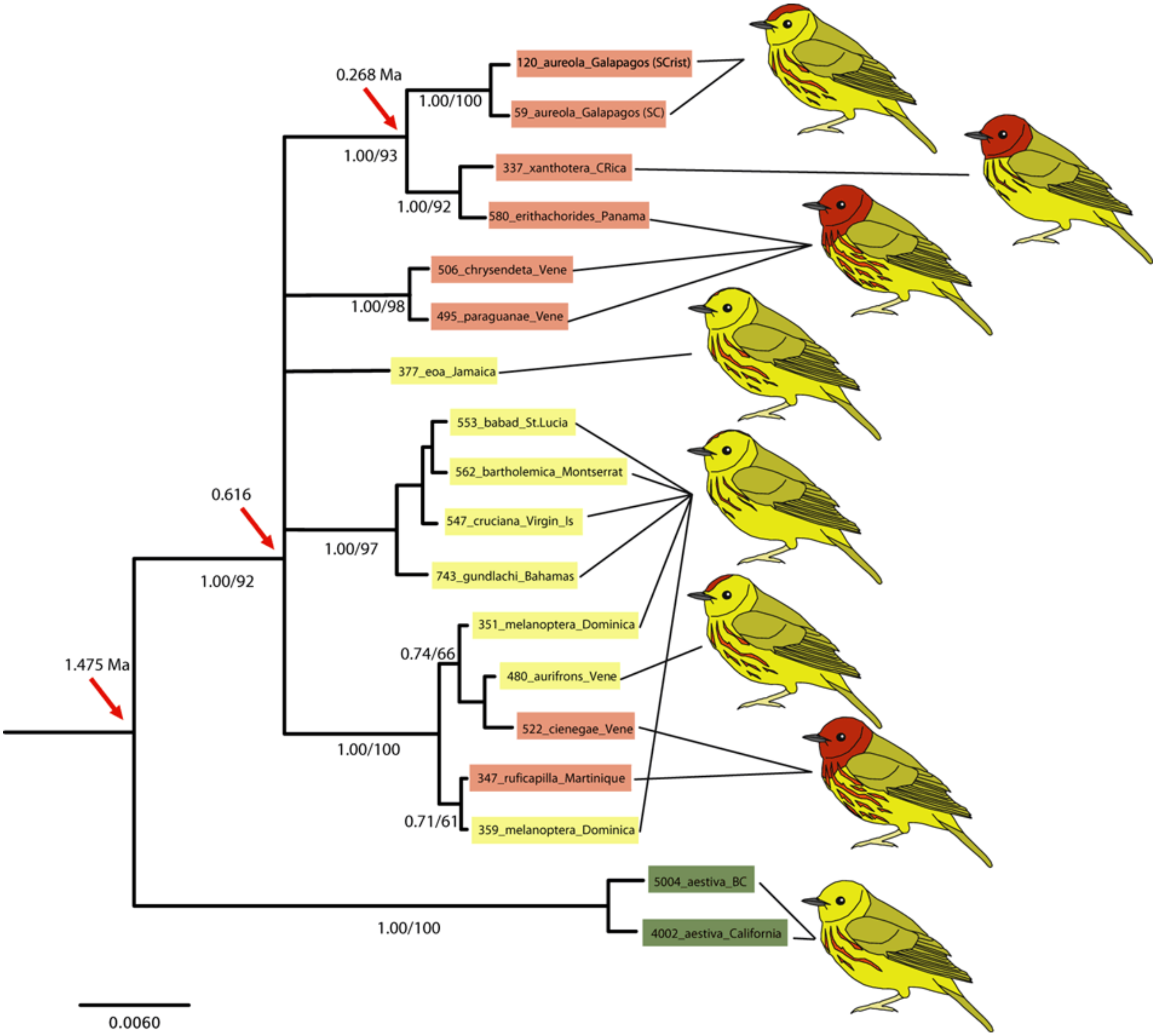

Fig. 1. Bayesian phylogeny of yellow warblers based on combined mtDNA sequences (ATPase, ND2, control region). Estimated posterior probabilities and ML bootstrap support are shown at each node, respectively. Red arrows depict divergence time estimates from a Bayesian Inference chronogram using BEAST based on ATPase and ND2. Colored terminal taxa correspond to taxonomic groups based on Browning (1994) and Olson (1980): green, North American migrant populations ‘*aestiva*’; yellow, West Indian golden ‘*petechia*’; red, Central and northern South America mangrove ‘*erithachorides*’. Plumage pattern corresponds to each subspecies based on plumage descriptions (Olson, 1980; Browning, 1994; Klein & Brown, 1994) and from museum skin collections. From Chaves et al. (2012).

Chaves et al. (2012) wrote: “Mean sequence divergence between the Galápagos Archipelago population and Yellow Warblers from the three Latin America sites [Venezuela, Costa Rica, Puerto Rico] was 3.7%, and between the Galápagos population and the three North American sites was 6.7%. Mean sequence divergence between the six Galápagos subpopulations and the six continental sites was 5.2 %. When the Galápagos population was compared to Yellow Warblers from all other sites, the smallest sequence divergence, 3.4%, was for Venezuela, and the largest value, 6.9%, was for western Canada.” Their results also show lack of phenotypic and genotypic concordance between two (*ruficapilla* and *cienagae*) members of the *erithachorides* group that cluster with three members of the *petechia* group. Specimen localities indicate that Chaves et al. (2012) sampled birds representing the *aestiva* group from British Columbia to New Brunswick, California, Oregon, Ohio, Michigan (none from Pennsylvania), and Hidalgo, Mexico. Samples representing the *petechia* and *erithachorides* groups included about half the recognized (Browning 1994, Lowther et al. 1999) taxa.

Are the two resident groups (*petechia* and *erithachorides* groups) separate species?

In addition to information concerning the systematics of the *petechia* and *erithachorides* groups mentioned above, additional consideration follows. Compared with the distinctiveness of the *aestiva* group, the taxonomic relationships of resident birds (the *petechia* and *erithachorides* group) as one, two, or more species, is less clear. Systematics of the resident groups, summarized here, demonstrated that species recognition is complicated. Hilty (2003), without providing details, listed *erithachorides* as a separate species. Haplotypes in populations from Dominica and Guadeloupe (Klein and Brown 1994) are considered by Ricklefs and Bermingham (2007) as representing a lineage [=*erithachorides*] from South America and a younger lineage [=*petechia*] from the Greater Antilles. This might explain *ruficapilla* from Martinique, which is by coloration similar to members of the *erithachorides* group (Browning 1994) and more similar in size to members of the *petechia* group (Wiedenfeld 1991). Lowther et al. (1999) placed *ruficapilla* among the *erithachorides* group. However, *ruficapilla* and *cienagae*, the latter traditionally considered part of the *erithachorides* group (Browning 1994, Lowther 1999), clustered with members of the *petechia* group (Chaves et al. 2012). The taxon *aureola*, considered to form a fourth group in the Yellow Warbler complex (Curson 2017), differs genetically and morphologically from the *aestiva* group and the two (*petechia* and *erithachorides*) tropical groups. However, following the dating of Chaves et al (2012), colonization by *aureola* on the Galapagos was considered by Sari and Bollmer (2018) as too recent for speciation. Divergence dates for *aureola* estimated by Carmi et al. (2016) were much greater than those reported by Chaves et al. (2012). No additional information concerning *aureola* was included in Carmi et al. (2016).

Contact

Known breeding ranges of members of the three (or four) groups of Yellow Warbler are many miles apart and are thus not in contact (AOU 1998). Cozumel Island, Mexico, is the historical range of *rufivertex*, a subspecies from the *petechia* group (e.g., Browning

1994), and is the exception to lack of contact. A population from the *erithachorides* group was documented on Cozumel Island by MacKinnon-Haskins and Dzib-Chay (2017), who believed the occurrence of a *erithachorides* representative is very recent (probably not earlier than 2008). Birds from the *erithachorides* group, including pairs, were restricted to mangroves, whereas birds (*rufivertex*) from the *petechia* group occurred in mixed vegetation, and both were found where mangroves and dune vegetation co-occur (MacKinnon-Haskins and Dzib-Chay 2017). Genetic studies on Cozumel Island are planned (MacKinnon-Haskins, pers. comm.). Dunn and Garrett (1997) also mentioned sightings of mangrove warblers on Isla Socorro and Revillagigedo, western Mexico.

In a footnote referencing the word “Cozumel” in the account on *bryanti,* Hellmayr (1935) wrote, "This locality is clearly erroneous. The specimen has no original label, but merely a printed tag "E Mus. O.S. & F.D.G. Cozumel I., Yucatan, 1885. G.F. Gaumer," the date being left in blank. It formed part of the collection upon which Salvin's (1888) account of the "Birds of the islands of the coast of Yucatan and the Bay of Honduras" was based. In this paper (p. 248) the author expressly states that "*D. petechia* [=*D. p. rufivertex*] is found in Cozumel Island, to the exclusion of *D. bryanti* and the migratory *D. aestiva*." Gaumer’s specimen localities or lack thereof have been questioned (e.g., Paynter 1955), and Parkes (1970:92) wrote: “Many [=not all, MRB, see, e.g., Parkes and Phillips 1967] of Gaumer’s specimens labeled “Cozumel Island” represent mainland species not otherwise known from the island...” Perhaps *bryanti,* a Mangrove Warbler and a larger bird (see Ridgway 1902), did historically occur on Cozumel, but was subsequently displaced by *rufivertex,* a Golden Warbler.

Recommendations:

The taxonomy of the so-called Yellow Warbler should reflect current findings. The northern migratory populations representing the *aestiva* group differ from the southern populations in the *petechia* and *erithachorides* groups by plumage color and pattern, genetic structure, behavior, and vocalizations. I recommend that *aestiva* be returned to specific status, similar to taxonomic decisions concerning Canada Goose (e.g., *Branta canadensis* and *B. hutchinsii*) and other taxa that were associated with the caveat that “Additional analysis may result in further splitting” (Banks et al. 2004). In that regard, further studies of the remaining “yellow” warblers may result in recognition of additional species.

Several species known as “yellow” warblers exist in the Eastern Hemisphere. Therefore, the northern taxa (formerly in the *aestiva* group) should be known as American Yellow Warbler, an English name already in use (e.g., Gill and Donsker 2017) for the northern birds. Warblers formerly in the *petechia* and *erithachorides* groups, as well as the taxon *aureola*, should be known as Mangrove Warblers because the involved taxa breed mostly in mangroves. As an alternative to Mangrove Warbler, the aforementioned warblers could be known as Tropical Yellow Warbler. In the instance of a split, in no instance should any of the taxa be known by the name Yellow Warbler. By historical definition, the moniker Yellow Warbler defines both northern and tropical birds and continued use for a different entity would serve only to confuse. Likewise, the name Mangrove Warbler should not be used for the tropical taxa because Mangrove Warbler historically refers to only one group of the tropical taxa. In the unlikely event of not recognizing more than one species, that is, if the status quo is maintained, I recommend that the English name for the complex be changed from Yellow Warbler to American Yellow Warbler. Doing so better defines the subject warbler as occurring mostly in the Americas and distinguishes them from other worldwide yellow warblers.

Effect on check-list:

If this proposal is accepted, all information (habitat and distribution) under the *aestiva* group in the Check-list (1998) would be moved under the species heading "*Setophaga aestiva* (Gmelin). American Yellow Warbler." All information (habitat and distribution) under the *petechia* and *erithachorides* groups in the Check-list (1998) would be moved under the heading "*Setophaga petechia* (Linnaeus). Tropical Yellow Warbler." The notes section under the species Tropical Yellow Warbler should be modified to read: Taxa within groups *S. petechia* (Linnaeus, 1766) [Golden Warbler] and *S. erithachorides* (Baird, 1858) [Mangrove Warbler] may constitute more than one species (xxx refs). Under American Yellow Warbler, a note might simply read: "See under Tropical Yellow Warbler." American Yellow Warblers (*Setophaga aestiva*) should precede Mangrove Warbler (*S. petechia*). Chestnut-sided Warbler (*S. pensylvanica*) would follow *S. petechia*.

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2018-C-3 N&MA Classification Committee pp. 373-420

Revise the classification and linear sequence of the Tyrannoidea

Background:

In recent years several studies have been published on the systematics of the Tyrannoidea complex and the Tyrannidae more narrowly (including Ohlson et al. 2008, Rheindt et al. 2008, Tello et al. 2009, and Ohlson et al. 2013). These studies reached conclusions that are mostly consistent amongst themselves but that show a number of discrepancies with the taxonomy and sequence of the AOS North American checklist.

The current AOS classification of Tyrannidae is based mostly on various morphology-based publications of Traylor and Lanyon from the late 20th century. Each of the recent studies consists of analyses of molecular data. Tello et al. (2009, see tree below) has nearly complete genus sampling, and Ohlson et al. (2013, see tree below) employed the most molecular data. Both papers present taxonomic recommendations along with phylogenetic hypotheses.

New information:

Although the checklist has been responsive to some of these studies in the creation of the Tityridae and by resolving most of the *incertae sedis* genera (2010, 2011 supplements), its treatment of Tyrannidae is unchanged from the 7th edition (AOU 1998). These recent studies, employing new data and analytic tools, support many elements of the preceding taxonomic work. A small number of revisions to the checklist could accommodate their new insights.

Recommendations:

Below I offer a series of recommendations to bring the checklist into closer accord with what I believe are currently the most strongly supported phylogenetic hypotheses. For sequence of genera within subfamilies, I have followed Ohlson et al. (2013). AOS sequence of higher ranked taxa is maintained in most cases. Appropriate taxonomic rank for various clades is controversial, and to address this I offer some alternatives (I believe that they can be voted on simultaneously). For reasons for adopting family rank in this complex for small and aberrant taxa see Ohlson et al. 2013[1] (p. 21) and Tello et al. 2008[2] (p. 448). Approval of 1b and 2-10 would result in a taxonomy which matches the recommendations of Ohlson et al. (2013).

1. ***Onychorhynchus*, *Terenotriccus* and *Myiobius*** are currently placed in Tyrannidae (Fluvicolinae). All studies found these three genera to form a clade and that their closest relatives are outside of the Tyrannidae.

1a) **Place these genera, along with *Oxyruncus*, into Tityridae.** These genera were found to be sister to *Oxyruncus*, and that resulting group sister to the genera that compose the current Tityridae (Tello et al. 2009, Ohlson et al. 2013). Merging them into Tityridae is the recommendation of Tello et al. (p. 441).

or

1b) If 1a fails, **place these three genera in a new family, Onychorhynchidae** Tello, Moyle, Marchese & Cracraft 2009**, following Tityridae in sequence**, with *Oxyruncus* remaining in Oxyruncidae. This is the recommendation of Ohlson et al. (p. 20).

and

1c) If 1a fails and 1b passes, **move Oxyruncidae to follow Onychorhynchidae,** to reflect its sister relationship to Onychorhynchinae.

2. **Change the composition and sequence of the group which includes *Myiornis* through *Tolmomyias*** (the AOS's current Platyrinchinae) **by adding *Mionectes, Leptopogon, Phylloscartes* and *Pseudotriccus* (all moved from Elaeniinae)**. All studies found a strongly supported clade (the Pipromorphinae of Ohlson et al. 2008 and Rheindt et al. 2008, and the Rhynchocyclidae of Tello et al. 2009 and Ohlson et al. 2013) which includes the following genera from our region:

Mionectes
Leptopogon
Pseudotriccus
Phylloscartes
Rhynchocyclus
Tolmomyias
Cnipodectes
Myiornis
Lophotriccus
Oncostoma
Poecilotriccus
Todirostrum
(Note that *Platyrinchus* is not a member of this clade.)

3. **Place Platyrinchinae at the beginning of Tyrannidae.** *Platyrinchus* and the genera above (plus some South American genera, and also *Piprites*) were found to be sister to the remaining tyrannid subfamilies (Elaeniinae, Hirundineinae, Fluvicolinae and Tyranninae), and thus should be placed first (Ohlson et al. 2008, Tello et al. 2009, Ohlson et al. 2013).

4. **Restrict Platyrinchinae to *Platyrinchus*** (see Ohlson et al. 2013, pages 20, 30 - note that the South American genera *Neopipo* and *Calyptura* would also be included in this taxon). **Adopt the name Rhynchocyclinae** Bonaparte 1854 **for the remainder of the subfamily (**listed as *Mionectes* through *Todirostrum* in 2 above)**, which would follow Platyrinchinae** (see Tello et al. 2009, pp. 447-8)**.** All authors found this to be an early divergence (see Ohlson et al. 2013, fig. 4). Note that the authors advocating separation of *Platyrinchus* from the *Rhynchocyclus* group also advocate 5, below.

5. If 4 passes, **raise the rank of both Platyrinchinae and Rhynchocyclinae to family level** (becoming Platyrinchidae and Rhynchocyclidae)**, and place them prior to Tyrannidae.** The divergences between these two groups, and to the remaining Tyrannidae, were found to be very deep (see Ohlson et al. 2013, fig. 4). For family rank see Ohlson et al. 2013 and Tello et al. 2009, pp. 446-8 (although the latter paper does not offer a taxonomic treatment for *Platyrinchus*).

(Note - the findings of Ohlson et al. 2013 and Tello et al. 2009 also appear to justify an alternative treatment in which the family Platyrinchidae would include subfamilies Rhynchocylinae and Pipritinae, in addition to Platyrhinchinae. Because neither author recommended this treatment, I decline to propose it here.)

6. **Merge the monotypic genus *Nesotriccus* into *Phaeomyias*, as species *Phaeomyias ridgwayi.*** Zucker et al. (2016) found this species nested within *Phaeomyias murina*. The authors propose splitting *P. murina* into three species. Setting aside the problem of species limits, maintenance of a monotypic genus for this taxon is incompatible with their results.

7. **Change the composition of Elaeniinae** by subtracting *Mionectes, Leptopogon, Phylloscartes* and *Pseudotriccus* (see 2), and **by:**

7a) **moving *Sublegatus* to Fluvicolinae.** See Tello et al. 2009, Ohlson et al. 2008, Rheindt et al. 2008, and Ohlson et al. 2013, all of which place *Sublegatus* within Fluvicolinae**.**

7b) **Adopt the following sequence for Elaeniinae:**

Zimmerius
Ornithion
Camptostoma
Elaenia
Myiopagis
Tyrannulus
Capsiempis
Phyllomyias

Phaeomyias (including *Nesotriccus*)
Serpophaga

8. **Change the composition of Fluvicolinae** by subtracting *Onychorhynchus*, *Terenotriccus* and *Myiobius* from Tyrannidae (see 1), adding *Sublegatus* from Elaeniinae (see 7a), and **by:**

8a) **moving *Machetornis* to Tyranninae.** See Ohlson et al. 2008, Tello et al. 2009, and Ohlson et al. 2013, which placed *Machetornis* within Tyranninae.

8b) **Adopt the following sequence for Fluvicolinae:**

Colonia
Myiophobus fasciatus
Sublegatus
Pyrocephalus
Fluvicola
Aphanotriccus (not sampled in these studies, but sister to *Lathrotriccus* - see Cicero & Johnson 2002)
Lathrotriccus
Mitrephanes
Sayornis
Empidonax
Contopus
Xenotriccus (not sampled in these studies)

9. **For Tyranninae, with *Machetornis* added** (see 8a)**, adopt following sequence:**

Attila
Legatus
Deltarhynchus (position uncertain - see Ohlson et al. 2008, page 327)
Rhytipterna
Sirystes
Myiarchus
Pitangus
Machetornis
Megarhynchus
Myiodynastes
Myiozetetes
Conopias (not sampled in these studies)
Empidonomus
Tyrannus

10. **Change the treatment of *Piprites* by creating a new family Pipritidae** Ohlson, Irestedt, Ericson & Fjeldså 2013**, including only *Piprites***, **and placing it at the beginning of the Tyrannoidea** (before Platyrinchidae if 5 passes)**.** Family rank is the recommendation of Ohlson et al. 2013 (p. 29).

Piprites is currently *incertae sedis* within the Tyrannioid superfamily [note that the list of species on the AOS website http://checklist.aou.org/taxa/ appears to be in error in listing *Piprites* as subfamily *incertae sedis* within the Tyrannidae. The 7th edition (page 416) lists it as one of "seven genera as a group, *incertae sedis*, to acknowledge that they are unequivocally tyrannoid but of uncertain affinity within the superfamily." The 52nd supplement (page 605) removed the other six genera from this category, but did not transfer the position of Piprites - "After the account for *Tyrannus savana*, change the heading Genera ***INCERTAE SEDIS*** to Genus ***INCERTAE SEDIS*** . . . The genus *Piprites* has presented a taxonomic challenge for more than a century. Recent genetic studies indicate that it is either the sister group to the Tyrannidae (Ericson et al. 2006, Ohlson et al. 2008) or an isolated lineage near the base of the Tyrannidae (Tello et al. 2009)." *Piprites* is not addressed in any subsequent supplement.]

This taxon was found to be sister to the *Platyrinchus* and *Rhynchocyclus* clades, and its divergence with those groups and with the remainder of Tyrannidae appears quite old (Ohlson et al. 2013).

[1] Ohlson et al. 2013 (page 21) - "The last decades has seen a drastic overturning of the conventional view of avian systematic relationships, making it ever harder to adhere to a “traditional view” in classification. There has been a general tendency in the past to merge small and aberrant taxa into larger families, both as a means of maintaining a simple classification, and because of a lack of a strict phylogenetic approach and data that could guide the taxonomic decisions in a transparent way. Even with a more well founded phylogenetic basis there has often been a reluctance to erect new family-level taxa, especially for small clades of “problematic” affinities. This has left a number of distinctive and comparatively old clades hanging in a taxonomic limbo, awaiting additional data that would allow inclusion in a well-established family. It has also led to a neglect of patterns that might determine the fate of clades, whether they fail to diversify, become relictual or undergo great phylogenetic expansion. Treating these small clades as family level taxa highlights their distinctiveness, deep evolutionary history and their hitherto unresolved relationships.

The phylogenetic tree of the NWS, like that of almost every other large radiation, contains lineages of widely different species richness and several taxa whose systematic positions have been contentious. Large amounts of data have been employed to clarify the phylogenetic positions of various debated taxa of NWS. We argue that the failure so far in associating these taxa, such as Platyrinchidae, *Oxyruncus* and *Xenops* unambiguously with any larger clades cannot be explained solely by insufficient data. Instead, these taxa stand out as isolated clades that were part of rapid successions of divergence events along with clades that today are rich in species (Fig. 4). These small clades are distinctive and internally coherent in terms of ecology and morphology and they have independent evolutionary histories that are likely to span at least 20 million years. Keeping these taxa in taxonomic limbo (i.e. as *incertae sedis*) becomes harder to justify and here we opt to highlight their isolation, distinctiveness and old age by treating them as family level taxa. Looking at avian systematics as a whole, there are many small families that most ornithologists would never consider subsuming into more inclusive taxonomic entities, even if their sister relationships are unambiguous (consider merging the Shoebill into Pelecanidae, for example). Concerning the New World suboscines, we would in several cases argue in favour of recognizing these clades as family level taxa, despite the “relatively little content” of monotypic families (Tello *et al.* 2009). These taxa are all “isolated” early offshoots from the larger radiations, and they are in most cases ecologically and morphologically distinctive from their closest living relatives. In our view, a treatment as family level taxa is more informative about the nature and phylogenetic position of taxa like *Oxyruncus, Xenops*, *Tachuris* and *Platyrinchus* compared to subsuming them into the larger groups from which they diverged early in their histories."

[2] Tello et al. 2008 (page 448) "In our effort to construct a phylogenetic classificatory framework with some long-term stability, we are eliminating the traditional, expanded concept of the Tyrannidae because nodes along the spine of that clade are nearly all ambiguously supported, including the basal node. In contrast, our concepts of Tyrannidae and Rhynchocyclidae are strongly monophyletic and thus likely to provide long-term stability for their names. We note, however, that if *Platyrhynchus* (sic) is confirmed to be the sister to the rhynchocyclines, then the family-group name would revert to Platyrhynchidae."

Literature Cited:

Cicero, C. and N. K. Johnson. 2002. Phylogeny and character evolution in the *Empidonax* group of Tyrant Flycatchers (Aves: Tyrannidae): a test of W. E. Lanyon's hypothesis using mtDNA sequences. Molecular Phylogenetics and Evolution 22: 289-302.

Ohlson, J., J. Fjeldså, and P. G. P. Ericson. 2008. Tyrant flycatchers coming out in the open: Phylogeny and ecological radiation of Tyrannidae (Aves, Passeriformes). Zoologica Scripta 37: 315-335.

Ohlson, J. I., M. Irestedt, P. G. P. Ericson, and J. Fjeldså. 2013. Phylogeny and classification of the New World suboscines (Aves, Passeriformes). Zootaxa 3613: 1-35.

Rheindt, F. E., J. A. Norman, and L. Christidis. 2008. Phylogenetic relationships of tyrant-flycatchers (Aves: Tyrannidae), with an emphasis on the elaeniine assemblage. Molecular Phylogenetics and Evolution 46: 88-101.

Tello, J. G., R. G. Moyle, D. J. Marchese, and J. Cracraft. 2009. Phylogeny and phylogenetic classification of the tyrant flycatchers, cotingas, manakins, and their allies (Aves: Tyrannides). Cladistics 25: 1-39.

Zucker, M. R., et al. 2016. The Mouse-colored Tyrannulet (*Phaeomyias murina*) is a species complex that includes the Cocos Flycatcher (*Nesotriccus ridgwayi*), an island form that underwent a population bottleneck. Molecular Phylogenetics and Evolution 101: 294-302.

Submitted by: Dale Dyer, Field Associate, Department of Ornithology
American Museum of Natural History, New York

Date of Proposal: 6 February 2017

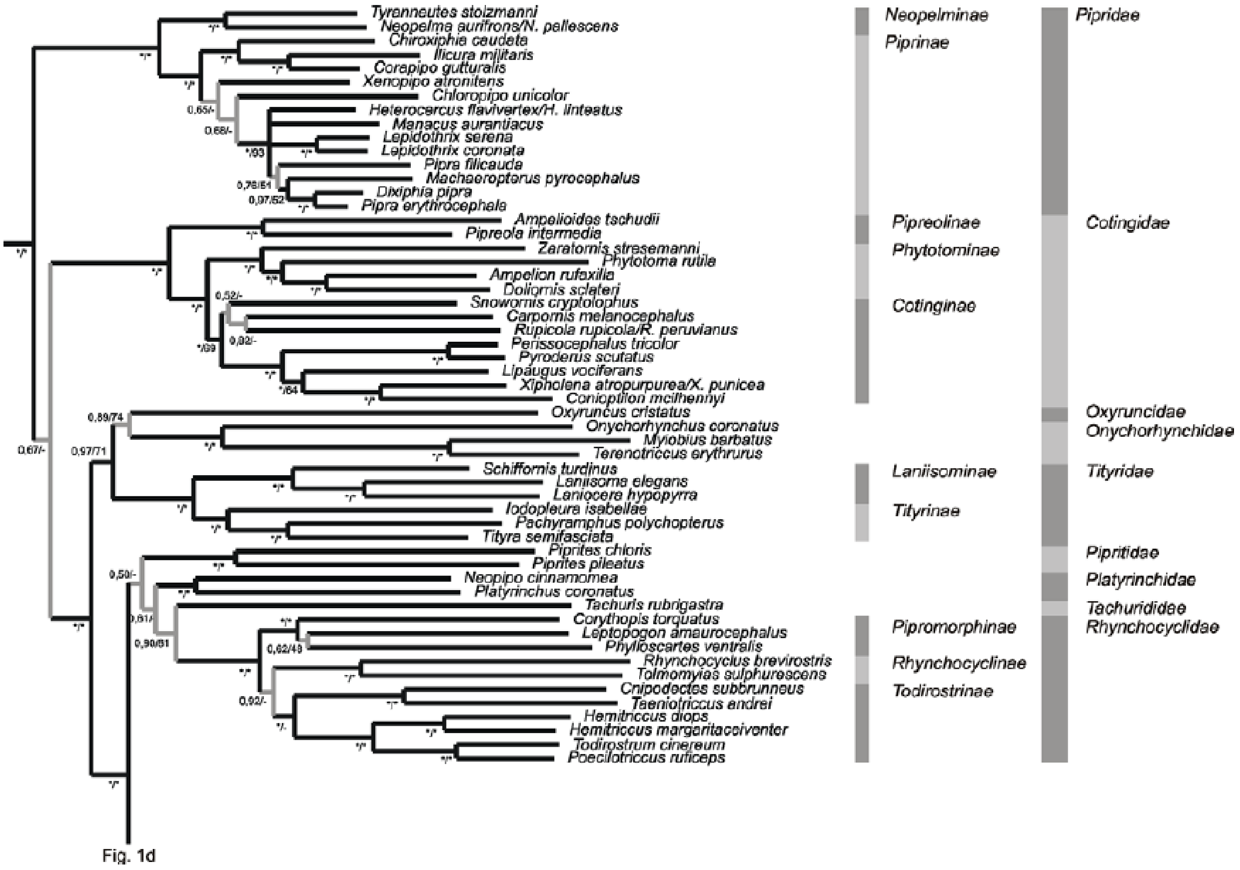

Fig. 1c from Ohlson et al. (2013). Bayesian consensus tree of part of Tyrannida (Pipridae, Cotingidae, and Oxyruncidae through Rhynchocyclidae) based on sequences of three nuclear introns (G3P intron 11, Myoglobin intron 2, and ODC introns 6 and 7) and the nuclear protein coding RAG-1 and RAG-2 genes. Branch support values are PP/ML. An asterisk denotes a PP value ≥ 0.98 and an ML value ≥ 90.This tree joins to Fig. 1d below as indicated at the bottom of the tree.

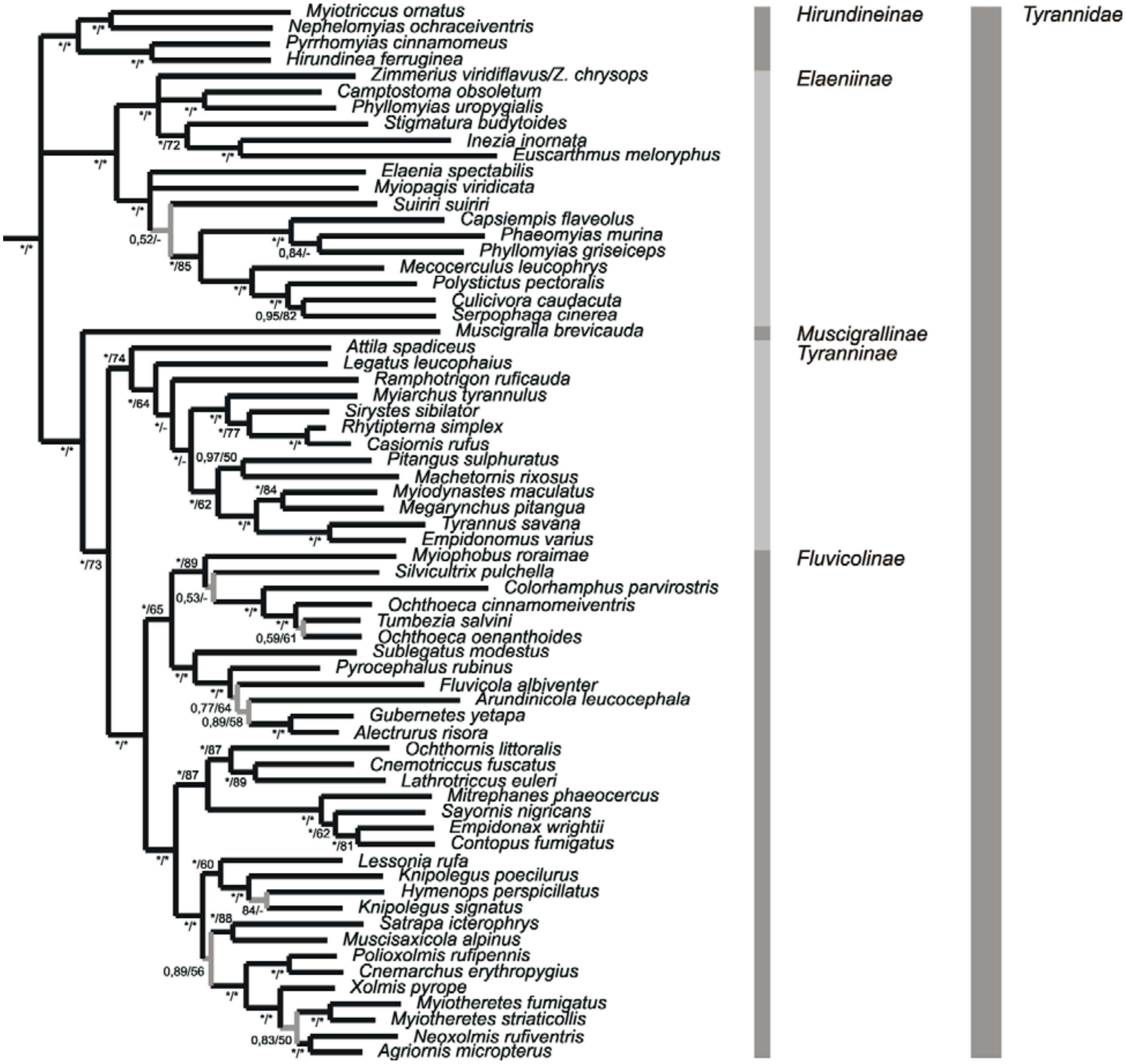

Fig. 1d from Ohlson et al. (2013), continued from Fig. 1c above. Bayesian consensus tree of part of Tyrannida (Tyrannidae) based on sequences of three nuclear introns (G3P intron 11, Myoglobin intron 2, and ODC introns 6 and 7) and the nuclear protein coding RAG-1 and RAG-2 genes. Branch support values are PP/ML. An asterisk denotes a PP value ≥ 0.98 and an ML value ≥ 90.


B
BP/ML/MP/BS
Tyrannidae (cont.)
Elaeniinae
Fluvicolinae
Tyranninae
Former Pipridae
E
D
F
Agriornis micropterus
Neoxolmis rufiventris
Myiotheretes fumigatus
Myiotheretes striaticollis
Xolmis pyrope
Cnemarchus erythropygius
Polioxolmis rufipennis
Muscisaxicola albilora
Satrapa icterophrys
Hymenops perspicillatus
Knipolegus signatus
Knipolegus poecilurus
Lessonia rufa
Cnemotriccus fuscatus
Lathrotriccus euleri
Ochthornis littoralis
Contopus fumigatus
Empidonax wrightii
Sayornis nigricans
Mitrephanes phaeocercus
Alectrurus risorus
Alectrurus tricolor
Gubernetes yetapa
Arundinicola leucocephala
Fluvicola pica
Pyrocephalus rubinus
Sublegatus modestus
"Myiophobus" roraimae
Ochthoeca cinnamomeiventris
Ochthoeca oenanthoides
Tumbezia salvini
Colorhamphus parvirostris
Silvicultrix pulchella
Colonia colonus
Attila spadiceus
Attila citriniventris
Legatus leucophaius
Rhamphotrigon ruficauda
Casiornis rufus
Rhytipterna simplex
Sirystes sibilator
Myiarchus swainsoni
Myiarchus tyrannulus
Empidonomus varius
Griseotyrannus aurantioatrocristatus
Tyrannus savana
Tyrannus vociferans
Myiozetetes luteiventris
Myiozetetes cayanensis
Megarynchus pitangua
Tyranniopsis sulphurea
Myiodynastes maculatus
Myiodynastes luteiventris
Machetornis rixosus
Philohydor lictor
Pitangus sulphuratus
Muscigralla brevicauda
Anairetes flavirostris
Uromyias agraphia
Culicivora caudacuta
Polystictus pectoralis
Pseudocolopteryx flaviventris
Serpophaga cinerea
Mecocerculus leucophrys
Pseudelaenia leucospodia
Capsiempis flaveolus
Phaeomyias murina
Phyllomyias griseiceps
Elaenia albiceps
Elaenia spectabilis
Myiopagis flavivertex_1
Myiopagis flavivertex_2
Myiopagis viridicata
Myiopagis gaimardii
Suiriri suiriri
Camptostoma obsoletum
Ornithion inerme
Tyranniscus uropygialis
Tyranniscus burmeisteri
Euscarthmus meloryphus
Euscarthmus rufomarginatus
Inezia inornata
Inezia subflava
Stigmatura budytoides
Zimmerius viridiflavus
Zimmerius villissimus
Hirundinea ferruginea
Pyrrhomyias cinnamomeus
"Myiophobus" ochraceiventris
Myiotriccus ornatus
Neopipo cinnamomea
0.005 substitutions/site
Xolmiini
Contopini
Fluvicolini
Fluvicolinae
Myiarchini
Tyrannini
Tyranninae
Elaeniini
Euscarthmini
Elaeniinae
Hirundineinae
Tyrannidae
Tyrannoidea (part)

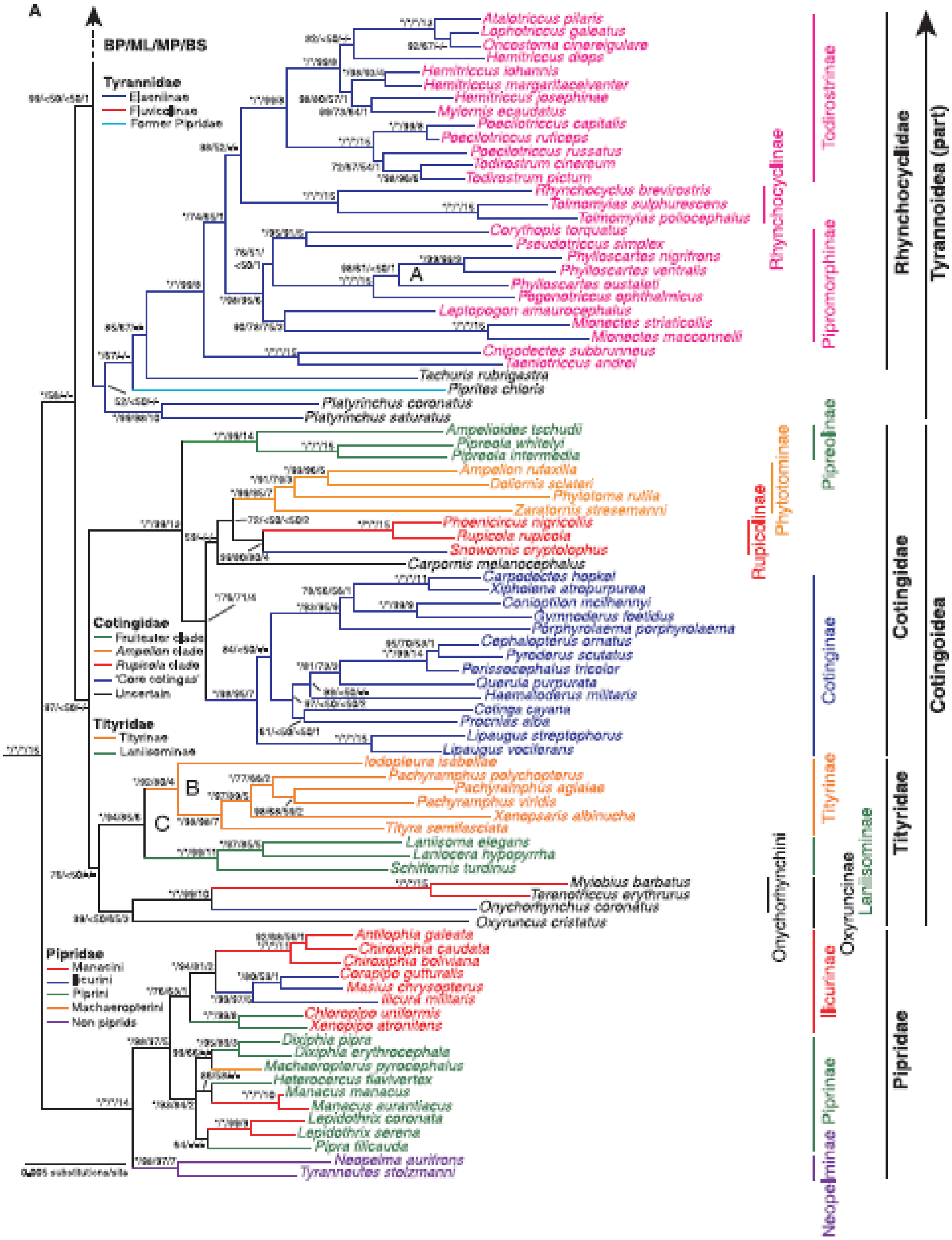

Fig. 3. Phylogenetic analyses of the Tyrannides: tree represents the majority-rule consensus obtained from Bayesian analysis of the combined RAG-1 and RAG-2 data using a complex partitioned model setting containing six partitions (see text). Numbers above branches indicate values of support: (i) posterior probabilities; (ii) maximum likelihood bootstraps; (iii) maximum parsimony bootstraps; (iv) Bremer decay indexes. Nodes that received 100% posterior probability or bootstrap support are represented by an asterisk. Nodes that were not recovered by a particular method are represented by “–”. Colored taxa names and lines represent previous taxonomic placement based on Fitzpatrick, 2004a (Tyrannidae); Ohlson et al., 2007 (Cotingidae); Barber and Rice, 2007 (Tityridae); Prum, 1992 (Pipridae). Letters represent relevant nodes discussed in the text.

Figure 1: Bayesian tree from Tello et al. (2009).

Amendment to Proposal 2018-C-3

The ongoing suboscine species-level UCE project was mentioned in the comments on Proposal 2018-C-3. Mike Harvey sent me the preliminary species-level tree and I took a close look at it yesterday, in part to try to place the genera not sequenced by Tello et al. (2009) or Ohlson et al. (2013) and in part to compare the UCE tree with the Tello/Ohlson trees. I have the following suggestions as to how to proceed with the various issues addressed by Proposal 2018-C-3. Although obviously we should not make changes based on the unpublished and preliminary species-level UCE tree, I think it would be wise to use the tree to help identify those proposed changes that will likely be stable vs those that will not be, and to make only those changes that will likely be stable. In general, the deep structure of the species-level tree closely matches that of the Tello and Ohlson trees, but the increased sampling at the genus and species level (and below in some cases) produces quite different topologies within subfamilies, not to mention revealing a fair degree of non-monophyly of genera. Therefore, changes to the linear sequences within subfamilies are not recommended at this time, but most other changes are recommended (including a few that the proposal overlooked):

1. ***Onychorhynchus*, *Terenotriccus* and *Myiobius:* 1a) Place these genera, along with *Oxyruncus*, into Tityridae; 1b)** If 1a fails, **place these three genera in a new family, Onychorhynchidae, following Tityridae in sequence**, with *Oxyruncus* remaining in Oxyruncidae; **1c)** If 1a fails and 1b passes, **move Oxyruncidae to follow Onychorhynchidae –** The Tello tree has very weak support (0.78 pp, <50% ML bootstrap) for the node uniting these three genera with Tityridae and Oxyruncidae. Support for this node in the Ohlson tree is moderate (0.97, 71%), and this node does not appear in the preliminary UCE tree (Oxyruncidae/Onychorhynchidae and Tityridae are successive sisters to the Tyrannidae). I would therefore not recommend option 1a, placing all these taxa in the Tityridae, but would instead suggest approving option 1b, which would leave Tityridae and Oxyruncidae as families and create the new family Onychorhynchidae (note that Oxyruncidae, with only one species, should precede Onychorhynchidae, *contra* the proposal). Another option would be to merge Oxyruncidae and Onychorhynchidae in the same family, but I don't recommend it because these may not be sister groups.

Moreover, these families, whether united or not, are sisters to the Tyrannidae (by themselves in the Ohlson and preliminary UCE trees, with Cotingidae in Tello) and should precede it under our guidelines for linear sequencing (because there are many more species in the Tyrannidae). Likewise, the Cotingidae and Pipridae are successive sisters to all other tyrannoids (in the Ohlson and preliminary UCE trees) and should precede the Tyrannidae and Tityridae in this sequence: Pipridae, Cotingidae, Tityridae, Oxyruncidae, Onychorhynchidae, Tyrannidae (the Tello topology would produce the slight variation Pipridae, Tityridae, Oxyruncidae, Onychorhynchidae, Cotingidae, Tyrannidae). I would recommend that we make these moves.

2. **Change the composition and sequence of the group which includes *Myiornis* through *Tolmomyias*** (the AOS's current Platyrinchinae) **by adding *Mionectes, Leptopogon, Phylloscartes* and *Pseudotriccus* (all moved from Elaeniinae) –** I

would recommend moving these taxa but not yet changing the linear sequence. Generic limits in this group will likely undergo major revisions, as will the linear sequence.

3. **Place Platyrinchinae at the beginning of Tyrannidae –** Approve: placement of Platyrinchinae before Elaeniinae (and Rhynchocyclinae – see below) is supported by all trees.

4. **Restrict Platyrinchinae to *Platyrinchus*** (see Ohlson et al. 2013, pages 20, 30 - note that the South American genera *Neopipo* and *Calyptura* would also be included in this taxon). **Adopt the name Rhynchocyclinae** Bonaparte 1854 **for the remainder of the subfamily (**listed as *Mionectes* through *Todirostrum* in 2 above)**, which would follow Platyrinchinae –** Approve: this is supported by all trees.

5. If 4 passes, **raise the rank of both Platyrinchinae and Rhynchocyclinae to family level** (becoming Platyrinchidae and Rhynchocyclidae)**, and place them prior to Tyrannidae –** Reject for now, until the complete topology with branch lengths can be assessed.

6. **Merge the monotypic genus *Nesotriccus* into *Phaeomyias*, as species *Phaeomyias ridgwayi* –** As was pointed out in the comments on this subproposal , it has a different basis than the rest, which principally use the trees in Tello et al. (2009) and Ohlson et al. (2013). This subproposal is based on Zucker et al. (2016), whose Fig. 1 clearly shows the paraphyly using mtDNA:

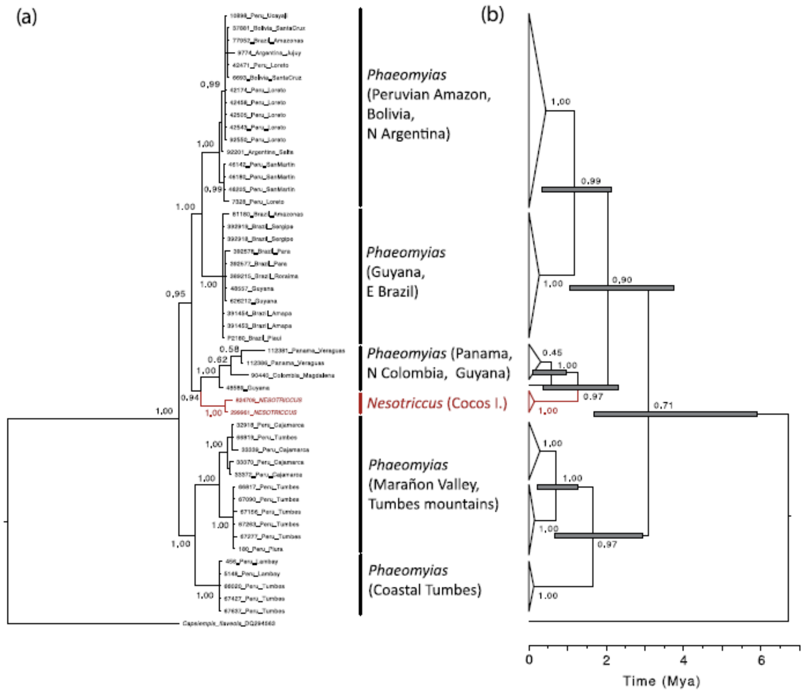

Fig. 1. Bayesian phylogenies of relationships within *Phaeomyias*, including *Nesotriccus* (marked in red), from ND2 data using MrBayes (a) and BEAST (b). Values at nodes represent support based on posterior probability. The BEAST tree is time-calibrated and gray bars indicate the limits of the high posterior density estimate of divergence time at each node. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

UCEs for only two individuals of *Phaeomyias* and one of *Nesotriccus* had been sequenced at the time, but according to the authors these were sufficient for "UCE and exon data [to] confirm that the close relationship between *Nesotriccus* and *Phaeomyias* is not a result of horizontal gene flow or deep coalescence of mitochondrial alleles." In the preliminary UCE tree, which samples 5 individuals of *Phaeomyias*, *Nesotriccus* nests within *Phaeomyias*, as in the mtDNA tree. Paraphyly of *Phaemoyias* with respect to *Nesotriccus* is a very clear result, so I'm slightly in favor of approving this subproposal (the question of species limits of *P. murina* should be considered first by SACC). As was noted in the comments, *Nesotriccus* has priority over *Phaeomyias*.

7. **Change the composition of Elaeniinae** by subtracting *Mionectes, Leptopogon, Phylloscartes* and *Pseudotriccus* (see 2), and **by:** 7a) **Moving *Sublegatus* to Fluvicolinae, and** 7b) **Adopting the following sequence for Elaeniinae –** I would recommend moving *Sublegatus*, which is supported by all the trees, but not yet changing our linear sequence. Although the sequence derived from the preliminary UCE tree is virtually identical to what's in the proposal, I think it best to be consistent and not fiddle with the lower level linear sequence of one subfamily when not addressing the rest.

8. **Change the composition of Fluvicolinae** by subtracting *Onychorhynchus*, *Terenotriccus* and *Myiobius* from Tyrannidae (see 1), adding *Sublegatus* from Elaeniinae (see 7a), and **by:** 8a) **Moving *Machetornis* to Tyranninae, and** 8b) **Adopting the following sequence for Fluvicolinae –** I would recommend moving *Machetornis*, which is supported by all the trees, but not yet changing our linear sequence. The sequence derived from the preliminary UCE tree is quite different to what's in the proposal or what I modified it to based on the Tello tree.

9. **For Tyranninae, with *Machetornis* added** (see 8a)**, adopt following sequence –** No. The sequence derived from the preliminary UCE tree is quite different to what's in the proposal or what I modified it to based on the Tello tree. However, we should move Tyranninae to precede Fluvicolinae: these subfamilies are sisters in all trees and Fluvicolinae has many more species.

10. **Change the treatment of *Piprites* by creating a new family Pipritidae, including only *Piprites*, and placing it at the beginning of the Tyrannoidea (before Platyrinchinae or -idae) –** Yes to moving *Piprites* to the beginning of the Tyrannidae (not Tyrannoidea – see above under #1), preceding Platyrichinae, but as a subfamily until the complete topology with branch lengths can be assessed.

If approved as suggested above, this would result in the following linear sequence of families:

Pipridae
Cotingidae
Tityridae
Oxyruncidae

Onychorhynchidae
Tyrannidae

and of subfamilies within Tyrannidae:

Pipritinae
Platyrinchinae
Rhynchocyclinae
Elaeniinae
Tyranninae
Fluvicolinae

We would transfer genera between groups as appropriate but would not otherwise change the linear sequences of genera or species. We would transfer *Phaeomyias murina* to *Nesotriccus*.

I think this would put the suboscines in good order and ready for the changes that will result from the species-level phylogeny, when it appears.

Terry Chesser, 29 March 2018

Split Cory's Shearwater (*Calonectris diomedea*) into two species

Effect on NACC:

This proposal would add a new species (Scopoli's Shearwater) to the checklist and would result in changes to the distributional statement of Cory’s Shearwater. In addition, the scientific name *C. diomedea* would be transferred from Cory’s Shearwater to Scopoli’s Shearwater, and the species with the English name Cory’s Shearwater would henceforth be known as *C. borealis*.

Background:

Cory's Shearwater was formerly a polytypic species comprised of three well-recognized subspecies: *diomedea*, *borealis*, and *edwardsii,* the latter now generally treated as a separate species. Both *borealis*, which breeds mainly on eastern North Atlantic islands, and *diomedea,* which breeds mainly on islands in the Mediterranean Sea, occur regularly off our Atlantic coast north to the southern mid-Atlantic region, but nearly all records off New England and Atlantic Canada are of *borealis*. Both taxa occur and have been documented in the Gulf of Mexico. The few documented sightings from the northeast Pacific all involve *borealis.* The Cape Verde Shearwater (*C. edwardsii*) occurs in North America as an accidental with perhaps as few as a single solid record.

New Information:

The arguments below largely follow Sangster et al. (2012), who split these species on the BOU list. The split has now been recognized by most global references (e.g., Dickinson and Remsen 2013, del Hoyo and Collar 2014, and Gill and Donsker 2017).

This split is well-supported under traditional BSC arguments. Although the two taxa have largely separate breeding ranges, *borealis* breeds in at least two colonies in the Mediterranean Sea (Almeria; Gomez-Diaz et al. 2006; Chafarinas Islands, Navarro et al. 2009) and a few pairs of *diomedea* have bred along the Bay of Biscay coast in western France (Mays et al. 2006). The Chafarinas Islands hold 10,000 breeding pairs of Cory's Shearwaters, and based on morphometric data from 82 birds (*diomedea* is smaller) 78% are *diomedea* and 22% are *borealis* (Gomez-Diaz et al. 2009, Navarro et al. 2009). The two forms on the Chafarinas Islands differ in feeding ecology and foraging areas during both chick-rearing and winter periods (Navarro et al. 2009). Subspecies *borealis* has been reported elsewhere in the breeding colonies of nominate *diomedea,* but these records are thought to have involved non-breeding birds (Lo Valvo and Massa 1998, Thibault and Bretagnolle 1998, Martinez-Abrain et al. 2002). Despite intensive monitoring of Atlantic and Mediterranean breeding colonies, reports of interbreeding between *borealis* and *diomedea* are limited to one record of a mixed pair raising a young bird in the Collumbretes Islands in 2011 (Martinez-Abrain et al. 2002), two birds showing phenotypic characters of one taxon and a genotype of the other taxon (Gomez-Dias et al. 2009), and one record of a male *borealis* or hybrid breeding with a female with characters intermediate, or atypical, of *diomedea* on Gireglia Island in 1993, 1994, and 1995 (Thibault and Bretagnolle 1998).

Duet calls of *borealis* have three brief syllables whereas most (97%-98%) of *diomedea* have two longer syllables (Bretagnolle and Lequette 1990, Thibault and Bretagnolle 1998, see also Robb et al. 2008). Of about 400 male calls of *borealis* and *diomedea* examined, none was detected from one taxon showing call characters of the other (Thibault and Bretagnolle 1998). Playback studies have documented differential responses to recordings of *borealis* and *diomedea* (Bretagnolle and Lequette 1990). *Calonectris edwardsii* gives calls like nominate *diomedea* but higher pitched.

Studies of the mitochondrial DNA of *borealis* and *diomedea,* as well as former conspecific *edwardsi* (Gomez-Diaz et al. 2006, 2009), indicated that individuals of these three taxa each formed monophyletic groups, and that *diomedea* and *edwardsi* were more closely related to each other than either was to *borealis*, as might have been expected from the vocalizations.

More recently, Zidat et al. (2017) analyzed nuclear genotypic (microsatellites) and phenotypic (chemical profiles of uropygial secretions) characters of birds of both species from the Chafarinas Islands, where they are sympatric, and compared their results to data from birds from Selvagem (*borealis* only) and Linosa (*diomedea* only). They found (a) that there were consistent interspecific differences in both the genotypic and phenotypic characters, and (b) that these differences were maintained in sympatry. They concluded that *borealis* and *diomedea* are reproductively isolated, supporting their separation as distinct species. Moreover, the chemical differences observed between species may well serve as cues to mate choice and species recognition.

Recommendation:

We recommend that *borealis* be split from *diomedea*, which would result in two monotypic species. Given the slightly overlapping ranges and almost no evidence of hybridization on islands where both occur (assortative mating), the evidence for the split is compelling and is buttressed by differences in vocalizations and other characters.

English names: Although AOS guidelines indicate that we should create English names for both daughter species that differ from that of the parental species (Cory’s Shearwater), unless there are compelling reasons not to, we suggest retaining the English names already in general usage for these Old World species. Cory's Shearwater would be retained for the eastern Atlantic breeding species, although the scientific name of Cory’s would change to *borealis*, and the name Scopoli's Shearwater would be used for the Mediterranean Sea breeding nominate *diomedea.*

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Submitted by: Jon Dunn and Terry Chesser

Date of Proposal: 7 February 2018

Split *Puffinus boydi* from Audubon's Shearwater *P. lherminieri*

Background:

The small shearwaters of the widespread *Puffinus assimilis-lherminieri* groups have received a bewildering variety of taxonomic treatments, ranging from all taxa being lumped in a single highly polytypic species to the now-general acceptance of several species. In Chesser et al. (2013), we recognized the small shearwater *baroli* of the eastern Atlantic islands (except the Cape Verde Islands) as specifically distinct based on its much closer genetic relationship to Audubon's Shearwater *P. lherminieri* than to *P. assimilis*, despite its much smaller size and plumage and soft part colors that are more similar to the latter. (For further information on that split and the group as a whole, see Proposal 2013-A-6, "Split Barolo Shearwater", http://checklist.aou.org/assets/proposals/PDF/2013-A.pdf).

The proposal on *baroli* left open the issue of whether the geographically adjacent Cape Verde taxon *boydi*, which differs strikingly from *baroli* in morphology and to some extent in vocalizations, should be considered a subspecies of *baroli* (as by Sangster et al. 2005), or of *lherminieri* (the status quo solution we tentatively accepted; Bannerman 1914, Murphy 1927, AOU 1998, Onley and Scofield 2007), or whether it should be treated as a monotypic species, *Puffinus boydi* (Hazevoet 1997, Clements 2009, Gill and Donsker 2018). Hazevoet (1997) advocated a PSC approach. The rationale given for the treatment of *boydi* as a monotypic species in Clements (2009) was that *boydi* and *baroli* differ significantly from each other in appearance and subtly on vocalizations at colonies, but whether *boydi* should be considered a subspecies of *lherminieri* was not explicitly addressed. The split by the IOC of *boydi* as a monotypic species (Gill and Donsker 2018) followed Robb et al. (2008) and Olson (2010); the BOU is also cited by the IOC, although Sangster et al. (2005) considered *boydi* a subspecies of *baroli*. A fourth recent treatment is followed by the Howard and Moore checklist (Dickinson and Remsen 2013) and the HBW (del Hoyo and Collar 2014, Carboneras et al. 2018), who consider both *boydi* and *baroli* as subspecies of *lherminieri*.

New information:

Evaluation of the taxonomic distinctness of *boydi* requires consideration of the paleontological record. A very small shearwater from Bermuda was named *Puffinus parvus* Shufeldt, 1916, but then synonymized with *lherminieri* by Wetmore (1931, 1962). Olson (2004) reexamined material of *P. parvus* and concluded that Wetmore's synonymy was erroneous, as *parvus* is "indeed a much smaller species" than *lherminieri*. The humerus of *parvus* shown on Fig. 1 of Olson (2004; https://www.biodiversitylibrary.org/page/35516036#page/607/mode/1up) is about 92% the length of that shown for *lherminieri* from Bermuda. Olson (2010) provided mensural comparisons of *parvus*, *boydi*, and Bermuda and other West Indian *lherminieri*, which showed the former two to be very similar in size, while these populations of *lherminieri* are much larger, virtually without overlap. Because *boydi* (=*parvus*) long existed on Bermuda until extirpated by human impacts, and only subsequent to its disappearance was Bermuda colonized briefly by *lherminieri*, Olson (2010) suggested that the two may have been in competition for some 400,000 years and that *lherminieri* was only able to successfully colonize Bermuda after the extirpation of *boydi*.

Robb et al. (2008) provided extensive illustrations, photos, and recordings of both *boydi* and *baroli*. These resources make it clear that *boydi* is much darker overall than *baroli*, with dark instead of white longer undertail coverts, darker underwing primary bases, and darker neck and face sides. The tail of *boydi* is also relatively and obviously longer than that of *baroli*. According to Howell et al. (2012), *boydi* differs from *lherminieri* in being slightly smaller with a shorter bill, but consistent plumage differences are unknown.

Based on the recordings and sonograms in Robb et al. (2008), flight vocalizations of the two eastern Atlantic populations are broadly similar but sound distinctly different; *boydi* gives fewer exhaled notes spread over a longer period, and inhaled notes that sound lower-pitched than for *baroli*. This book cited an unpublished analysis showing significant differences in vocalizations (Sangster, in litt., in Robb et al. 2008). Few recordings are publicly available for *P. lherminieri*, but a 1968 recording from Bermuda (ML 42998), sounds very similar to *boydi* (but much less similar to *baroli*) to me.

There is agreement among phylogenetic studies that *baroli*, *boydi*, and *lherminieri* are all genetically close (e.g., Austin et al. 2004, Martínez-Gómez et al. 2015, Kawakami et al. 2018; see tree below), the latter showing *baroli* and *boydi* to be sister taxa, with the clade they form being sister to *lherminieri* (including *loyemilleri* of Panamanian islets, synonymized in del Hoyo and Collar 2014).

So, key points relevant here are:

1) The synonymization of *P. parvus* of Bermuda with *boydi* (Olson 2010) is based on their similar size and apparent lack of qualitative osteological differences, but different *Puffinus* species in the same clade and same size class could well be osteologically indistinguishable anyway. (I think a lot of perfectly good modern taxa would be wrongly synonymized on osteological criteria alone.) Add to this the probability that the evidently sedentary or at most short-distance migrant *boydi* would occur both in the Cape Verde Islands and Bermuda, but nowhere else, and the case seems less than solid. If *boydi* and *parvus* are different taxa, despite being inseparable osteologically, then 2) is irrelevant to species status of the former. Perhaps ancient DNA analyses will help answer this eventually.

2) The contention that the presence of *boydi* (=*parvus*) on Bermuda kept *lherminieri* from colonizing due to competition until the extirpation of *boydi* there (Olson 2010) seems speculative, especially given the size difference demonstrated between *boydi* and Caribbean *lherminieri*, which might allow coexistence instead. The lack of evidence for *lherminieri* on Bermuda contemporaneously with *parvus* could be due to other factors. And one may question whether the later

Part of Fig. 2 of Kawakami et al. (2018)

colonization by a larger replacement taxon (*lherminieri* in this case) rules out the two taxa being conspecific. Thus, although Olson (2010) makes an intriguing case for species status of *boydi*, this is based on the assumptions, first that the synonymy of *parvus* into *boydi* is correct, and second, that *lherminieri* was in fact competitively excluded from Bermuda by *parvus*.

3) If either of the above are considered to require further evidence, then we are left with having to decide the status of *boydi* based only on its considerably smaller size than *lherminieri*, to which it is genetically, vocally, and morphologically otherwise so similar.

Effect on AOS-CLC:

Although *boydi* has evidently not been recorded in the AOS-CLC area, it is included implicitly in the breeding range statement for *Puffinus lherminieri* ("in the eastern Atlantic on the Cape Verde Islands"; AOU 1998: 21). Thus, even if we vote to treat it as a separate species, the impact on the AOS-CLC area is minimal; we would need to remove the statement about occurrence of *lherminieri* in Cape Verde, and should have a Note indicating why *boydi* is now considered a separate species. Because *boydi* is considered to be largely resident around the Cape Verde Islands, with reports of presumed short-distance migrants from western Senegal (Hazevoet 1997), it is not a likely migrant or vagrant to the AOS area. Substantiation of vagrant records would require extraordinarily good documentation.

Recommendation:

Given the vocal, morphological, and genetic similarities between *boydi* and *lherminieri*, as well as the uncertainties of the case for species status on the basis of past competitive exclusion, **I recommend** continuing to treat *boydi* as a subspecies of *lherminieri* (option 1 below). It is possible that analysis of large sample sizes of homologous vocalizations might show consistent differences between *boydi* and *lherminieri*, but this seems unlikely, and such data do not yet exist. Treatment of *boydi* as a subspecies of *lherminieri* but retaining *baroli* as a distinct species creates a paraphyletic species (*boydi* + *lherminieri*) according to recent phylogenies (Austin et al. 2004, Kawakami et al. 2018), but even so, in my opinion *baroli* should be retained as a separate species due to its distinctive morphology and vocalizations. (Most committee members already voted for the split of *baroli*, so I did not make relumping it an option.)

Option 1: Continue to consider *boydi* a subspecies of *lherminieri*. In the event this passes, no common name change is needed, nor is any modification to the range statement for *lherminieri*. However, a statement in the Notes section acknowledging that *boydi* is sometimes treated as specifically distinct would be needed.

Option 2: Consider *boydi* a subspecies of *baroli*. In the event this passes, then we would have to consider common name options again, Macaronesian Shearwater being the obvious choice due to familiarity and geographical appropriateness, although Barolo Shearwater has also been used even when *boydi* is included (e.g., Neves et al. 2012). We would also have to modify the account of *baroli* accordingly.

Option 3: Consider *boydi* to be a distinct, monotypic species. In the event this passes, then the name Boyd's Shearwater has received wide usage in recent years and should be adopted. Although Hazevoet (1997) used Cape Verde Little Shearwater, this overlong name does not reflect phylogenetic relationships, interferes with the name of the Little Shearwater, and is unfamiliar. If Option 3 passes, the Cape Verde Islands need to be removed from the range statement of *lherminieri* and a Note added to that species account about the split.

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

Date of proposal: 10 February 2018

(a) Split extralimital *Gracula indica* from Hill Myna *G. religiosa* and (b) move *G. religiosa* from the main list to Appendix 1

Background:

The Hill Myna *Gracula religiosa* is included on the Checklist on the basis of a population (of the *religiosa* group) introduced and established in Puerto Rico. In the 7th edition (AOU 1998), we noted that escaped birds had also been present in Hawaii and Florida for many years but that populations had not become established there.

New Information:

Taxonomy:
It has become increasingly common for the Hill Myna to be split into two species, Common Hill Myna *Gracula religiosa* and Southern Hill Myna *Gracula indica*, in recent years. The two species were split as long ago as Feare and Craig (1998), the 5th edition of Clements (Clements 2000), Rasmussen and Anderton (2005), the original IOC list (Gill and Wright 2006), and the Handbook of Birds of the World chapter on starlings (Craig and Feare 2009). Of major global references, only Dickinson and Christidis (2014) treat the Hill Myna in the traditional sense. Unfortunately, most of the references cited above offered no rationale for the split, the exception being Rasmussen and Anderton (2005), who based their treatment on "[s]everal consistent morphological differences, and even more striking vocal differences, [which] confirm the previously suggested treatment of this [*G. indica*] as a species distinct from *G. religiosa*." HBW Alive mentions the "long, narrow serrated wattle on hindcrown", "much shorter wings", "proportionately finer bill", and "striking vocal differences" as characters that distinguish *indica* from *religiosa* (Craig and Feare 2018).

Two other taxa sometimes considered part of *G. religiosa*, and endemic to small islands off western Sumatra, are also now sometimes treated as species: *G. robusta* (Nias Hill Myna), separated due to its much larger size, and *G. enganensis* (Enggano Hill Myna). Our distributional statement is not specific enough to determine whether these taxa were included in our *G. religiosa sensu lato*, but these are borderline splits that will not be reflected in the Checklist and I don't know that we need to deal with them one way or another.

The English names used in AOU 1998 were Eastern Hill-Myna for the *religiosa* group and Southern Hill-Myna for the *indica* group. However, the English names in general usage, as indicated above, are Common Hill Myna for *G. religiosa sensu stricto* and Southern Hill Myna for *G. indica*.

Status:
The species account for Hill Myna on the CD-ROM in Oberle (2010) includes the following statement: “There are no recent sightings on Puerto Rico’s north and east coasts where it had been breeding.” Following up on this, I have learned that there has been only one report of this species in Puerto Rico in the past 15 years and that it has likely not bred on the island in decades (M. Oberle, in litt., drawing on the additional knowledge of Sergio Colón, the eBird editor for Puerto Rico, and the unpublished Puerto Rico Breeding Bird Atlas).

Other than suspected escapes, the Hill Myna has not been reported since the 1990s in Hawaii, where it is on the state’s non-established species list (Pyle and Pyle 2017; E. VanderWerf, in litt.; H. D. Pratt, in litt.). In Florida, the species has declined and is listed on Appendix B of the state list as a non-established exotic (Greenlaw et al. 2014); because its population has decreased sharply, it seems unlikely that it will be proposed to be established in Florida in the near future (A. W. Kratter, in litt.).

Recommendation:

I recommend (a) that we split *G. indica* from *G. religios*a, following most current references, and that we adopt the English names in general usage, which given our naming conventions would be Common Hill-Myna for *G. religiosa* (and Southern Hill-Myna for extralimital species *G. indica*); and **(b)** that we transfer Common Hill-Myna to Appendix 1 under Category 3: An introduced population [that] has failed to become established. This would necessitate a new species account in paragraph form.

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Submitted by: Terry Chesser

Date of Proposal: 13 February 2018

Split *Melozone occipitalis* from White-eared Ground-Sparrow *M. leucotis*

Background:

Melozone leucotis is distributed from southern Mexico to central Costa Rica. Three subspecies have been described based on plumage differences: (1) *M. l. leucotis* from Costa Rica between 500 and 2000 m; (2) *M. l. nigrior* from the northern highlands of Nicaragua above 500 m; and (3) *M. l. occipitalis* from Chiapas, Mexico, to El Salvador. Historically, *M. l. occipitalis* has sometimes been treated as a separate species based on plumage differences, size, and allopatric distribution. Sandoval et al. (2017a) wrote that "*Melozone l. occipitalis* (Salvin, 1878) was originally described as a different species from *M. l. leucotis* based on morphological differences (longer tails than *M. l. occipitalis*) and plumage patterns (e.g., pileum color, distinct yellow neck stripe, and smaller black breast spot in *M. l. occipitalis*; Ridgway 1901)."

New Information:

Sandoval et al. (2017a) conducted a rigorous phenotypic comparison between the three recognized subspecies of *Melozone leucotis*. They "found substantial variation between the northern subspecies and the two southern subspecies of *Melozone leucotis* in terms of morphometric features, plumage patterns, plumage color, and vocalizations. In particular, *Melozone leucotis occipitalis* from Chiapas, Mexico, Guatemala, and El Salvador is distinguishable from the two more southern subspecies, *M. l. leucotis* from Costa Rica and *M. l. nigrior* from Nicaragua (Stiles & Skutch 1989, Howell & Webb 1995), on the basis of morphometric characteristics (the southern subspecies has longer tarsi, but shorter tail), plumage patches (the northern subspecies has a shorter breast spot), plumage color (the southern subspecies exhibit less brightness in the black throat, breast, and forehead, but higher brightness in the crown), and voice (the northern subspecies has calls with higher minimum frequency and frequency of maximum amplitude; songs with lower frequency of maximum amplitude but longer song duration; and duets with lower maximum frequency). These phenotypic and vocal differences indicate significant divergence between the northern and southern taxa, and suggest the need to reconsider the taxonomic relationship between the northerly subspecies, *M. l. occipitalis*, and the complex of the southerly subspecies, *M. l. leucotis* and *M. l. nigrior*."

Sandoval et al. (2017a) also showed that morphometrics differed between the sexes per subspecies: "We found significant morphological variation across the three *M. leucotis* subspecies in our analyses of both males and females; *M. l. nigrior* grouped together with *M. l. leucotis* whereas *M. l. occipitalis* grouped separately for both sexes" (Table 1, Fig. 1).

Plumage patterns of *M. l. occipitalis* showed marked differences compared to *M. l. leucotis* and *M. l. nigrior*: “*Melozone l. occipitalis* has a grey crown stripe, a broader yellow line on the side of the neck, and a small black breast spot, but *M. l. nigrior* and *M. l. leucotis* have a black crown stripe, a thinner yellow line on the side of the neck, and a bigger black breast spot". Plumage reflectance also differed: "We found notable differences in the chromatic component of plumage reflectance for six of the 10 body regions analyzed using a visual model...” (Figs. 2 & 3).

Vocal evidence showed that male solo song duration was longer, and had lower frequency of maximum amplitude in *M. l. occipitalis* than in *M. l. leucotis and M. l. nigrior* (Table 2, Fig. 4). Calls showed higher minimum frequency, (Table 2, Fig. 4).

Additionally, a genetic study (Sandoval et al. 2017b) that included mitochondrial and nuclear genes showed that the genetic differences between *M. l. nigrior* and *M. l. leucotis/M. l. nigrior* were similar or higher to other actually recognized species inside the genus (Fig. 5).

Recommendation:

The phenotypic and genetic differences between *M. occipitalis* and *M. l. leucotis/M. l. nigrior* are similar to differences observed within the *Arremon torquatus* complex (Cadena & Cuervo 2010), and between *M. biarcuata* and *M. cabanisi* (Sandoval et al. 2014), which were recently elevated from subspecies to species (Chesser et al. 2012, 2017, ~~Remsen et al. 2013??~~). Based on this new evidence, **I recommend** a vote of YES for splitting *M. occipitalis* from *M. leucotis* (including *M. l. leucotis* and *M. l. nigrior*).

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Submitted by: Luis Sandoval
Escuela de Biología, Universidad de Costa Rica

Date of proposal: 14 February 2018

Table 1. Morphometric difference between subspecies of *M. leucotis* (Sandoval et al. 2017a). Bold text indicates statistically different morphometric measurements, and numbers connected by the same letter per measurement are statistically different.

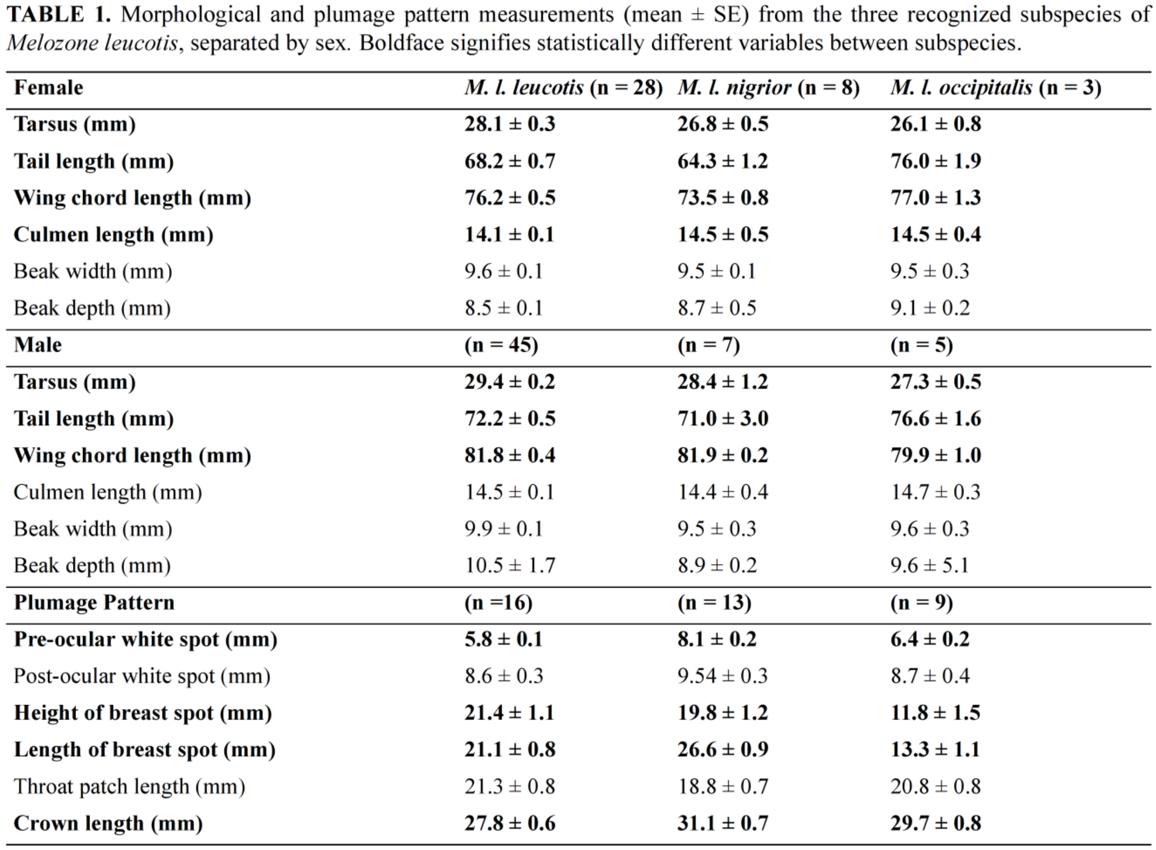


TABLE 1. Morphological and plumage pattern measurements (mean ± SE) from the three recognized subspecies of *Melozone leucotis*, separated by sex. Boldface signifies statistically different variables between subspecies.

Female	***M. l. leucotis* (n = 28)**	***M. l. nigrior* (n = 8)**	***M. l. occipitalis* (n = 3)**
Tarsus (mm)	**28.1 ± 0.3**	**26.8 ± 0.5**	**26.1 ± 0.8**
Tail length (mm)	**68.2 ± 0.7**	**64.3 ± 1.2**	**76.0 ± 1.9**
Wing chord length (mm)	**76.2 ± 0.5**	**73.5 ± 0.8**	**77.0 ± 1.3**
Culmen length (mm)	**14.1 ± 0.1**	**14.5 ± 0.5**	**14.5 ± 0.4**
Beak width (mm)	9.6 ± 0.1	9.5 ± 0.1	9.5 ± 0.3
Beak depth (mm)	8.5 ± 0.1	8.7 ± 0.5	9.1 ± 0.2
Male	**(n = 45)**	**(n = 7)**	**(n = 5)**
Tarsus (mm)	**29.4 ± 0.2**	**28.4 ± 1.2**	**27.3 ± 0.5**
Tail length (mm)	**72.2 ± 0.5**	**71.0 ± 3.0**	**76.6 ± 1.6**
Wing chord length (mm)	**81.8 ± 0.4**	**81.9 ± 0.2**	**79.9 ± 1.0**
Culmen length (mm)	14.5 ± 0.1	14.4 ± 0.4	14.7 ± 0.3
Beak width (mm)	9.9 ± 0.1	9.5 ± 0.3	9.6 ± 0.3
Beak depth (mm)	10.5 ± 1.7	8.9 ± 0.2	9.6 ± 5.1
Plumage Pattern	**(n =16)**	**(n = 13)**	**(n = 9)**
Pre-ocular white spot (mm)	**5.8 ± 0.1**	**8.1 ± 0.2**	**6.4 ± 0.2**
Post-ocular white spot (mm)	8.6 ± 0.3	9.54 ± 0.3	8.7 ± 0.4
Height of breast spot (mm)	**21.4 ± 1.1**	**19.8 ± 1.2**	**11.8 ± 1.5**
Length of breast spot (mm)	**21.1 ± 0.8**	**26.6 ± 0.9**	**13.3 ± 1.1**
Throat patch length (mm)	21.3 ± 0.8	18.8 ± 0.7	20.8 ± 0.8
Crown length (mm)	**27.8 ± 0.6**	**31.1 ± 0.7**	**29.7 ± 0.8**

Table. 2. Vocal differences between subspecies of *M. leucotis* (Sandoval et al. 2017a). Bold text indicates vocal measurement statistically different.

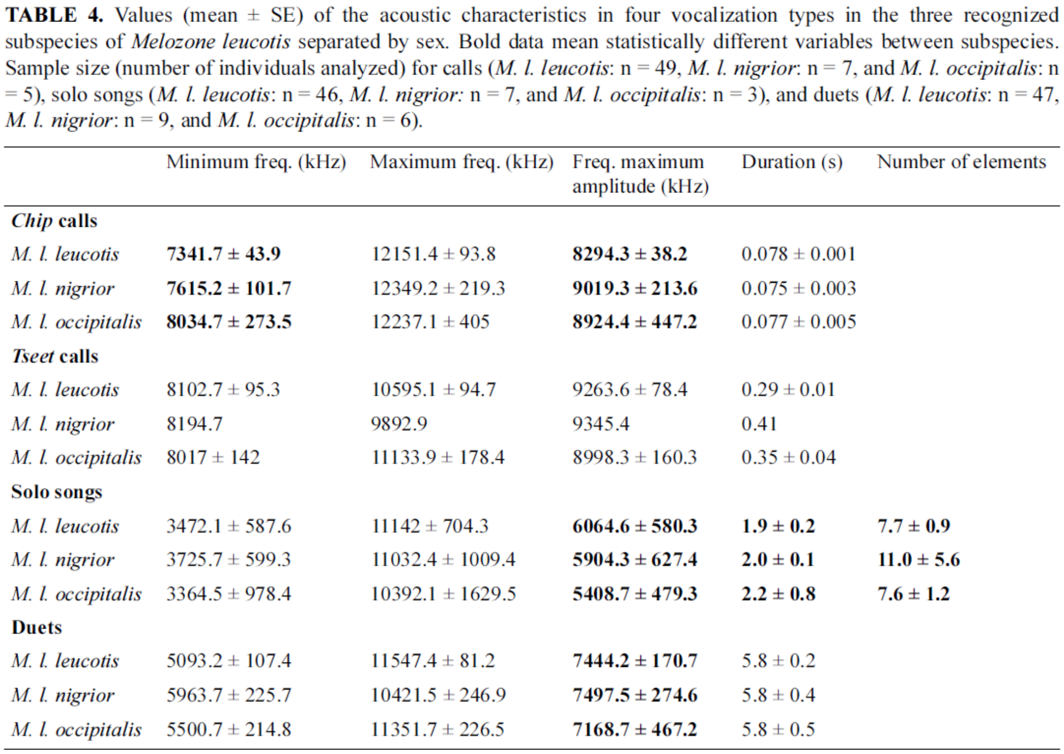


TABLE 4. Values (mean ± SE) of the acoustic characteristics in four vocalization types in the three recognized subspecies of *Melozone leucotis* separated by sex. Bold data mean statistically different variables between subspecies. Sample size (number of individuals analyzed) for calls (*M. l. leucotis*: n = 49, *M. l. nigrior*: n = 7, and *M. l. occipitalis*: n = 5), solo songs (*M. l. leucotis*: n = 46, *M. l. nigrior:* n = 7, and *M. l. occipitalis*: n = 3), and duets (*M. l. leucotis*: n = 47, *M. l. nigrior*: n = 9, and *M. l. occipitalis*: n = 6).

	Minimum freq. (kHz)	Maximum freq. (kHz)	Freq. maximum amplitude (kHz)	Duration (s)	Number of elements
***Chip* calls**					
M. l. leucotis	**7341.7 ± 43.9**	12151.4 ± 93.8	**8294.3 ± 38.2**	0.078 ± 0.001	
M. l. nigrior	**7615.2 ± 101.7**	12349.2 ± 219.3	**9019.3 ± 213.6**	0.075 ± 0.003	
M. l. occipitalis	**8034.7 ± 273.5**	12237.1 ± 405	**8924.4 ± 447.2**	0.077 ± 0.005	
***Tseet* calls**					
M. l. leucotis	8102.7 ± 95.3	10595.1 ± 94.7	9263.6 ± 78.4	0.29 ± 0.01	
M. l. nigrior	8194.7	9892.9	9345.4	0.41	
M. l. occipitalis	8017 ± 142	11133.9 ± 178.4	8998.3 ± 160.3	0.35 ± 0.04	
Solo songs					
M. l. leucotis	3472.1 ± 587.6	11142 ± 704.3	**6064.6 ± 580.3**	**1.9 ± 0.2**	**7.7 ± 0.9**
M. l. nigrior	3725.7 ± 599.3	11032.4 ± 1009.4	**5904.3 ± 627.4**	**2.0 ± 0.1**	**11.0 ± 5.6**
M. l. occipitalis	3364.5 ± 978.4	10392.1 ± 1629.5	**5408.7 ± 479.3**	**2.2 ± 0.8**	**7.6 ± 1.2**
Duets					
M. l. leucotis	5093.2 ± 107.4	11547.4 ± 81.2	**7444.2 ± 170.7**	5.8 ± 0.2	
M. l. nigrior	5963.7 ± 225.7	10421.5 ± 246.9	**7497.5 ± 274.6**	5.8 ± 0.4	
M. l. occipitalis	5500.7 ± 214.8	11351.7 ± 226.5	**7168.7 ± 467.2**	5.8 ± 0.5	

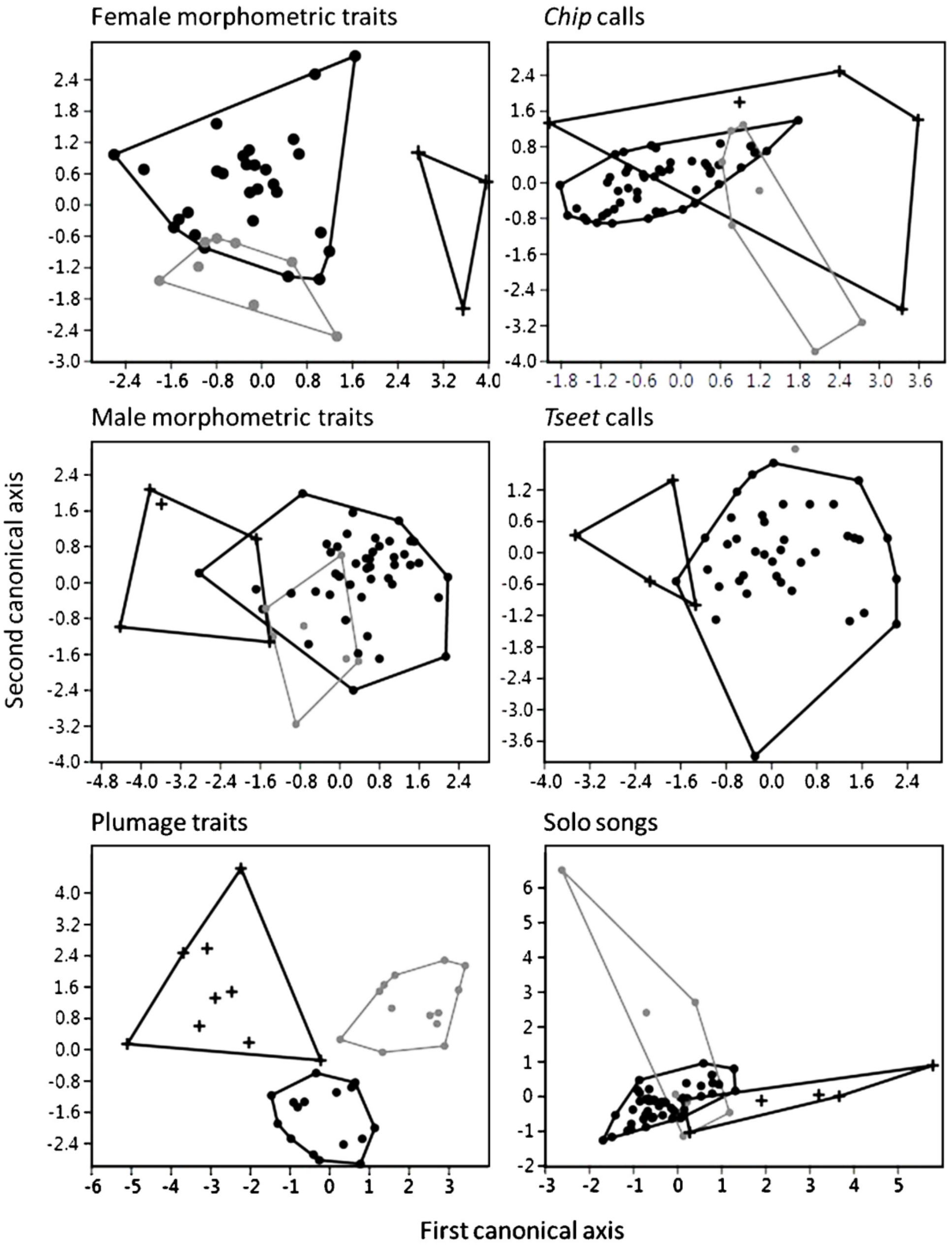


FIGURE 3. Plot of the first two discriminant functions for morphometric measurements, plumage patterns, and vocalizations showing separation between the three subspecies of *Melozone leucotis* (black circles: *M. l. leucotis*, gray circles: *M. l. nigrior*, addition sign: *M. l. occipitalis*) based on the best model for each comparison (see text for details on percentage of classification and variables included in each model).

Fig. 1. Morphometric and vocal differences between subspecies of *M. leucotis* (Sandoval et al. 2017a).

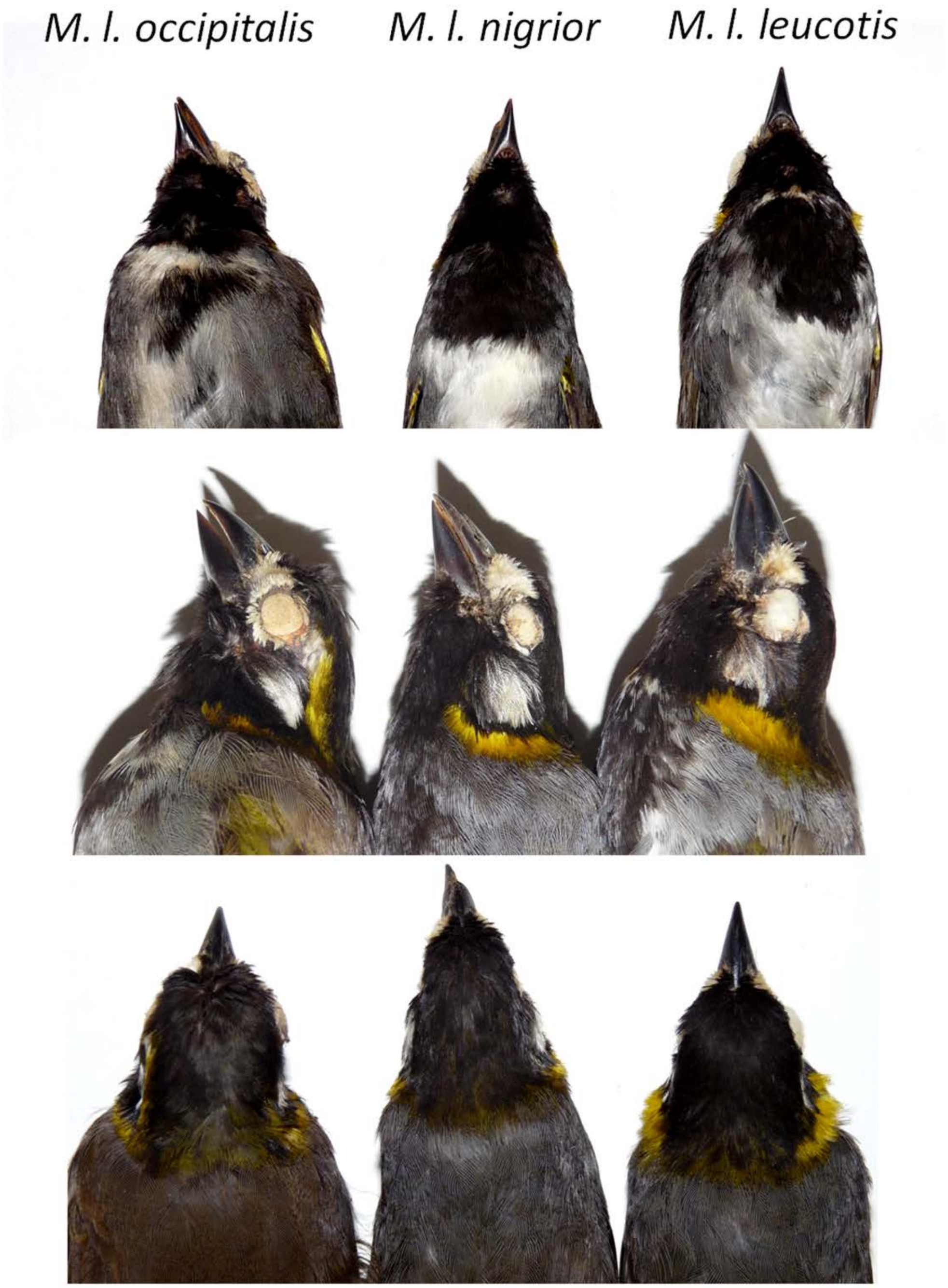


FIGURE 2. Photographs of museum specimens reveal plumage color and pattern differences between the three subspecies of *Melozone leucotis*. Photographs were taken under the same light conditions at the Field Museum of Natural History, Chicago. The top row compares the ventral surfaces, the middle row shows lateral surfaces, and the bottom row shows dorsal surfaces.

Fig. 2. Plumage pattern differences between *M. leucotis* subspecies (Sandoval et al. 2017a).

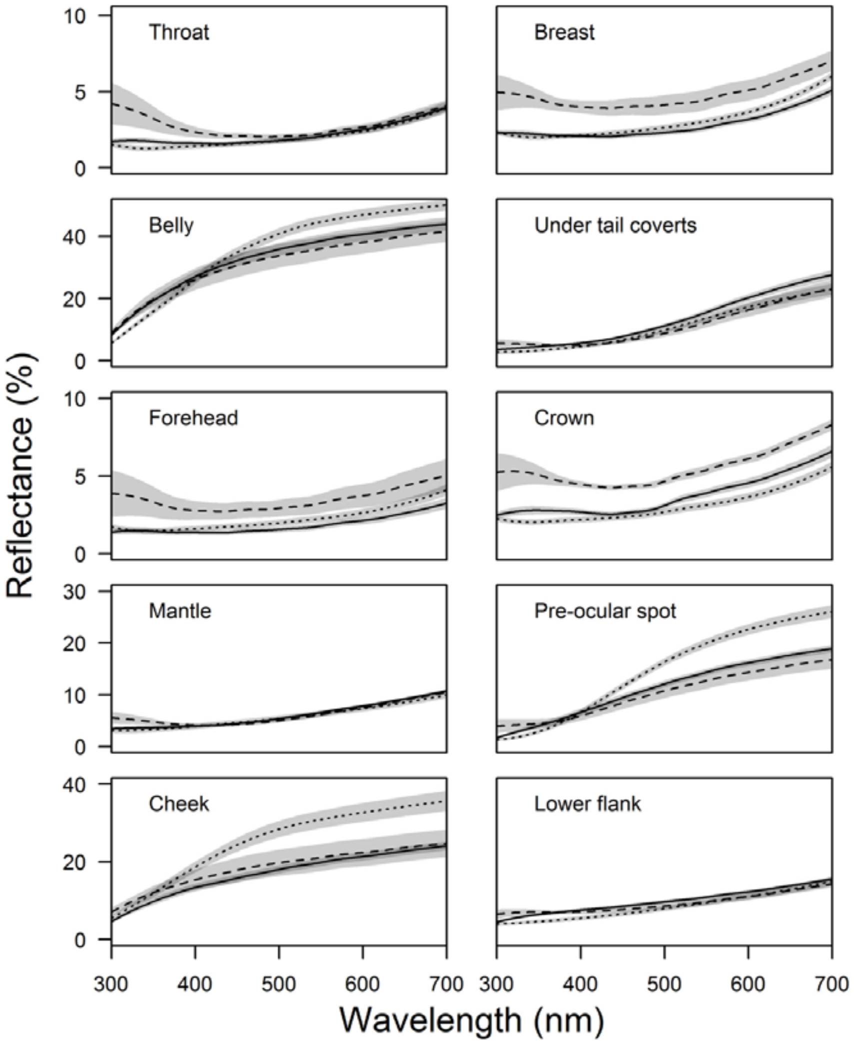


FIGURE 4. Mean reflectance spectra for ten body regions measured from three *Melozone leucotis* subspecies, *M. l. leucotis* (solid lines, $N = 13$), *M. l. nigrior* (dotted lines, $N = 13$), and *M. l. occipitalis* (dashed lines, $N = 8$). The gray area around each line represents standard error of the mean calculated at every 1nm.

Fig. 3. Mean reflectance spectra for 10 body regions in *M. leucotis* subspecies (Sandoval et al. 2017a). Solid lines represent *M. l. leucotis,* dashed lines *M. l. occipitalis,* and dotted lines *M. l. nigrior.* Gray area around each line is standard error every 1 nm.

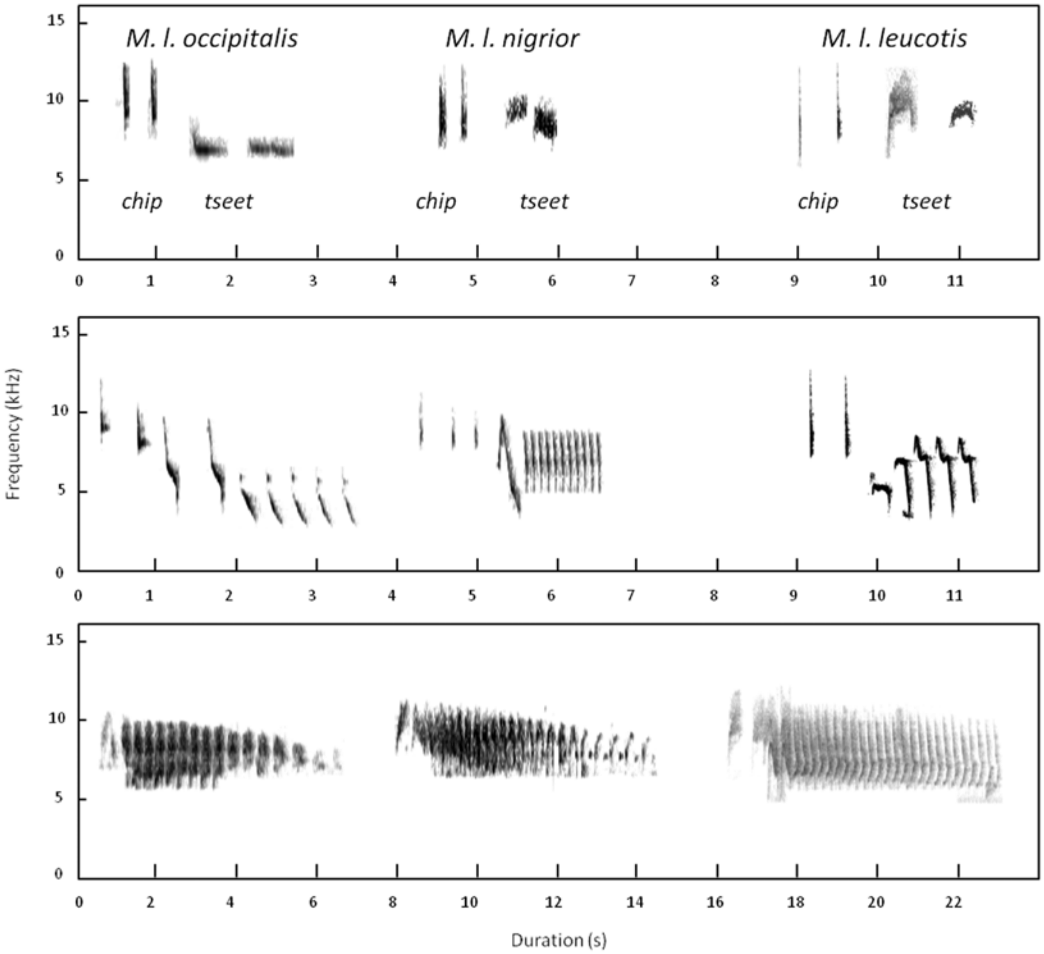


FIGURE 5. Sound spectrograms of two call types, male solo songs, and duets of the three subspecies of *Melozone leucotis.*

Fig. 4. Sonograms of calls, solo songs, and duets of *M. leucotis* subspecies (Sandoval et al. 2017a).

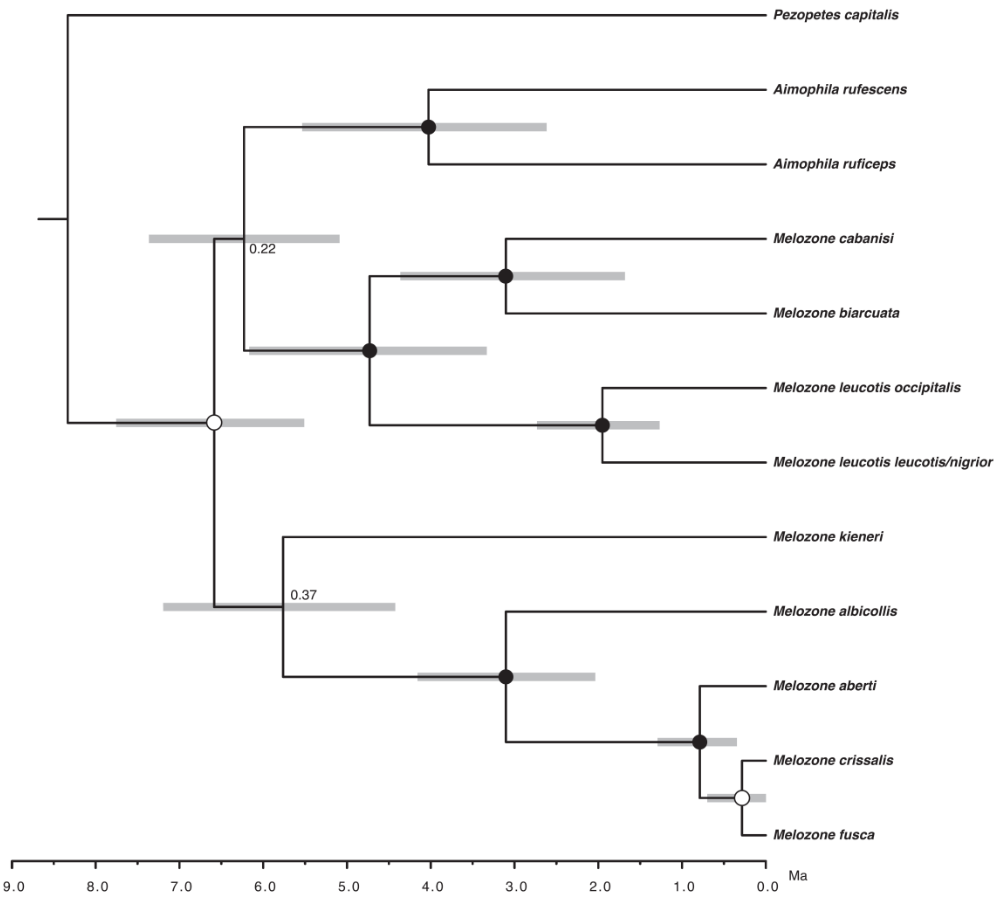


Fig. 4. A time-calibrated maximum clade credibility tree for sparrows in the genera *Melozone* and *Aimophila*, constructed using all available loci. Grey bars shown indicate confidence intervals (95% posterior densities) surrounding estimated divergence dates. Black dots indicate strong (≥0.95 posterior probability) support and the white dot indicates support between 0.95 and 0.75.

Fig. 5. Concensus tree of *Melozone* and *Aimophila* species based on nuclear and mitochondrial loci (Sandoval et al. 2017b).

Split White-collared Seedeater (*Sporophila torqueola*) into two species

Effect on NACC:

If approved, this proposal would split one Checklist species, *Sporophila torqueola*, into two species: *Sporophila torqueola* and *Sporophila morelleti*.

Background:

The White-collared Seedeater (*Sporophila torqueola*) complex typically includes five subspecies, including two subspecies groups that are broadly similar in plumage patterning, but vary markedly in the coloration of the belly and rump:

Sporophila torqueola [*torqueola* group; Cinnamon-rumped seedeater]

- *S. t. atriceps* (S. F. Baird, 1867) Pacific lowlands of Mexico from C & S Sinaloa and W Durango S to Nayarit and N Jalisco; S Baja California.
- *S. t. torqueola* (Bonaparte, 1850) C Mexico from Jalisco and Guanajuato E to Morelos and W Puebla, S to Colima, Michoacán, Guerrero and W & S Oaxaca.

Sporophila torqueola [*morelleti* group; White-collared seedeater]

- *S. t. sharpei* (Lawrence, 1889) Sharpe's Seedeater extreme S USA (lower Rio Grande Valley, in S Texas) and NE Mexico (Nuevo León and Tamaulipas S through E San Luis Potosí to N Veracruz).
- *S. t. morelleti* (Bonaparte, 1850) White-collared Seedeater E Mexico (N Veracruz) S on Caribbean slope (including Mujeres I, off NE Quintana Roo), and on Pacific slope from El Salvador, to extreme W Panama.
- *S. t. mutanda* (Griscom, 1930) S Mexico (S Chiapas) S to El Salvador.

Note that sometimes *S. t. sharpei* is recognized as a separate group (e.g., Howell and Webb 1995).

A series of molecular studies have confirmed that *S. torqueola* belongs to the Sporophilinae—a subfamily of tanagers with an exceptionally high speciation rate (Mason and Burns 2013; Burns et al. 2014; Burns et al. 2016). However, little was heretofore known about genetic and phenotypic differentiation within *S. torqueola*, which spans from Mexico to western Panama. A recent publication uncovered deep molecular divergence within *Sporophila torqueola* that corresponds to phenotypically diagnosable lineages (Mason et al. 2018), suggesting that species limits should be reconsidered within this complex.

New information:

A recent phylogenomic and phenotypic study has provided new insights into the evolutionary history of the White-collared Seedeater (*Sporophila torqueola*) species complex. Specifically, Mason et al. (2018) examined genetic and phenotypic variation (bill/body morphology and plumage) among three currently recognized subspecies groups (Clements et al. 2016). With respect to morphological variation, Mason et al. (2018) compared 663 specimens, including at least 25 individuals of each sex from each subspecies. They measured culmen length, bill length from the gonys, depth of the bill at the nostril, width of the bill at the nostril, wing chord length, tarsus length, hallux length, and length of the central rectrix. Mason et al. (2018) also recorded the presence or absence of multiple plumage characters: partial eye ring, primary wing bars, white edging on the secondaries and tertials of the wing feathers, and a white spot at the base of the primaries. Using a principal components analysis, the authors found clustering by phenotype that corresponded to currently recognized subspecies groups; these were also diagnosable with a multinomial logistic regression approximately 90% of the time (Fig. 1). The phenotypic differentiation seen here is similar to interspecific differences between other species of *Sporophila*, such as members of the southern capuchino radiation (Campagna et al. 2017), which are far more similar genetically yet are still recognized by all taxonomic authorities.

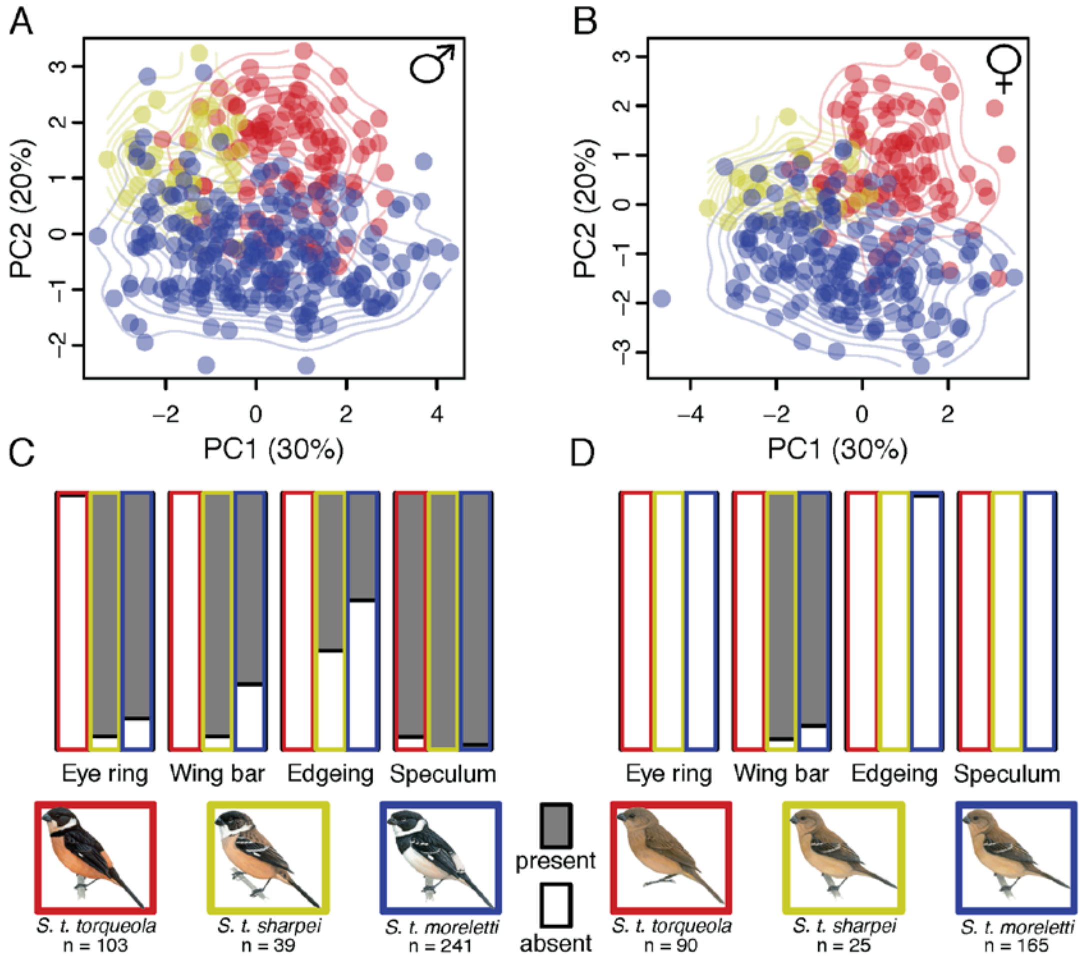
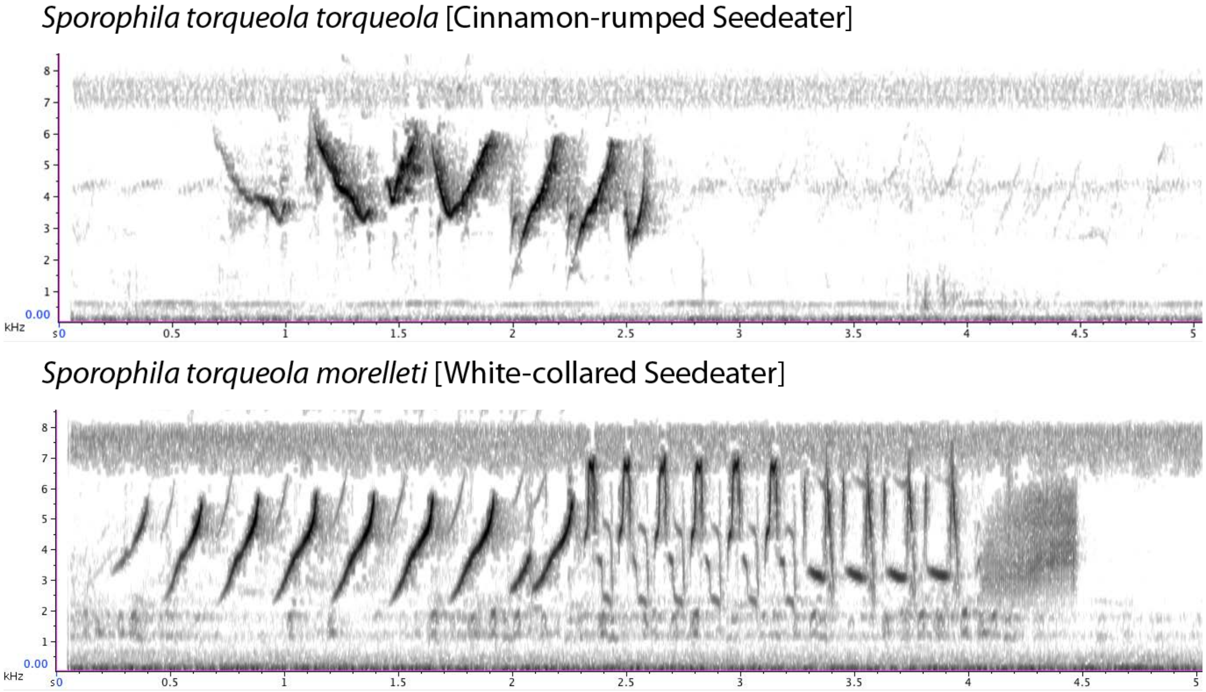


Figure 1: Morphometric analyses of three subspecies within the *Sporophila torqueola* species complex. Scatterplot of principal component axis 1 and principal component axis 2 for males (a) and females (b). Contour lines show the interpolated bivariate kernel density for each subspecies. Barplots showing frequency of plumage characters for males (c) and females (d). Colors that correspond to each subspecies and the presence or absence of a plumage character are shown at the key in the bottom along with sample sizes for each sex and subspecies.

Vocal variation was not quantified by Mason et al. (2018), but a qualitative examination of songs available on Macaulay Library and xeno-canto suggests that vocal differences are present between the *torqueola* and *morelleti* groups. Specifically, the *torqueola* group songs are generally shorter and lack the rapid, buzzy trill that is common at the end of *morelleti* group songs (Fig. 2). We recommend that members of the committee listen to various songs of each taxon and compare spectrograms to make their own judgement about divergence in vocal signals as no published comparison exists (see xeno-canto (link here) and Macaulay Library (link here)).



Sporophila torqueola torqueola [Cinnamon-rumped Seedeater]

Sporophila torqueola morelleti [White-collared Seedeater]

Figure 2: Spectrograms of (top) *Sporophila t. torqueola* and (bottom) *S. t. morelleti*. Although there is substantial variation in both subspecies groups, these spectrograms are representative of typical vocal displays and illustrate some differences: songs of *torqueola* tend to be shorter and lack the rapid, buzzy trills that are common at the end of *morelleti* songs.

To examine genetic differentiation, Mason et al. (2018) sequenced a panel of ultraconserved elements, a widely used method for acquiring a large panel (1000s) of loci via in-solution target capture. These highly conserved genomic regions contain variable sites as one extends toward the margins of the conserved sequences and are informative at both deep and shallow evolutionary scales. Mason et al. (2018) sampled 68 individuals of *S. torqueola* and 4 *S. minuta* as an outgroup, including multiple representatives of each subspecies group (Fig. 3).

Using this panel of loci, Mason et al. (2018) performed a series of population genetic

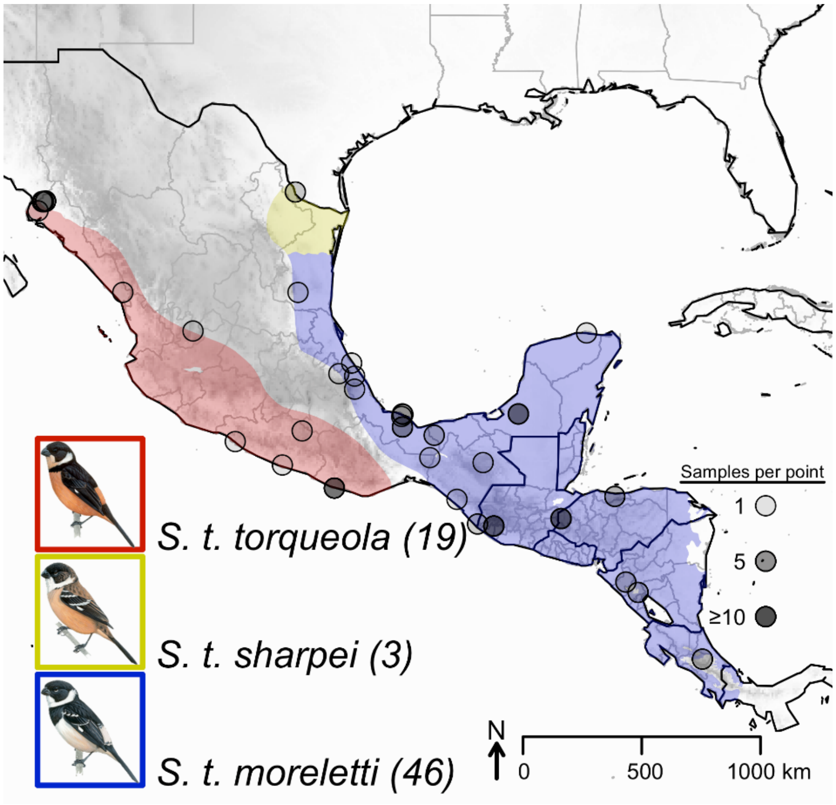


Figure 3: Map showing sampling localities of samples used in this study. Sampling points have been made slightly transparent to help visualize the density of samples at localities with more than one sample. Sample numbers are shown next to each species' portrait. See Table S1 for more detailed information on sampling localities used in genetic analyses.

analyses, and found evidence of deep molecular divergence between the *torqueola* subspecies group (*S. t. torqueola* and *S. t. atriceps*) of western Mexico and the *morelleti* subspecies group (*S. t. morelleti, S. t. sharpei,* and *S. t. mutanda*) (Fig. 4). A coalescent-based species delimitation analysis strongly supported a taxonomic split to recognize *S. t. torqueola* as a separate species from *S. t. morelleti* and *S. t. sharpei* (Bayes Factor = 4216.14). Furthermore, Mason et al. (2018) constructed demographic models that suggested little to no gene flow between *S. t. torqueola* and *S. t. morelleti* and *S. t. sharpei*. There is no known contact zone between the two divergent lineages, but these data suggest that introgression between these lineages does not occur.

To contextualize the genetic divergence between the *torqueola* and *morelleti* subspecies group in the broader evolutionary history of the genus *Sporophila*, Mason et al. (2018) extracted mtDNA bycatch from their UCE data set and aligned these sequences to cyt b sequences for other *Sporophila* species on GenBank (Mason and Burns 2013). The authors used BEAST to infer a phylogeny of the resulting alignment, and found that the *torqueola* and *morelleti* subspecies groups are not sister taxa (Fig. 5). Rather, the *torqueola* group is more closely related to a lineage containing *S. corvina* and *S. intermedia* than to the *morelleti* group. In turn, the *morelleti* group is more closely related to a lineage containing *S. schistacea* and *S. fringilloides*, among other taxa, albeit with low node support.

Most taxonomic references currently recognize a single species of *Sporophila torqueola* (Dickinson and Christidis 2014; Clements et al. 2016; Gill and Donsker 2017) although certain references already recognize the *torqueola* and *morelleti* groups as separate

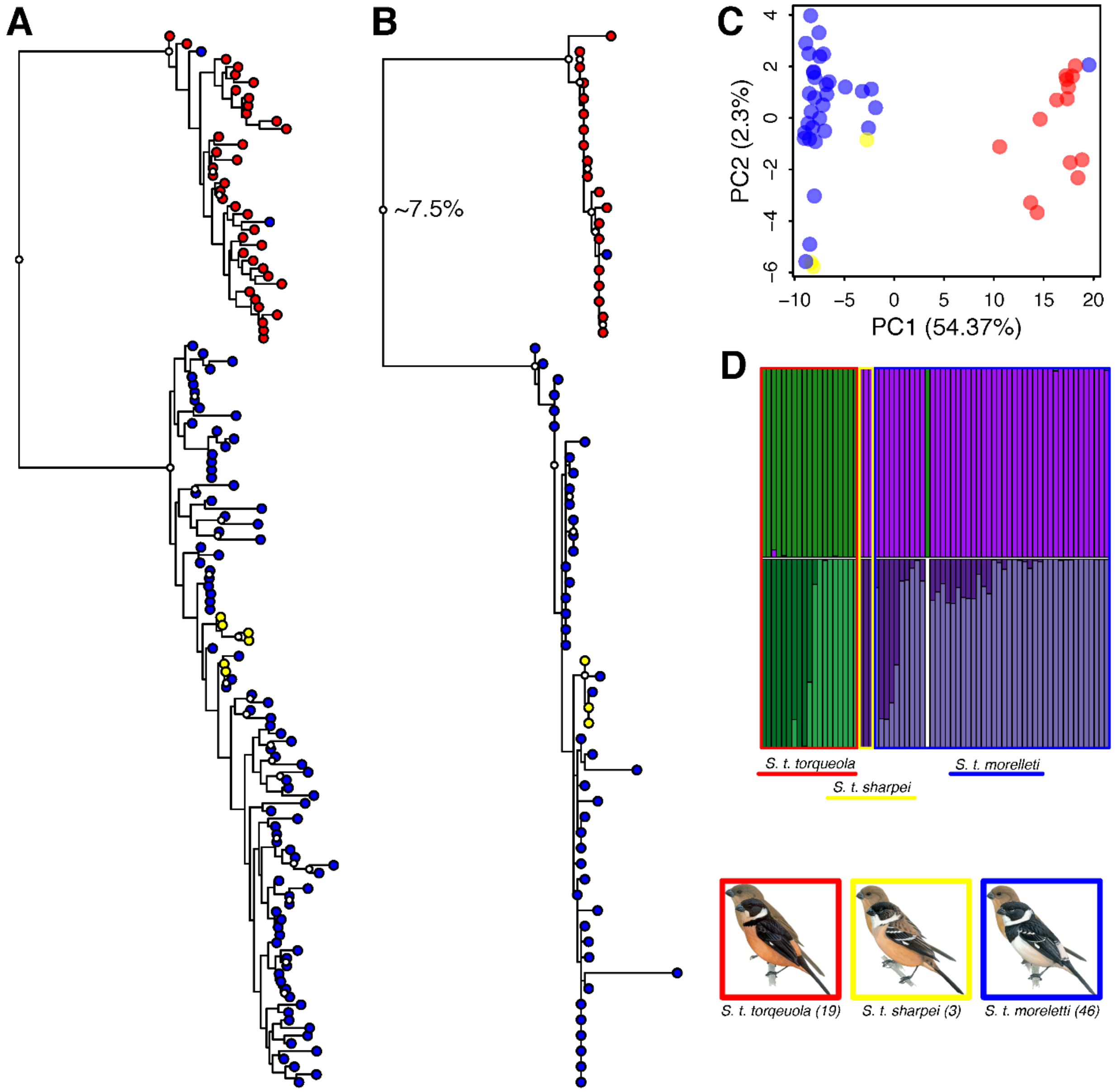


Figure 4: Phylogenetic and population genetic analyses of *S. torqueola* with outgroup removed. (a) RAxML phylogeny built with 1,000 loci with highest number of parsimonious sites. Built by searching for the best tree and performing rapid bootstrapping in the same run (-f a setting). Nodes with white circles have bootstrap support above 70. Tip colors correspond to taxa in the lower right corner. (b) RAxML phylogeny of cyt b mtDNA sequences. Built by searching for the best tree and performing rapid bootstrapping in the same run (-f a setting). Nodes with white circles have bootstrap support above 70. Tip colors correspond to taxa in the lower right corner. (c) PCA plot constructed by filtering data set to include individuals with <85% missing data (n = 50) and loci with <75% missing data (n = 4,067). Dot colors correspond to taxa in the lower right corner. (d) STRUCTURE plot with optimal K value (2) determined by the Evanno method. Individuals are sorted according to taxa and by decreasing latitude within taxa, with rectangular boundary colors corresponding to taxa in the lower right corner. (e) STRUCTURE output for hierarchical analyses (optimal K = 2 for both) performed by subsetting the data set for each of the clusters identified and removing mismatched individuals in panel (d)

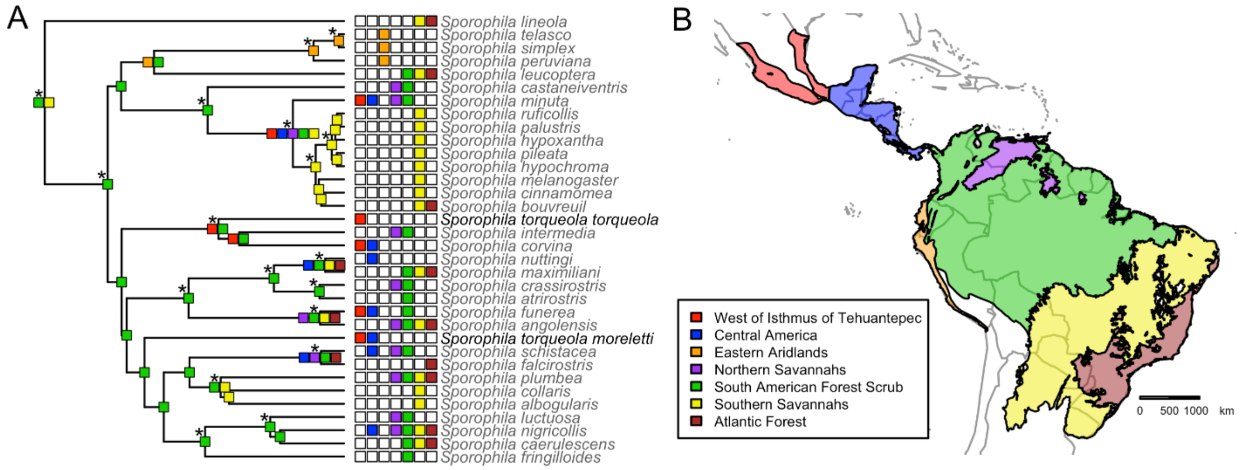


Figure 5: (a) Inferred phylogeny of the genus *Sporophila* estimation of the probabilities of ancestral ranges via the best-fit model in BioGeoBEARS (DEC model). Asterisks indicate strongly supported nodes with over 95 posterior probability. The most likely ancestral range is indicated for each node, while the range for each extant species is shown at the tips of the phylogeny. The ancestral range of *Sporophila* was most likely forest scrub in central South America, and multiple lineages have crossed the Isthmus of Tehuantepec, including two lineages that are currently considered conspecific (*S. t. torqueola* and *S. t. morelleti* shown in bold). (b) Biogeographic regions used in the BioGeoBEARS analyses conducted in this study. The colors corresponding to the key in the lower left represent the same biogeographic regions in panel (a).

species (del Hoyo and Collar 2018; Rising 2018) or suggest this as an alternative taxonomic treatment (Howell and Webb 1995). The common name “Cinnamon-rumped Seedeater” is already in use for the *torqueola* (western) subspecies group (Howell and Webb 1995; BirdLife International 2017; Rising 2018), and is a suitably descriptive common name that is readily available—we suggest it should be adopted as the common name for this newly recognized species if this proposal passes. We believe that the common name White-collared Seedeater should be retained for the subspecies *sharpei*, *morelleti*, and *mutanda*, of which *morelleti* has priority. ‘White-collared Seedeater’ is an accurate description of this species’ phenotype and succinctly describes how it differs from closely related species with which it overlaps. It is also the more widespread of the two lineages recovered in Mason et al. (2018), and its common name has been widely used throughout Central America since its initial description.

Recommendation:

I recommend following the suggestion of Mason et al. (2018) to split *Sporophila torqueola* into two species, based on genetic and phenotypic differences. Mason et al. (2018) uncovered deep polyphyly within *S. torqueola* in the mtDNA phylogeny and deep intraspecific nuclear divergence in UCE loci. They also found diagnosable differences in plumage and bill morphology and qualitative differences in song. The phenotypic differences observed here are commensurate with interspecific differences observed among other *Sporophila* species, such as the southern Capuchino lineage. Thus, both phenotypic and genetic (nuDNA and mtDNA) data support recognizing the Cinnamon-rumped Seedeater and White-collared Seedeater as separate species.

The recommended new taxonomy would be as follows:

Sporophila torqueola Bonaparte, 1850 (Cinnamon-rumped Seedeater)

- *Sporophila torqueola atriceps*
- *Sporophila torqueola torqueola*

Sporophila morelleti Bonaparte, 1850 (White-collared Seedeater)

- *Sporophila morelleti sharpei*
- *Sporophila morelleti morelleti*
- *Sporophila morelleti mutanda*

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

Date of proposal: 20 February 2018

Proposal 2018-C-8b (Amendment to 2018-C-8):

Adopt the English name Morelet's Seedeater for *Sporophila morelleti*

The English names recommended in Proposal 2018-C-8, the split of *Sporophila morelleti* from White-collared Seedeater *S. torqueola*, are White-collared Seedeater for *morelleti* and Cinnamon-rumped Seedeater for *torqueola*. As stated in the proposal, these names are being used by HBW for the daughter species, and Howell and Webb (1995) noted that the *torqueola* group is sometimes considered specifically distinct under the name Cinnamon-rumped Seedeater (implying use of White-collared for *morelleti*?). However, we generally use or at least consider former English names, if available, for daughter species; these are often Ridgway's names or AOU names. Ridgway used the English name Cinnamon-rumped Seedeater for *torqueola*, but used Morellet's Seedeater for *morelleti*. The first edition of the checklist (AOU 1886) also used Morellet's Seedeater for *morelleti*, then the checklist used Sharpe's Seedeater (for the subspecies *morelleti sharpei*) in the 2nd through 4th editions (AOU 1895, 1910, 1931), before using White-collared Seedeater for the lumped species *S. torqueola* in the 5th and 6th editions (AOU 1957, 1983). In AOU 1998, we used Cinnamon-rumped Seedeater for the *torqueola* subspecies group and mentioned both White-collared Seedeater and Morellet's Seedeater as names for the *morelleti* subspecies group. In another variation, Davis (1972) used Morellet Seedeater for *morelleti*.

Ridgway's names conform to our guidelines of using names different from the parental species for both daughter species, to minimize confusion about the identity of particular taxa, unless there are compelling reasons to retain the parental name for one of the daughter species. We generally consider retaining a name in cases in which (1) one daughter species is North American and the other largely or exclusively extralimital (e.g., Northern Harrier split), (2) the relative distributions of the daughter species are vastly different in size (e.g., Cassia Crossbill split), (3) a descriptive name is appropriate for one daughter species but not for the other, or much more appropriate for one than the other (e.g., Winter Wren split). None of these reasons would seem to apply in this case: both daughter species are North American, their range sizes are not vastly different, and both have the partial white collar.

Moreover, although the name White-collared Seedeater is in use for *morelleti* (as above), it's not clear how well established this name is for *morelleti*, rather than for *torqueola sensu lato*. I don't think that its recent adoption is indicative of widespread establishment, and I don't think we want to simply accept names chosen by global lists for birds in our area without considering alternatives that better conform to our guidelines for English names.

The species *morelleti* was described by Bonaparte from specimens in the Paris Museum collected by "the French traveller Morelet" near Petén, Guatemala, in 1847

(Salvin and Godman 1885). As seems to have happened all too frequently, the name of the honoree was misspelled in the description, so that we have *morelleti* rather than *moreleti*. This misspelling was corrected by Salvin and Godman (1885) to *moreleti* but the incorrect spelling has priority and there is no internal evidence in Bonaparte's description to merit a correction. According to Jobling (2010), Pierre Marie Arthur Morelet (1809-1892) was a "French naturalist, artist, and collector in the Azores, Canary Islands, and tropical America." His surname is used in the English names of Morelet's Crocodile (*Crocodylus moreletii*) and Morelet's tree frog (*Agalychnis moreletii*), but apparently in the English name of no bird species.

Recommendation: I recommend that we follow our guidelines and reinstate Ridgway's name and the original AOU name for the daughter species *morelleti*, correcting the spelling to Morelet's Seedeater, unless there is compelling evidence that the name White-collared Seedeater is well established for *morelleti* and would cause much confusion if not adopted.

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Terry Chesser, 5 April 2018

Lump Taiga Bean-Goose *Anser fabalis* and Tundra Bean-Goose *A. serrirostris*

Background:

The bean goose complex consists of six taxa. One of these, *brachyrhynchus*, formerly was classified as a subspecies of *Anser fabalis* by some authors but now universally is recognized as a separate species (Pink-footed Goose). The other five taxa were also long included in *Anser fabalis*, but currently NACC recognizes two polytypic species, Taiga Bean-Goose *A. fabalis* (with subspecies *fabalis*, *johanseni*, and *middendorffii*), and Tundra Bean-Goose *A. serrirostris* (with subspecies *rossicus* and *serrirostris*). This split was implemented in the Forty-eighth Supplement (Banks et al. 2007), and is based on NACC Proposal 2006-B-7, submitted by Richard Banks. Dick's proposal in turn drew heavily on Sangster and Oreel (1996), which should be consulted for a fuller discussion of the complicated taxonomic history of these taxa, and for a discussion of the morphological differences between them.

Description of the problem:

To begin, it's worth revisiting Sangster and Oreel (1996). A large part of this paper is devoted simply to establishing that the *fabalis* and *serrirostris* groups represent real taxa, and that the differences between them are discrete, not clinal. Dick's proposal paraphrases the take home message from Sangster and Oreel:

"Furthermore, field observations on the wintering grounds in western Europe have revealed that, besides [very subtle!] differences in plumage and proportions, Taiga and Tundra Bean Geese show differences in vocalizations, feeding habitat and diet, photosensitivity, activity pattern, behavior, phenology and responses to extreme cold (Berry 1938, Coombes 1951, Mathiasson 1963, Huyskens 1977, 1986, van Impe 1980b, van den Bergh 1985, Barthel 1989, 1995)".

NACC took all of these assertions at face value, although note that, in their short paper, Sangster and Oreel did not elaborate on how the *fabalis* and *serrirostris* groups differed in any features other than plumage and proportions. Also note that some of the references cited to buttress these claims are in Dutch or French, and I admit that I have only an incomplete understanding of what those papers have to say on the subject. I have consulted what I can find in English, although my sample happens to include some of the earliest and least quantitative of the lot. Regarding vocalizations, for example, Berry (1938) wrote that "the call notes of flocks of *segetum* [= *serrirostris*], and *arvensis* [= *fabalis*], are, to me, as distinct as are those of *A. anser* [Graylag Goose] and *A. albifrons* [Greater White-fronted Goose]"; and similarly Coombes (1951) reported that the two groups have "some different habits and a different voice". The only other description of the vocal differences that I have found (in English) is in Yokota et al.

(1982), who reported that the vocalizations of *middendorffii (fabalis* group) are deeper than are those of nominate *serrirostris*. On the other hand, they also described *middendorffii* as larger bodied than *serrirostris*, with a longer bill and neck. For all I know, then, any differences in voice between different taxa of bean geese are nothing more than allometric effects of differences in the size of the body and bill.

Another reference cited by Sangster and Oreel, Matthiasson (1963), presented a detailed review of the biology of bean geese in one region of Sweden. He acknowledged the existence of different subspecies, but recognized only a single species, and most of this paper simply referred to "Bean Goose". Matthiasson described two populations in this region, one of which (*rossicus*, of the *serrirostris* group) occurs in passage earlier in the fall, and the other (*fabalis*) of which appears later in the fall, and lingers into winter. I find nothing surprising about this. He also noted a subtle difference between October and November with respect to the length of time it takes geese to settle into the evening roost sites. He proposed that the difference in activity pattern between October and November is because these are two different populations, but he was very explicit that this is only an hypothesis, not something he had documented. I'm willing to concede that his hypothesis may well be correct, but I'm less certain of the taxonomic implications of this behavioral difference. He also correlated the fall departure of *rossicus* from his region with the onset of frost; I assume that this is the basis for the different "responses to extreme cold" mentioned by Sangster and Oreel. Again, I concede the difference, but am not that impressed by the significance of this as a taxonomic character. Although Mathiasson (1963) was very focused on these differences between the two taxa in roost behavior and triggers for migration, I did not notice anything in his account related to differences in habitat or vocalizations between them.

Coombes (1951) reported that *fabalis* wintering in Britain occupy a different habitat than do *serrirostris* wintering in the Netherlands. The differences in habitat are not described, and in any event, what significance the habitat differences of populations that winter in allopatry might have to populations that winter in sympatry elsewhere in western Europe is not clear. The closest I have come to finding significant support for ecological and behavioral differences between the *fabalis* and *serrirostris* groups is in van Impe (1980). This is a long paper, in French, on the two groups at a wintering site in the southern part of the Netherlands ; I have relied on the English summary. Among other observations are that "*A. f. fabalis* grazes on meadows during the winter. *A. f. rossicus* feeds on the harvest waste of sugar beets and potatoes during early winter; later, its preferences change and it visits newly sown wheat fields and stubble fields sown with grasses ... *A. f. fabalis* always drinks fresh water while *rossicus* largely depends upon brackish water. Because the former visits meadows it is mainly a grazer and occasionally a digger. *A. f. rossicus*, however, is predominately a digger and during this activity it uses more energy" etc. This account raises, to me, as many questions as it answers. How widespread are these patterns? – as noted above, Mathiasson (1963) did not report any habitat differences at his study site in southern Sweden, so is this a taxon-specific difference, or simply a peculiarity at van Impe's study site? And how significant is the difference between meadows and stubble fields? – this does not seem like a very compelling difference to me, but perhaps the full text makes this clearer.

In any event, Sangster and Oreel admitted that the differences that they enumerated between the *fabalis* and *serrirostris* groups amount to their recognition only as phylogenetic species. Recognition of the two as biological species hinges on a supposition that mate choice occurs on the wintering grounds: "Because there are no recoveries of Taiga and Tundra Bean Geese ringed in the Netherlands from each other's range during the breeding season, formation of mixed pairs, if any, must occur on a very small scale [this presumably is based on Burgers et al. 1991]. This suggests that interbreeding of Taiga and Tundra Bean Geese is rare, perhaps nonexistent, and that they can be recognized as species under the Biological Species Concept". It's hardly surprising that different taxa have different breeding ranges. Sangster and Oreel don't report any observations of pair formation on the wintering grounds or on migration, and they have no information at all on pairs on the breeding grounds, either in the core ranges for either taxon or at potential zones. This makes it difficult to evaluate the significance of their claim; this is another of their points where I find the supposition plausible, but that it is presented with little or no supporting documentation.

New information:

There is surprisingly little phylogenetic information available on these geese, but their relationships were investigated by Ruokonen et al. (2008). This is a single study, and it relies entirely on mitochondrial DNA, so take it for what it's worth. But the inferred relationships amount to a third possibility that no one had counted upon: "We found three mitochondrial clades geographically distributed to (1) Greenland, Iceland, and Svalbard (*A. brachyrhynchus*), (2) the eastern taiga zone (former subspecies *A. fabalis middendorffii*), and (3) the western taiga and tundra zone (subspecies *A. fabalis rossicus, serrirostris*, and *fabalis*)". In other words, the major genetic break in the bean geese is not between the *fabalis* and *serrirostris* groups, but rather is *within* the *fabalis* group. There are subclades that refer to *serrirostris* + *rossicus* and to *fabalis*, but with shallower genetic divergence. So, the implication is that one could follow Sangster and Oreel and maintain the split between nominate *fabalis* and the *serrirostris* group, but then also must recognize *middendorffii* as a species. Or, one could revert to a single species of bean goose. But these genetic results are not consistent with NACC's version of a two species classification.

Sangster and Oreel were adamant that intergradation between the *fabalis* and *serrirostris* groups does not occur. Both Dickinson and Remsen (2013) and del Hoyo and Collar (2014), however, suggest that intergradation does occur, although with uncertainty over its extent. Neither checklist cites a source for these comments about intergradation. I suspect that Liebherr and Rutschke (1993) and Yokota et al. (1982) are the key references here, but I only came across these at a late stage of preparing this proposal, and have not yet seen the former; with luck, someone on the committee will track it down and share their findings. Reeber (2015) characterized the former thusly: "However, Liebherr & Rutschke, having analysed 1,114 birds in the hand in Germany between 1987 and 1991, were more cautious, and deemed the distinctions [between the *fabalis* and *serrirostris* groups] very difficult, particularly because of frequent overlap in the different features". Yokota et al. (1982) estimated, without much discussion, that 10-20% of Bean Geese wintering in Japan are intermediates between *serrirostris* and *middendorffii*, apparently as assessed from field observations.

When NACC considered the original proposal to split the bean geese, the comments suggested that the main concern among the committee members was not the nature of the evidence presented by Sangster and Oreel, but rather, surprise that, 10 years on, the British Ornithologists' Union had yet to adopt the split. In fact, the BOU never did accept this split. The two species approach currently is the official stance of the BOU (BOU 2018), but that is solely because the BOU Records Committee dissolved its Taxonomic Subcommittee a few years ago, and the BOU checklist now follows the taxonomy of the International Ornithological Union's IOC World Bird List. And the IOC has split these, citing (ironically) Banks et al. (2007). On the other hand, the bean goose split was not adopted by Dickinson and Remsen (2013), the most conservative, at the species level, of the major global avian checklists. Nor was the split adopted by del Hoyo and Collar (2014) on behalf of the HBW/BirdLife International checklist, which is the checklist that recognizes the greatest number of bird species: "In view of the contradictory findings of these various studies, and the fact that races intergrade to an uncertain extent, it would seem safer for the time being to retain the widely recognized treatment of two species". Also note that waterfowl specialists, who generally accept more splits in ducks and geese than does NACC, also recognize only a single species of bean goose (e.g. Kear 2005, Reeber 2015).

Recommendation:

The evidence for recognizing two species of bean geese is not as well supported as NACC believed when it adopted this split, and the admittedly limited genetic data shows that the relationships among these geese may be more complicated than previously was recognized. In the meantime, NACC is one of the few taxonomic authorities that recognizes two species of bean goose. **I recommend** that NACC return to the one species approach, at least until such time as truly compelling evidence would suggest otherwise.

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Submitted by: Tom Schulenberg, Cornell Lab of Ornithology

Date of Proposal: 26 February 2018

Recognize Mexican Duck *Anas diazi* as a species

Background:

Mexican Duck, *Anas diaz*i, is one of many taxa in the Mallard (*A. platyrhynchos*) complex in which males and females are similar. This taxon apparently flew under the radar for a surprisingly long time. It was described, as a species, only as late as 1886 (Ridgway 1886), with a type locality in Puebla, southern Mexico. The pre-Colombian distribution of *diazi* in the United States is not well known. Henry (1856) reported *Anas obscura* (= American Black Duck *Anas rubripes*) from the Rio Grande Valley in New Mexico, a record that presumably would apply to *diazi*; but it is not clear from his account if he obtained specimens. The next record seems to be that of Huber, who (re)discovered a population of *diazi* along the Rio Grande in south central New Mexico in the early 20th century (Huber 1920). It was not detected in southern Arizona until as late as 1947 (Brandt 1951). Currently its distribution in the American southwest includes southeastern Arizona, New Mexico, and the Trans-Pecos region of Texas. It's difficult if not impossible to determine if *diazi* formerly was this widespread but undetected until the early 20th century, although the potential for confusion with Mallard makes this plausible. (For that matter, I haven't found confirmed references to it from Mexico before it was described, although maybe I haven't searched the early literature on Mexico with due diligence.) Or perhaps its range has expanded in the Southwest, even as natural wetlands were affected or destroyed, through increasing levels of irrigation and water impoundment in the region; something along those lines seems to have happened recently in coastal northwestern Mexico, outside its historical distribution (see also Lavretsky et al. 2015).

Description of the problem:

Hybridization between *diazi* and *platyrhynchos* has been known at least since Lindsey (1946; note that the earliest specimen showing signs of hybridization was collected in 1883, i.e., even before the recognition of *diazi* as a taxon). Aldrich and Baer (1970) also noted hybridization between *diazi* and *platyrhynchos*, but continued to recognize *diazi* as a species, in part based on the lack of a quantitative assessment of levels of hybridization. Hubbard (1977) provided just that kind of a quantitative assessment, based on a traditional hybrid zone index of plumage characters of specimens from Canada south to southern Mexico (Puebla). Hubbard found, not surprisingly, that "even 'pure' populations are variable" in both taxa (although more so in *diazi*), and also found indications of effects on plumage from adventitious factors (e.g., bleaching from water conditions), such that he emphasized that "one should dwell less on the absolute scores of populations than on the trends and the relative scores that they exhibit". And that general trend was for characters to become more *diazi* like from north to south, with an inflection point in this trend in New Mexico. Hubbard also reported an increased rate of hybridization over time, based on partitioning the specimens from Dona Ana County (New Mexico) into two temporal periods, 1893-1920 and 1938-1970. Hubbard comes across as conflicted on the taxonomic implications of his findings, e.g., "The major inconsistency in regarding *diazi* and *platyrhynchos* as conspecific is the fact that the major shifts in mensural and plumage characters occur rather abruptly, a finding which may indicate that counter-selection against gene flow is operative". Even so, he ended up recommending the classification of *diazi* as a subspecies *of platyrhynchos,* with the caveat that this assessment "must be regarded as tentative and subject to revision". On the basis of Hubbard's survey, the classification committee considered *diazi* to be a subspecies of *platyrhynchos* (AOU 1983), and this remains the current treatment.

New information (and reconsideration of some old):

Hubbard's study received both support and criticism in subsequent papers. Scott and Reynolds (1984) were not convinced by Hubbard's demonstration of an increased frequency of hybridization between the two time periods, since Hubbard's sample sizes for each period were small, and the reported difference is not statistically significant. Scott and Reynolds also suggested that Hubbard's "specimens are probably not random samples of the populations presented" since "increasing awareness of the intergrade nature of the New Mexico population could easily cause a higher percentage of 'hybrids' to be deposited in museums than were actually present in the birds taken by earlier hunters and collectors". I suppose this is possible, but no evidence is presented that this is the case, and we'll probably never know one way or the other. Otherwise Scott and Reynolds found another area of apparent hybridization between *platyrhynchos* and *diazi*, in the Río Conchos Valley in Chihuahua, although the overall picture in Mexico is for "no evidence for genetic swamping by the Northern Mallard phenotype". Whether hybridization still occurs in Chihuahua also is not known, although Baldassarre (2014) suggested that this is unlikely, due to a change in the migratory pattern of Mallards: formerly "a conspicuous component as far south as the Valley of México … today the Northern Mallard is almost unknown in central Mexico and is scarce even in northern Chihuahua" (Scott and Reynolds 1984). Furthermore, *diazi* has been undergoing a population increase in Mexico (Perez-Arteaga et al. 2002), so it is possible that hybridization is even less likely as the decline in *platyrhynchos* in Mexico is coupled with a surge in the population of *diazi*.

And Hubbard's survey has not been replicated in more than 40 years. All we have are several sets of anecdotal observations. One highly skilled observer, for example, comments that his experience in southeastern Arizona "is not of the 'extensive' hybridization that influenced the decision to lump the two. Rather, it is of no obvious hybridization" (Webster 2006). Similarly, in southwestern New Mexico *diazi* reportedly greatly outnumbers *platyrhynchos*, "which again indicates some geographic separation between Mexican Ducks and Mallards" (Sandy Williams, cited by Baldassarre 2014).

This observation of course does not reflect whether hybridization would occur in this region if populations of the two taxa were comparable, but at a minimum indicates that any zone of hybridization is likely to be narrower than is portrayed by AOU (e.g. AOU 1998, "extensive hybridization in southeastern Arizona, southern New Mexico, and west-central Texas"). Hybridization also is thought to be highly unlikely in Texas, as "there are no breeding populations of green-headed Mallards in … the entire Trans-Pecos" (Lockwood and Freeman 2014).

The hybrid zone index has been an important tool in systematics. It's worth keeping in mind, however, that the hybrid zone index is a proxy for estimating gene flow. We don't know the genetic profile of any specimen that Hubbard relied on in his research (and recall his caveats not to focus on the absolute values of his hybrid index zone scores at even the population level). Directly measuring gene flow would have been a pipe dream in Hubbard's day, but times have changed. A few years ago, NACC considered Proposal 2011-B (submitted by Richard Banks), which summarized the morphological and genetic evidence that had been published up to that point (Livezey 1991, Johnson and Sorenson 1999, McCracken et al. 2001, Gonzalez et al. 2009). There is considerably more information available now than there was even a few years ago, however, so it is worth taking a fresh look at the current state of our knowledge (Lavretsky et al. 2014a, 2014b, 2015).

The sampling scheme varies across these papers, and in most cases, samples of *diazi* are only from Mexico, i.e., potentially far from the zone of introgression. All of Johnson and Sorenson's (1999) samples were from the United States, however, and Lavretsky et al. (2015) sampled no few than 105 *diazi*, from the United States (New Mexico, Texas) south to southern Mexico (Puebla). Only a few of these papers examined variation in nuclear DNA. Lavretsky et al. (2014a) considered variation across *platyrhynchos*, *diazi*, *A. fulvigula* (Mottled Duck), and *A. rubripes* in 17 nuclear introns, and Lavretsky et al. (2015) conducted genomic scans of 3532 autosomal loci. The general pattern was for nuNDA to show little resolution, not only between *diazi* and *platyrhynchos*, but also between these two taxa and nominate *fulvigula*, *A. fulvigula maculosa*, and *rubripes* (but see also Lavretsky et al. 2014b).

On the other hand, there is a considerable diversity of mitochondrial DNA haplotypes. Most mtDNA haplotypes are shared across most or all taxa in the complex, but other haplotypes reveal signs of structure. In terms of mtDNA, *A. fulvigula maculosa* is the most divergent taxon, and is the only member of the group that does not share haplotypes with any of the other members of the complex (Lavretsky al. 2014a; but see McCracken et al. 2001). On the other hand, *rubripes* has a large number of unique haplotypes, with no evident structure, and also shares haplotypes with Mallard. Weak structure is shown by *diazi* and nominate *fulvigula*, both of which also share haplotypes with each other, and, in the case of *diazi*, with *platyrhynchos* (Lavretsky et al. 2014a). Finally, Lavretsky et al. (2015) also examined divergence in Z-linked loci in *diazi* and *platyrhynchos*, and found an elevated level of divergence in these loci (are there similar studies relating to Z-linked loci for other taxa in this complex? – if so, I have not seen them).

Anyone hoping that genetic approaches would yield a straightforward case for or against recognizing *diazi* as a species is going to come away disappointed. Autosomal nuDNA, to date, is of little use in distinguishing taxa in the New World *platyrhynchos* complex, "demonstrating that taxa were broadly polyphyletic and indicating that many polymorphisms were shared among taxa" (Lavretsky et al. 2014a). The situation with regard to level of mtDNA divergence across these taxa is similar. There is a large number of mtDNA haplotypes, many of which are unique to particular taxa, but these haplotypes collectively show only very low levels of divergence from each other, and some are shared between different combinations of taxa (*diazi* and *platyrhynchos*, *diazi* and *maculosa*, and *rubripes* and *platyrhynchos*). One takeaway from this, of course, is that *diazi* is just another face in the crowd; it is not well differentiated genetically from *platyrhynchos*, but it also is not any less differentiated than is any other member of the group. This overall pattern could be a signal of incomplete lineage sorting, although high levels of gene flow between these taxa cannot be ruled out (Lavretsky et al. 2014a). Finally, there is some evidence of selection on Z-linked loci, which could be consistent with recognition of *diazi* as a species (Lavretsky et al. 2015).

What other considerations may come into play here? Despite the obvious differences in male plumage between *platyrhynchos* and the other taxa, courtship displays apparently differ little between the members of this complex (Johnsgard 1961). AOU (1983) acknowledged widespread hybridization between *platyrhynchos* and *rubripes*, but suggested that continued recognition of *rubripes* as a species was warranted on the basis of assortative mating ("they tend to segregate as species"). AOU (1983) did not discuss levels of assortative mating between *platyrhynchos* and *diazi*, although this silence perhaps implies that these taxa do not segregate in this fashion. The evidence, however, points both ways. Lindsey (1946) noted a high incidence of hybrids, and reported no assortative behavior, among *diazi* and *platyrhynchos* at a park in Albuquerque; for what it's worth, Hubbard (1977) was of the opinion that "considering the artificial conditions this should not be counted as reflecting the condition in the wild". Other authors report that indeed there is segregation between *diazi* and *platyrhynchos*. In an unpublished study (Bevill and Davis 1969, Bevill 1970), "the two forms tended to stay apart and did not form any mixed pairs" (Hubbard 1977). Bellrose (1976) offered more details: "In an area frequented by both mallards and Mexican ducks, he [Bevill] observed 26 mated Mexican duck hens. All but one hen mated with drakes of their own species …". Similarly, Hubbard cited another unpublished study (Nymeyer 1975), which found no mixed pairs at one locality, but 7 pairs of *diazi* and 8 of *platyrhynchos*; and at another location, there were 11 pairs of *diazi*, 10 pairs of *platyrhynchos*, 4 mixed pairs of *diazi* x *platyrhynchos*, and 1 apparent pair of *diazi* x *Anas acuta* (Northern Pintail). As Hubbard pointed out, field identification of *diazi* x *platyrhynchos* hybrids is difficult; but whether these observations refer to *diazi* or *diazi*-like ducks may not matter, since the clear pattern is for *diazi* or *diazi*-like individuals to pair assortatively. Hubbard himself recognized this: "Far more *diazi*-like birds were paired with similar birds (and vice versa in the case of *platyrhynchos)*, and this is a strong indication that pairing is not random in this complex". Brown (1985) suggests that in Arizona, *diazi* forms pairs by early fall, which "tends to reproductively isolate them from Mallards on the basis of behavior as most adult Mexican Duck hens are paired prior to the arrival of wintering Mallards". (Note that this contrasts with Hubbard, who reported that "differences in the timing of breeding in these two forms … cannot be strongly emphasized and may not be significant".)

What does it all mean?

We have no current assessment of rates of hybridization between *diazi* and *platyrhynchos*, but we must assume that introgression at some level is ongoing. The best that can be said is that *diazi* is only very modestly divergent, genetically, from *platyrhynchos* (but the same is true as well of *rubripes* and *fulvigula*, especially *A. fulvigula maculosa*). On the other hand, there is evidence that the zone of hybridization is much narrower than earlier was thought; there is evidence of assortative mating where *diazi* and *platyrhyncho*s are in contact; and there is evidence of selection on Z-linked loci, all of which point towards recognition of *diazi* as a species.

Hubbard (1977) explicitly, and AOU (1983) implicitly, compare the interactions between *diazi* and *platyrhynchos* with those between *rubripes* and *platyrhyncho*s. (Keep in mind that authors who lumped not only *diazi* but also *fulvigula* with *platyrhynchos* continued to maintain *rubripes* as a species, e.g. Delacour 1956, Mayr and Short 1970.) At the time of Hubbard (1977) and AOU (1983), hybridization between *diazi* and *platyrhynchos* was known but could be seen as the exception, not the rule. Aldrich and Baer (1970), for example, cited Johnsgard (1967) as reporting that "obvious Mallard x Black Duck hybrids rarely exceed more than 2 per cent of combined populations indicating that assortative mating is operating effectively". Now we know that hybridization between *platyrhynchos* and *rubripes* no longer is rare, but instead occurs at relatively high levels. But do we know what that level actually is? Johnsgard (1967) inferred rates of hybridization from the proportions of hybrids versus parental types in wing samples of waterfowl shot by hunters and examined by personnel from U.S. Fish and Wildlife Service. Kirby et al. (2000), using a similar methodology, estimated a rate of hybridization that was up to 6 times higher than Johnsgard's. This disparity probably is more reflective of a revised set of criteria for recognizing hybrids and backcrosses than an increased rate of hybridization, although perhaps the latter also plays some role. The key point is that both studies calculated the proportion of hybrids in relation to parental types in a nonbreeding sample, incorporating an unknown (but surely significant) proportion of *rubripes* originating from breeding areas that are not any zone of contact with *platyrhynchos*. What we are interested in, of course, is the rate of hybridization where the two taxa *are* in contact as breeders. We can infer, however, that the rates of hybridization in populations in contact must be much higher than anything reported by either Johnsgard (1967) or Kirby et al. (2000). Anecdotally, hybridization is considered to be rampant in the Northeast and the Mid-Atlantic region, especially where saltmarsh breeding *rubripes* seem to pair with an ever-increasing presence of locally breeding *platyrhynchos*.

Also note that Johnsgard (1967) assumed that assortative mating was taking place based on his (under)estimate of the rate of hybridization. Direct assessments of assortative mating between *platyrhynchos* and *rubripe*s seem to be quite few, of which the most significant may be Brodsky and Weatherhead (1984). At their study, in Ontario, *platyrhynchos* outnumbered *rubripes*, and in both taxa males outnumbered females. In both taxa, pairs formed assortatively but only until all available female *platyrhynchos* had paired with like males; "surplus" male *platyrhynchos* then courted and paired with female *rubripes;* furthermore*, platyrhynchos* tended to form pairs earlier in the season than did *rubripes.* Needless to say, it would be interesting to know more about the dynamics of assortative pairing from other regions, especially in areas (such as the coastal Northeast and Mid-Atlantic) where hybridization is particularly prevalent.

Other than *rubripes*, hybridization with other members of the Mallard complex was scarcely known at all during Hubbard's time. We now know that hybridization of *platyrhynchos* with nominate *fulvigula* also occurs frequently (affecting up to 10% of the Florida population, Williams et al. 2005), and may be increasing in *maculosa* (e.g., Ford et al. 2017). Introgression is rampant on Hawaii between feral populations of *platyrhynchos* and native Hawaiian Duck *A. wyvilliana*, such that populations on Oahu are completely introgressed with *platyrhynchos* (Browne et al. 1993); the same may be true on Hawaii (Browne et al. 1993), and there is a hybrid swarm on Maui as well (Engilis et al. 2002). Hybridization on New Zealand between *platyrhynchos* and Pacific Black Duck *A. superciliosa* is so extensive that the genetic extinction of the nominate subspecies could occur (Rhymer et al. 1994); hybridization also occurs on Australia, but appears to be restricted to populations in urban areas, and so is not widespread (Kear 2005). And there is extensive hybridization in eastern Asia between *platyrhynchos* and Eastern Spot-billed Duck (*A. zonorhyncha*) (Kulikova et al. 2004). The only members of the Mallard complex in which hybridization is *not* reported are a few species that are not (yet?) in any appreciable contact with *platyrhynchos*, such as Laysan Duck *A. laysanensis* of the outer Hawaiian Islands. And again, note that *rubripes* and *fulvigula*, recognized as species by NACC, are no more differentiated genetically than is *diazi*.

Recommendation:

Many taxa in the global Mallard complex, and all members of the New World Mallard complex (except for the most isolated geographically taxon, *laysanensis*), hybridize with *platyrhynchos* when these come into contact. This is the case even though there is some level of assortative mating between any of these taxa and *platyrhynchos* (with the apparent exception of *wyvilliana*, where assortative mating apparently does not occur). Obviously, these taxa are not genetically identical, but the evidence to date points to only very low levels of genetic divergence across the New World Mallard complex. In all of these respects, *diazi* does not stand out as being different from any other member of the group. In particular, the interactions between *diazi* and *platyrhynchos* do not appear, on the basis of admittedly incomplete information in both cases, to be any different from those between *rubripes* and *platyrhynchos*, with the exception that contact between *diazi* and *platyrhynchos* occurs in a geographically restricted area, but on a broad front between *rubripes* and *platyrhynchos*.

Evaluating all the available evidence, then, and adopting a classification that is consistent across all taxa, one could treat all New World members of the Mallard complex the same way as *diazi:* that is, lump *wyvilliana*, *rubripes,* and *fulvigula* all into *platyrhynchos*. As mentioned above, there is ample precedent for such an approach (e.g., Delacour 1956, Mayr and Short 1970). The more conservative option is to grant *diazi* the status accorded to the other taxa, and recognize it as a species. But the current classification, reflecting an idea that *diazi* somehow is an outlier in the global Mallard complex, increasingly seems to be the untenable position. **I recommend** the conservative approach: split *diazi*. That's easier than lumping *rubripes* and the rest, and more consistent with the entirety of the data than treating *diazi* as an outlier.

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Transfer *Loxigilla portoricensis* and *L. violacea* to *Melopyrrha*

Background:

In the current AOS Checklist of North and Middle American Birds, the genus *Loxigilla* consists of four species that occur on islands in the Caribbean: *Loxigilla portoricensis, L. violacea*, *L. noctis*, and *L. barbadensis*. Traditional classification (e.g., Paynter and Storer 1970) placed this genus near other finches on Caribbean islands such as *Loxipasser*, *Tiaris*, *Melanospiza*, and *Melopyrrha*. Later studies (e.g., Burns et al. 2002, Barker et al. 2013) showed that these species are all tanagers and closely aligned with Darwin's finches.

New Information:

Burns et al. (2014) studied phylogenetic relationships of tanagers using two mitochondrial gene regions (ND2 and cyt *b*) in addition to one exon (RAG1) and three introns (MB-I2; FGB-I5; sex-linked ACO1-I9). About 95% of tanager species were included in the study, including all *Loxigilla* species and potential close relatives. The trees of this study (see figure) showed *Loxigilla* to be polyphyletic, with *L. noctis* and *L. barbadensis* forming a strongly supported clade, and *L. portoricensis* and *L. violacea*, together with *Melopyrrha nigra*, forming a strongly supported clade in another part of the tree. These two clades are separated by several strongly supported nodes. Thus, Burns et al. (2014) recommended merging *portoricensis* and *violacea* "into *Melopyrrha* Bonaparte, 1853, (type species = *M. nigra*), and retaining *Loxigilla* (type species = *L. noctis*) for the other two species of *Loxigilla*, *L. noctis* and *L. barbadensis*". Later, after reviewing the taxonomic literature, Burns et al. (2016) instead recommended using *Pyrrhulagra* Bonaparte, 1850, for *L. portoricensis, L. violacea*, and *Melopyrrha nigra*, following Gray's (1855) designation of *portoricensis* as the type species of *Pyrrhulagra*, which has priority over *Melopyrrha*. del Hoyo and Collar (2016) followed this recommendation by retaining *Loxigilla* Lesson, 1831, for *L. noctis* and *L. barbadensis*, but recognizing *Pyrrhulagra* for *portoricensis*, *violacea*, *Melopyrrha nigra*, and *M. taylori* (which they split from *nigra*).

Although Ridgway, Hellmayr, and others have accepted Gray's (1855) subsequent designation of *portoricensis* as the type species of *Pyrrhulagra*, Bonaparte and Schlegel (1850, p. v) had clearly designated *noctis* as the type species five years earlier:

> avec le Dr. SCHIFF de Francfort nous appellons *Pyrrhulagra* un nouveau genre dont *Fringilla noctis*, L. est le type, et qui contient deux ou trois espèces semblables par la couleur si non par le bec. [rough translation: with Dr. Schiff in Frankfurt we name *Pyrrhulagra* a new genus of which *Fringilla noctis*, L. is

the type, and which contains two to three species similar in color if not in the beak.]

Thus, it appears that *Pyrrhulagra* is an objective junior synonym of *Loxigilla*, unless Bonaparte and Schlegel (1850) is for some reason unavailable as a source of new names. James Jobling, author and editor of the HBWAlive Key to Scientific Names in Ornithology, has looked into this question thoroughly and has confirmed (in litt.) that Bonaparte and Schlegel (1850) "is available as a vehicle for the designation of types and the introduction of new names," and that *Fringilla noctis* Linnaeus, 1758, is indeed the type species of *Pyrrhulagra* Bonaparte 1850. Therefore, *Melopyrrha* appears to be the oldest available genus name for the group containing *portoricensis*, *nigra*, and *violacea*.

Recommendation:

We recommend that the committee transfer *Loxigilla portoricensis* and *L. violacea* into *Melopyrrha*, and that the linear sequence between *Euneornis* and *Melanospiza* be changed to:

Melopyrrha portoricensis
Melopyrrha nigra
Melopyrrha violacea
Loxipasser anoxanthus
Loxigilla noctis
Loxigilla barbadensis

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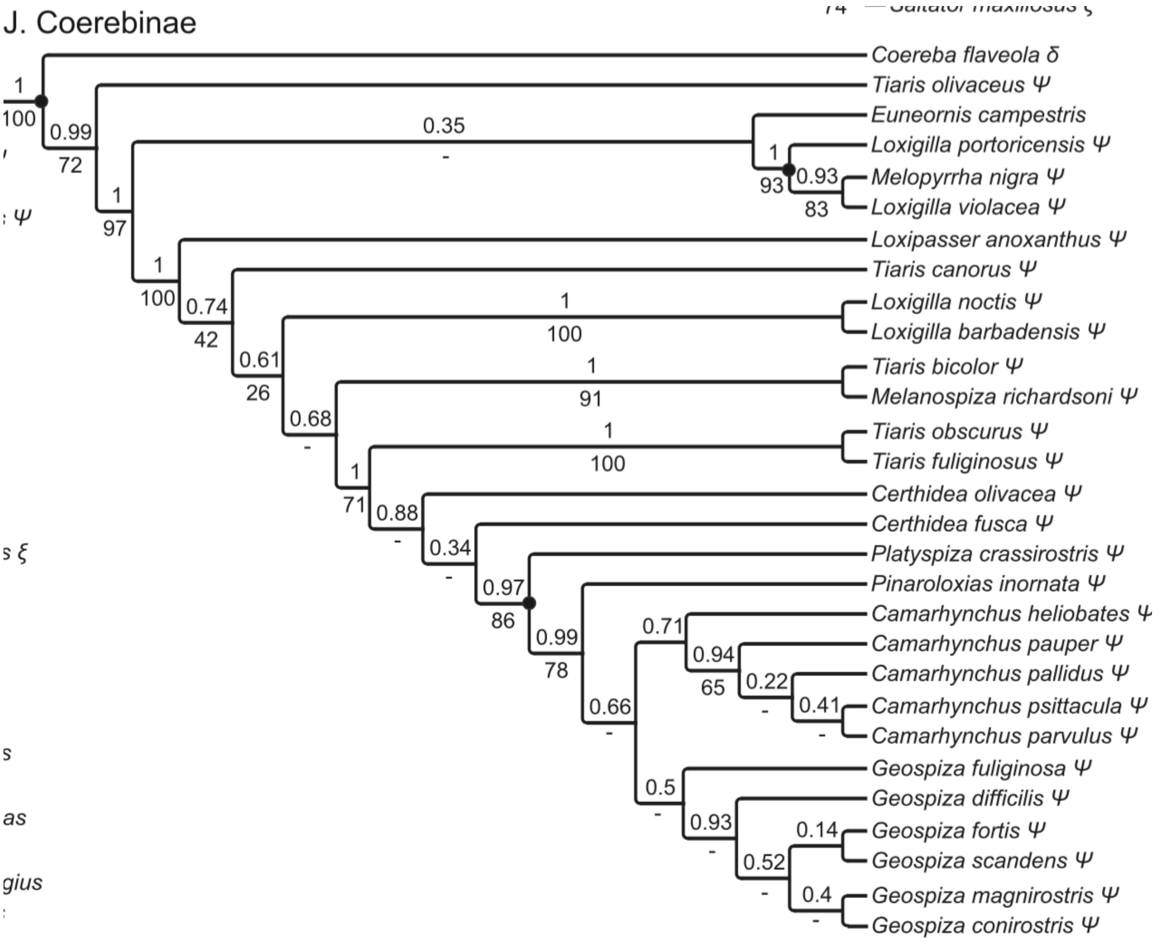
Submitted by: Kevin Burns and Terry Chesser

Date of Proposal: 26 February 2018



Phylogenetic relationships of the taxa in question from Burns et al. (2014) showing results of the concatenated analysis of six genes. The tree structure is derived from the maximum clade credibility tree with arbitrary branch lengths. For each node, the posterior probability from the BEAST analysis is given above the branch leading to that node, and the maximum likelihood value from the RAxML analysis is given below the branch.

Split Gray Nightjar *Caprimulgus indicus* into three species, recognizing *C. jotaka* and *C. phalaena*

Effect on NACC:

This proposal revisits an issue considered by the committee in 2004, when a 2-way split of *Caprimulgus indicus* was rejected. If approved, this proposal would split one checklist species, Gray Nightjar *C. indicus*, into three species, recognizing *C. indicus, C. jotaka,* and *C. phalaena* as separate species. Among these three species, only *C. jotaka* has been recorded as a vagrant within the NACC geographic area. Therefore, *C. jotaka* would replace *C. indicus* on the checklist.

Background:

Nightjars in the genus *Caprimulgus* are crepuscular, aerial insectivores with a collectively widespread distribution. Recent research has highlighted phenotypic differences among geographically restricted taxa that have prompted many taxonomic authorities to revise species limits to recognize multiple species (e.g., Rasmussen and Anderton 2005). One such potential split has relevance to the NACC checklist, in that the Gray Nightjar (currently *C. indicus*) periodically occurs as a vagrant in the Aleutian Islands of Alaska (Howell et al. 2014). This taxon has now been split into three species by most global taxonomic references (Clements et al. 2017; Gill and Donsker 2017; del Hoyo et al. 2018a, b; but see Dickinson and Remsen 2013); therefore, it seems timely to revisit this issue.

New information:

Rasmussen and Anderton (2005) examined phenotypic variation among geographically restricted subspecies within the Gray Nightjar (*Caprimulgus indicus*) and recognized two species in South Asia, *C. indicus* and *C. jotaka*. They noted differences in vocalizations, wherein *C. jotaka* produces “a rapid, percussive series of downturned, monosyllablic, whiplash ‘SCHurk’SCHurk’SCHurk...’ notes that run together”, whereas *C. indicus* produces a rather slow, metronomic series of distinct disyllabic notes, “FWlk-\m-/FWlk-\m-/FWlk-\m-/” (Fig. 1). Furthermore, Rasmussen and Anderton (2005) noted that the eggs of *C. jotaka* are bluish-white to creamy white with heavy dark brown blotches, while *C. indicus* eggs are buff to rich salmon-buff with dense pale chestnut to olive-brown blotches. With respect to wing size, Rasmussen and Anderton (2005) reported longer wings in *C. jotaka* (196–210 mm) compared to *C. indicus* (182–195 mm) and darker overall appearance (blackish patches, streaks and bars larger, on crown, upperparts, underparts, and tail) in *C. jotaka* compared to *C. indicus*. As noted, most taxonomic references (e.g., Clements et al. 2017, Gill and Donsker 2017, del Hoyo et al. 2018) have gone on to recognize the species *C. phalaena* as distinct from *C. jotaka*. This taxon, restricted to the Pacific island nation of Palau, is much smaller in size (mean winglength 160 mm) and differs in plumage coloration, being largely black with rufous flecking on chin, throat, and crown (del Hoyo et al. 2018b). Gill and Donsker (2017) split these taxa based on differences in vocalizations, citing recordings archived at Xeno-Canto and the Macaulay Library, as well as the descriptions in Pratt et al. (1987) and Pratt and Etpison (2008). Pratt et al. (1987) described the voice as a "series of knocking sounds, like a small hammer striking hard wood" with rising pitch and cadence: "tawk - tock - tac-tac-tac-tac-tac."

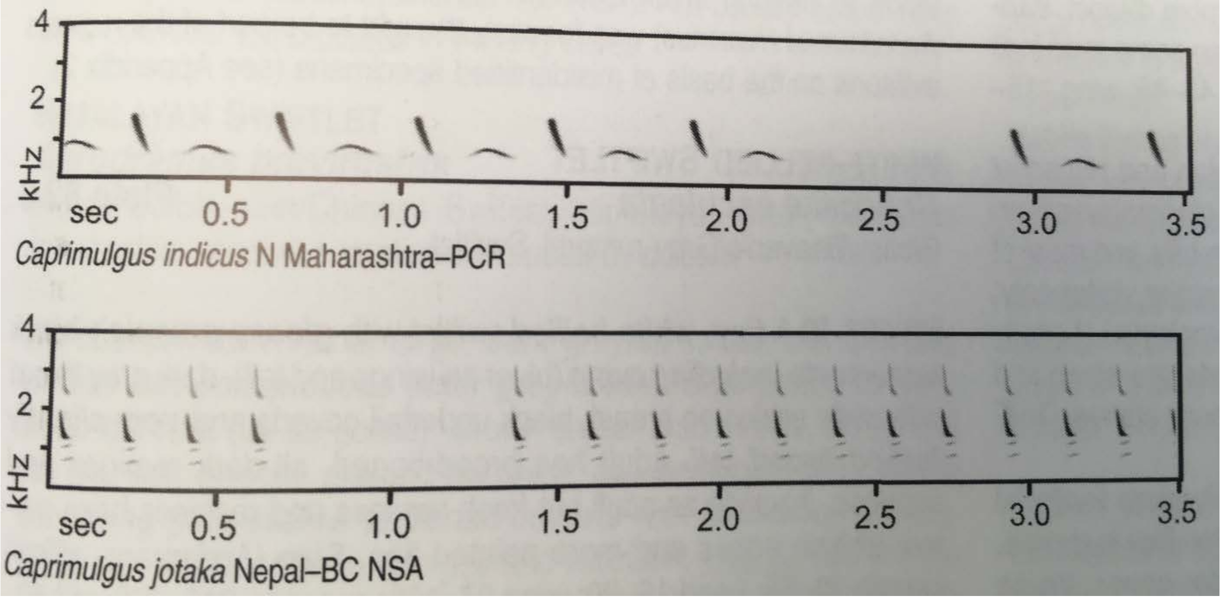


Figure 1: Spectrogram reproduced from Rasmussen and Anderton (2005) that illustrates vocal differences between *C. indicus* (top) and *C. jotaka* (bottom).

Recommendation:

We recommend (a) that the committee recognize the split of the Old World species *C. jotaka* and *C. indicus*, first suggested by Rasmussen and Anderton (2005) based on differences in vocalizations, egg coloration and patterning, and plumage. This would remove *C. indicus* from the checklist and add *C. jotaka*. *Caprimulgus phalaena*, like *indicus sensu stricto*, is not known from the NACC area, but is also recognized by most taxonomic references, and **we recommend (b)** recognizing this extralimital taxon as well, due to differences in vocalizations, size, and plumage.

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Submitted by: Nicholas A. Mason and Carla Cicero, Museum of Vertebrate Zoology, UC Berkeley, and Terry Chesser

Date of proposal: 26 February 2018

Split Barn Owl (*Tyto alba*) into three species

Background:

Taxonomic references currently recognize from one to four species in the Barn Owl (*Tyto alba*) species complex. The AOS recognizes one cosmopolitan species (AOU 1998), as does HBW, which additionally groups 28 subspecies into eight species groups (del Hoyo & Collar 2014). Clements et al. (2016) differentiate *T. deroepstorffi* (Andaman Islands) from *T. alba*, whereas the Howard and Moore Checklist recognizes three species: *T. alba*, *T. delicatula*, and *T. deroepstorffi* (Dickinson & Remsen Jr. 2013). The IOC (Gill & Donsker 2018) recognizes four species of barn owl:

- *T. alba* (Western Barn Owl), 10 subspecies, widespread in Africa and Europe
- *T. furcata* (American Barn Owl), 12 subspecies, widespread in North, Middle, and South America
- *T. javanica* (Eastern Barn Owl), 7 subspecies, distributed from south and southeast Asia to Australasia and southwestern Pacific
- *T. deroepstorffi* (Andaman Masked Owl), from the Andaman Islands

A different subset of three allopatric species has been recognized based on molecular phylogenies derived from sequences of the mitochondrial *cytb* gene and the nuclear *RAG-1* gene (Wink et al. 2009): the Common Barn Owl, *T.alba*, which has ten subspecies distributed in Africa, Eurasia, and South-east Asia; the American Barn Owl, *T.furcata*, with at least five subspecies from North, Central, and South America; and the Australian Barn Owl, *T. delicatula*, with at least four subspecies restricted to the easternmost part of Southeast Asia, Australia, New Zealand, and Polynesia (Alibadian et al. 2016). Morphological traits such as overall size, plumage coloration and pattern, amount of feathering on the tarsus, and power of tarsus and toes have been proposed to correlate with the three-species subdivision (Alibadian et al. 2016).

New Information:

Alibadian et al. (2016) published a molecular study of systematic relationships within the Barn Owl species complex, and estimated the timing of divergence events. Alibadian et al. (2016) analyzed 40 samples belonging to ten taxa, which included populations distributed across the world (Table 1). They obtained sequences of three mitochondrial genes, cyt b (620 bp), CO1 (660 bp), 16S (568 bp), and one nuclear gene, RAG-1 (990 bp). They inferred a maximum likelihood phylogenetic tree (RAxML v. 7.0.4) and a Bayesian inference tree (MrBayes v. 3.2). They also conducted a molecular dating analysis (BEAST v. 1.8), an estimation analysis of the ancestral distribution of the three groups (LAGRANGE), and statistical analyses of ecological niche overlap (MAXENT v. 2.0, ENMTOOLS).

Phylogenetic analyses revealed three main clades with strong geographic structure. The first group, the *furcata* clade, included subspecies from mainland North and South

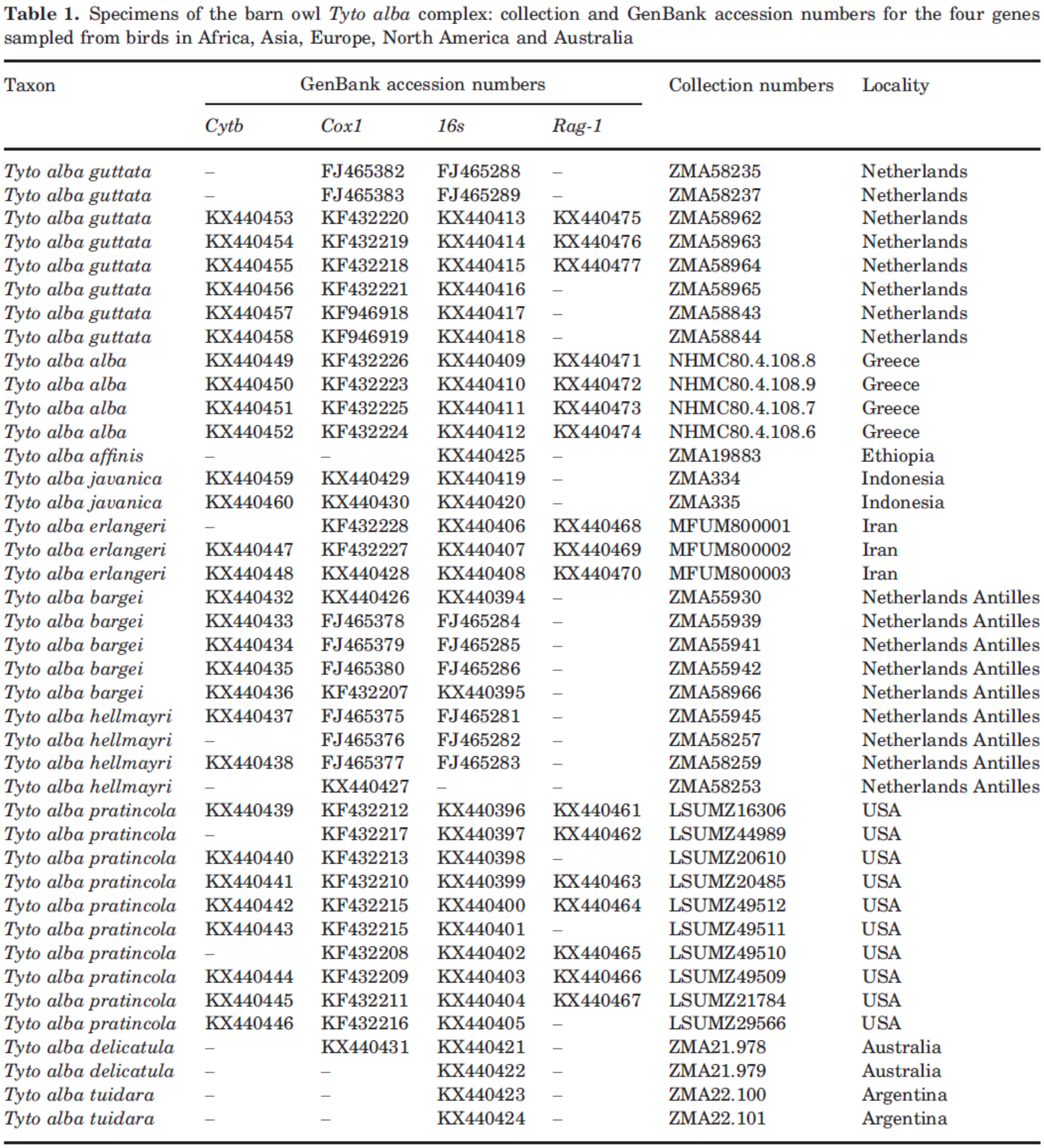
Table 1. Specimens of the barn owl *Tyto alba* complex: collection and GenBank accession numbers for the four genes sampled from birds in Africa, Asia, Europe, North America and Australia

Taxon	GenBank accession numbers				Collection numbers	Locality
	Cytb	*Cox1*	*16s*	*Rag-1*		
Tyto alba guttata	–	FJ465382	FJ465288	–	ZMA58235	Netherlands
Tyto alba guttata	–	FJ465383	FJ465289	–	ZMA58237	Netherlands
Tyto alba guttata	KX440453	KF432220	KX440413	KX440475	ZMA58962	Netherlands
Tyto alba guttata	KX440454	KF432219	KX440414	KX440476	ZMA58963	Netherlands
Tyto alba guttata	KX440455	KF432218	KX440415	KX440477	ZMA58964	Netherlands
Tyto alba guttata	KX440456	KF432221	KX440416	–	ZMA58965	Netherlands
Tyto alba guttata	KX440457	KF946918	KX440417	–	ZMA58843	Netherlands
Tyto alba guttata	KX440458	KF946919	KX440418	–	ZMA58844	Netherlands
Tyto alba alba	KX440449	KF432226	KX440409	KX440471	NHMC80.4.108.8	Greece
Tyto alba alba	KX440450	KF432223	KX440410	KX440472	NHMC80.4.108.9	Greece
Tyto alba alba	KX440451	KF432225	KX440411	KX440473	NHMC80.4.108.7	Greece
Tyto alba alba	KX440452	KF432224	KX440412	KX440474	NHMC80.4.108.6	Greece
Tyto alba affinis	–	–	KX440425	–	ZMA19883	Ethiopia
Tyto alba javanica	KX440459	KX440429	KX440419	–	ZMA334	Indonesia
Tyto alba javanica	KX440460	KX440430	KX440420	–	ZMA335	Indonesia
Tyto alba erlangeri	–	KF432228	KX440406	KX440468	MFUM800001	Iran
Tyto alba erlangeri	KX440447	KF432227	KX440407	KX440469	MFUM800002	Iran
Tyto alba erlangeri	KX440448	KX440428	KX440408	KX440470	MFUM800003	Iran
Tyto alba bargei	KX440432	KX440426	KX440394	–	ZMA55930	Netherlands Antilles
Tyto alba bargei	KX440433	FJ465378	FJ465284	–	ZMA55939	Netherlands Antilles
Tyto alba bargei	KX440434	FJ465379	FJ465285	–	ZMA55941	Netherlands Antilles
Tyto alba bargei	KX440435	FJ465380	FJ465286	–	ZMA55942	Netherlands Antilles
Tyto alba bargei	KX440436	KF432207	KX440395	–	ZMA58966	Netherlands Antilles
Tyto alba hellmayri	KX440437	FJ465375	FJ465281	–	ZMA55945	Netherlands Antilles
Tyto alba hellmayri	–	FJ465376	FJ465282	–	ZMA58257	Netherlands Antilles
Tyto alba hellmayri	KX440438	FJ465377	FJ465283	–	ZMA58259	Netherlands Antilles
Tyto alba hellmayri	–	KX440427	–	–	ZMA58253	Netherlands Antilles
Tyto alba pratincola	KX440439	KF432212	KX440396	KX440461	LSUMZ16306	USA
Tyto alba pratincola	–	KF432217	KX440397	KX440462	LSUMZ44989	USA
Tyto alba pratincola	KX440440	KF432213	KX440398	–	LSUMZ20610	USA
Tyto alba pratincola	KX440441	KF432210	KX440399	KX440463	LSUMZ20485	USA
Tyto alba pratincola	KX440442	KF432215	KX440400	KX440464	LSUMZ49512	USA
Tyto alba pratincola	KX440443	KF432215	KX440401	–	LSUMZ49511	USA
Tyto alba pratincola	–	KF432208	KX440402	KX440465	LSUMZ49510	USA
Tyto alba pratincola	KX440444	KF432209	KX440403	KX440466	LSUMZ49509	USA
Tyto alba pratincola	KX440445	KF432211	KX440404	KX440467	LSUMZ21784	USA
Tyto alba pratincola	KX440446	KF432216	KX440405	–	LSUMZ29566	USA
Tyto alba delicatula	–	KX440431	KX440421	–	ZMA21.978	Australia
Tyto alba delicatula	–	–	KX440422	–	ZMA21.979	Australia
Tyto alba tuidara	–	–	KX440423	–	ZMA22.100	Argentina
Tyto alba tuidara	–	–	KX440424	–	ZMA22.101	Argentina

America and Curaçao (*T. a. pratincola, T. a. hellmayri, T. a. tuidara, T. a. bargei*). The second group, the *alba* clade, included subspecies from the Netherlands, Greece, Iran, and Ethiopia (*T. a. guttata, T. a. alba, T. a. erlangeri, T. a. affinis*). The third group, the *javanica* clade, contained samples from Indonesia, India, and Australia (*T. a. javanica, T. a. stertens, T. a. delicatula*) (see tree below). The dating analysis indicated that the Barn Owl complex originated during the Middle Miocene, and the biogeographical reconstruction suggested an origin in the Old World. A low amount of ecological niche overlap was estimated among all three lineages.

Alibadian et al. (2016) proposed that the taxonomy of *Tyto alba* be redefined and that at least three species should be recognized. However, because not all *T. alba* subspecies were included in the study, the authors established the species limits based mainly on the geographic distribution of the subspecies sampled. The authors proposed restricting the specific epithet *alba* to populations from the Afrotropical and Palearctic regions to at least eastern Iran. They suggested elevating the *furcata* clade (populations from Nearctic and Neotropical regions, including at least part of the Caribbean) to species status under the name *Tyto furcata*. The *javanica* clade, including populations from Indonesia, India, and Australia (*T. a. javanica, T. a. stertens, T. a. delicatula*), was proposed for elevation under the name *Tyto javanica*, because the name *javanica* has priority over *delicatula.*

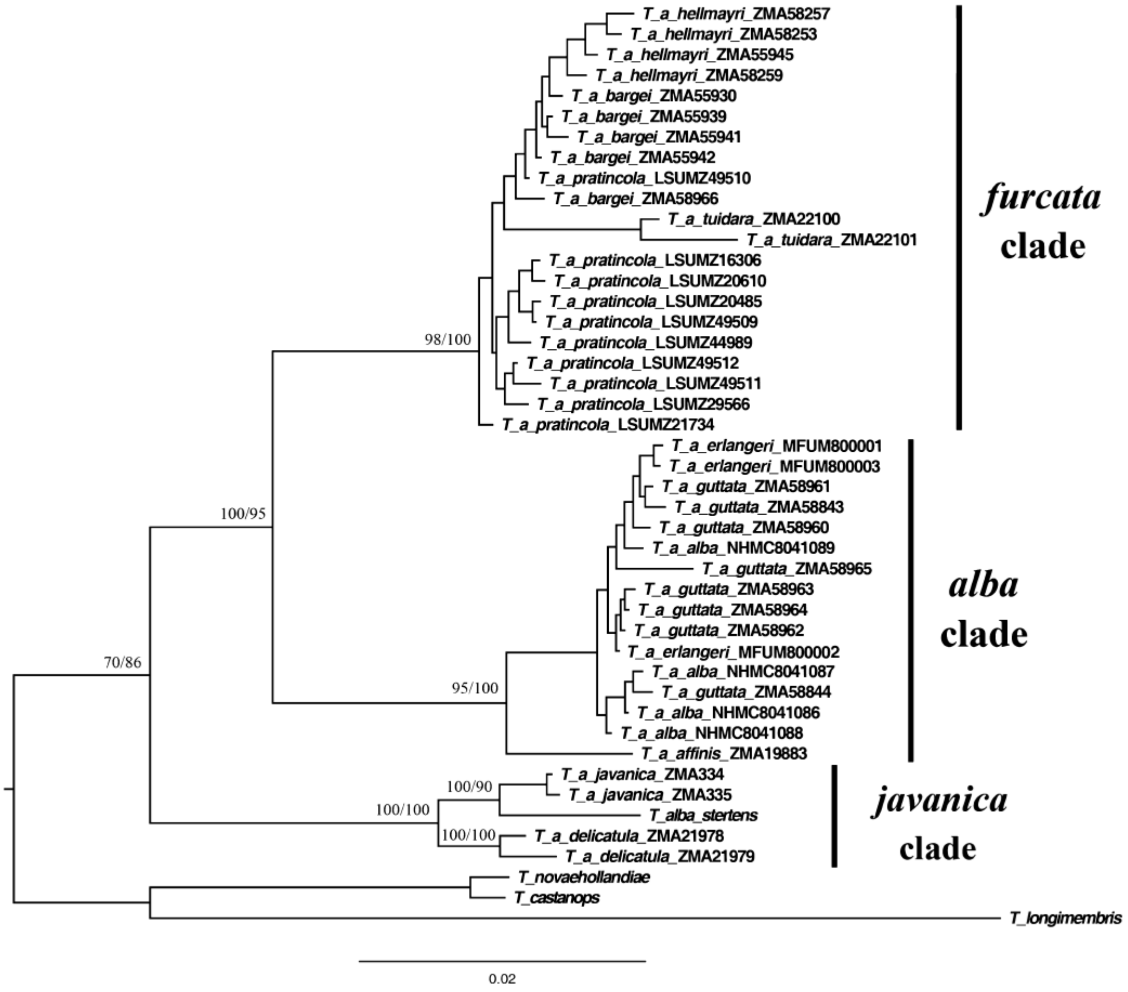

Figure 1. Fifty-percent majority-rule consensus tree sampled from the posterior distribution of the most-partitioned analysis based on 2838 bp of *16s*, *Cox1*, *Cytb*, and *Rag1*. Posterior probability values from the Bayesian analysis are indicated as the first number and the second number represents maximum likelihood bootstrap values.

Uva et al. (2018) published another molecular study of the systematic relationships of the barn owls and relatives, estimated divergence times using fossil calibrations, and reconstructed ancestral ranges. Uva et al. (2018) analyzed 179 genetically different individuals belonging to 16 species of *Tyto* and 1 species of *Phodilus*, which included over 30 subspecies distributed worldwide (see map below). They obtained sequences of five mitochondrial markers (ND6, CO1, control region, cytochrome b, and 16S) and two nuclear markers (C-MOS and RAG-1). They inferred maximum likelihood phylogenetic (RAxML) and Bayesian inference trees (BEAST v. 1.8.4) and constructed a haplotype network of the Common Barn Owl based on the cyt-b sequences (TCS, POPart).

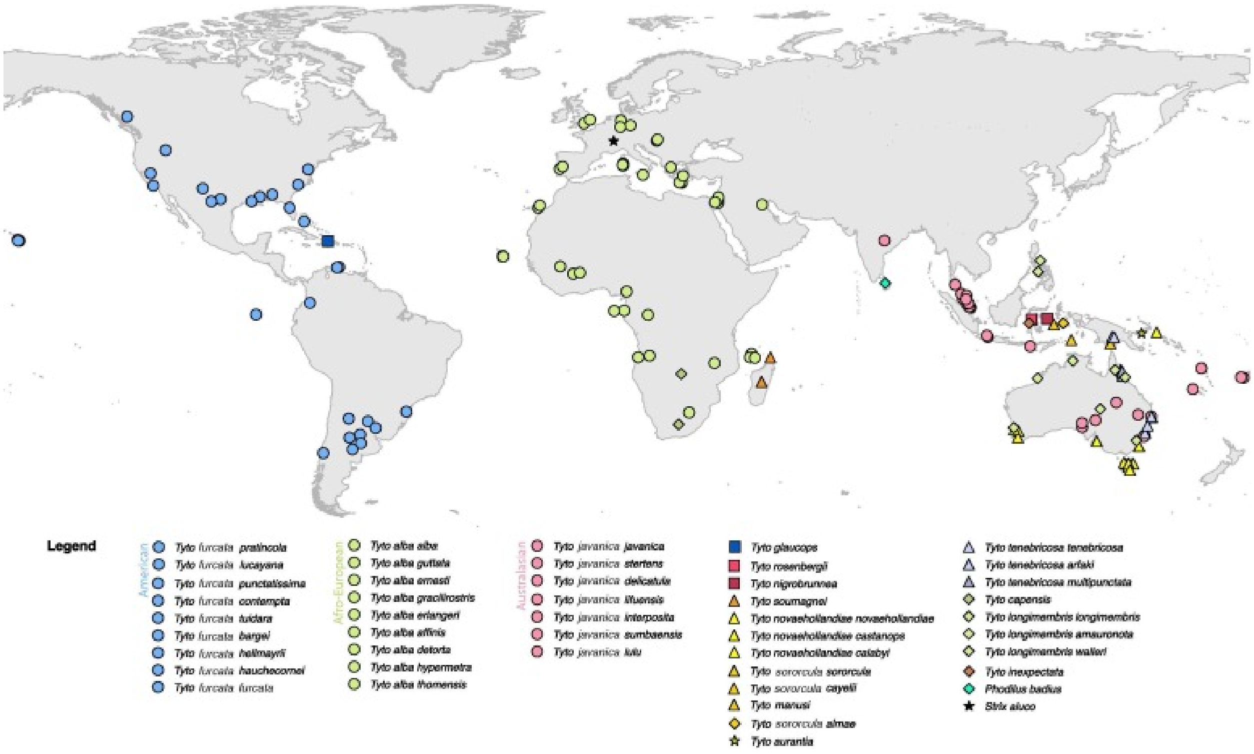

Figure 1. Sample location map - sample locations, legend following the classification of Gill and Donsker (2018). When samples were missing precise locations, approximate coordinates were given.

Phylogenetic and haplotype network analyses (Figure 3) recovered three main lineages within the Common Barn Owl group, which differed by 5.82 to 9.33% in cyt-b sequence, supporting the results from Alibadian et al. (2016). The scientific and common names used by Uva et al. (2018) followed the IOC World Bird List.

- Australasian clade: samples of the Eastern Barn Owl, *T. javanica*, from Australia and Indonesia, including the Sulawesi Masked Owl, *T. rosenbergii*, *T. javanica* from India, Malaysia and Java, and *T. nigrobrunnea.*
- American clade: samples of the American Barn Owl *T. furcata,* and the Ashy-faced Owl, *T. glaucops*. This group also includes a subclade of two island endemics from Galapagos (*T. f. punctatissima*) and Hispaniola (*T. g. glaucops*).
- Afro-European clade: samples of the crown group of all Western Barn Owls, *T. alba*, and the São Tomé Barn Owl, *T. a. thomensis*.

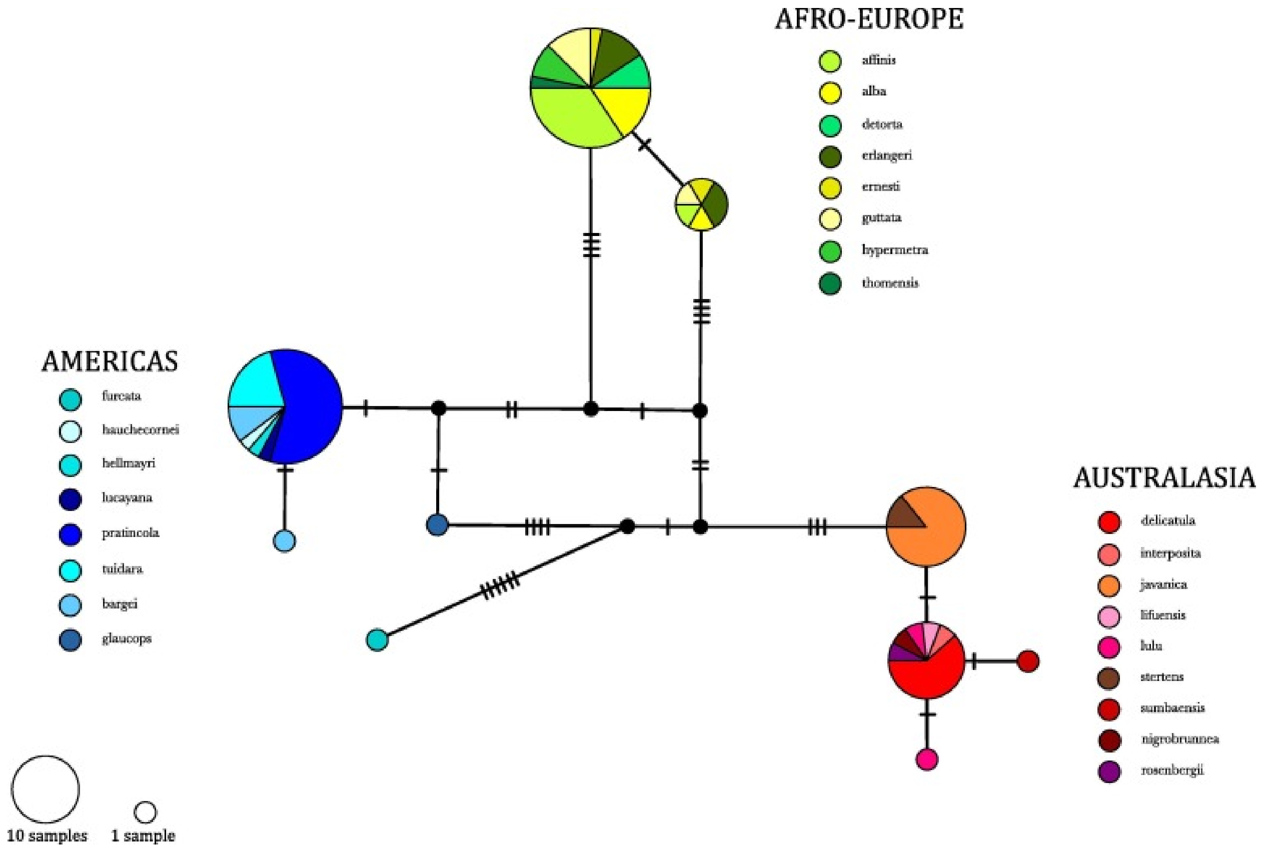

Figure 3. Genetic structure within the Common Barn Owl group, including all taxa nested within the three major clades - TSC haplotype networks drawn for cyt-b sequences, following the classification in Gill and Donsker (2018).

The dating analysis indicated that the Barn Owl complex originated during the Late Miocene (ca. 6 mya). The biogeographical reconstruction suggested an origin in the Australasian and African regions.

Uva et al. (2018) concluded that the Common Barn Owl consists of three evolutionary units, as in Alibadian et al. (2016), and indicated that three species should be recognized:

- African and European populations: *Tyto alba*, Western Barn Owl
- North, Cental and South American populations: *Tyto furcata*, American Barn Owl
- South and southeastern Asian and Australian populations: *Tyto javanica*, Eastern Barn Owl

Recommendation:

We recommend splitting *Tyto alba* into three species to better reflect the evolutionary trajectory of the clade. The phylogenetic evidence suggests geographic and genetic isolation of the three lineages (Wink et al. 2009, Nijman & Alibadian 2013, Alibadian et al. 2016, Uva et al. 2018), in addition to their correlated morphological traits (Alibadian et al. 2016).

(1) Afrotropical and Palaearctic populations: *Tyto alba*, Western Barn Owl
(2) American populations: *Tyto furcata*, American Barn Owl
(3) Eastern Asian and Australian populations: *Tyto javanica*, Eastern Barn Owl

The recommended English names are based on those proposed by Uva et al. (2018), which are currently used by the IOC World Bird List (Gill & Donsker 2018).

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Submitted by: Rosa Alicia Jiménez and Carla Cicero, Museum of Vertebrate Zoology

Date of Proposal: 26 February 2018, revised 15 March 2018

Split LeConte’s Thrasher (*Toxostoma lecontei*) into two species

Background:

LeConte’s Thrasher (*Toxostoma lecontei*) inhabits sparsely vegetated habitats and sand dunes in arid regions of the southwestern United States and northwestern Mexico. Three subspecies are typically recognized within LeConte’s Thrasher: *T. l. lecontei*, *T. l. arenicola*, and *T. l. macmillanorum* (Fig. 1). Zink et al. (1997) found that *T. l. arenicola* and *T. l. lecontei* + *T. l. macmillanorum* were reciprocally monophyletic in mtDNA gene trees, and suggested that *T. l. arenicola* should be elevated to species status. However, a NACC proposal to implement this taxonomic split did not pass (8–1 vote; see http://checklist.aou.org/nacc/proposals/comments/2015_A_comments_web.html - 2015–A–8 for comments). Many NACC committee members cited the lack of information regarding vocal displays, playback responses, contact zone information, and nuclear DNA as reasons to not split *T. lecontei*. A recent study examined phenotypic and genetic (mtDNA and nuDNA) variation within *T. lecontei* in more detail, suggesting that species limits within *T. lecontei* should be reconsidered.

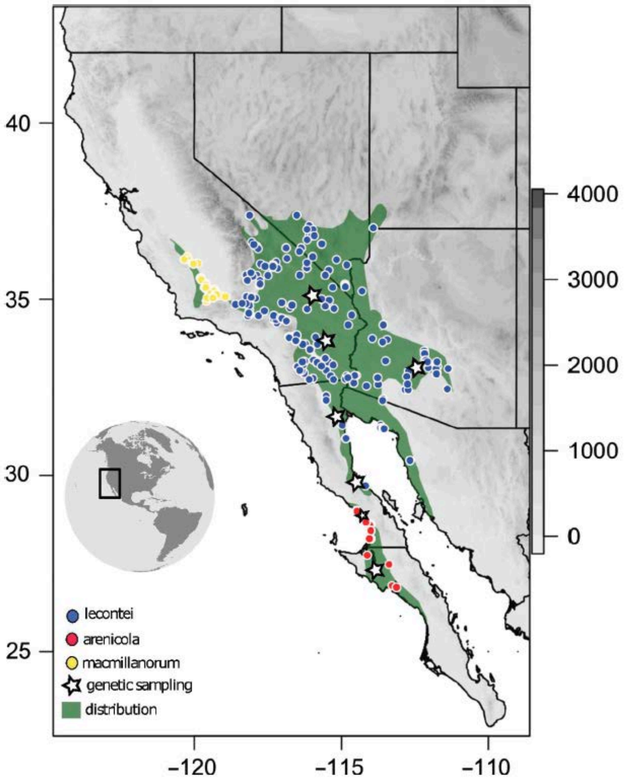

Figure 1: Map with locality information for the morphological (blue, red and yellow circles) and genetic sampling (stars). Current distribution polygon reproduced with permission from BirdLife and NatureServe; elevation grayscale on right in meters, longitude on the x-axis, and latitude on the y-axis.

New information:

Vázquez-Miranda et al. (2017) presented new phenotypic and genetic analyses that provide new insights into the evolutionary history and taxonomy of *T. lecontei*. Specifically, Vázquez-Miranda et al. (2017) examined phenotypic differentiation among the three currently recognized subspecies within *T. lecontei*. Vázquez-Miranda et al. (2017) measured tarsus length, culmen length, flat wing, and tail length of 551 specimens (327 males, 224 females) of the three subspecies from 159 localities (Fig. 1). Zink et al. (1997) had collected data on dorsal coloration, which were also included in analyses conducted by Vázquez-Miranda et al (2017). Principal component analyses revealed considerable overlap in both morphometric characters (Fig. 2) and coloration characters (Fig. 3).

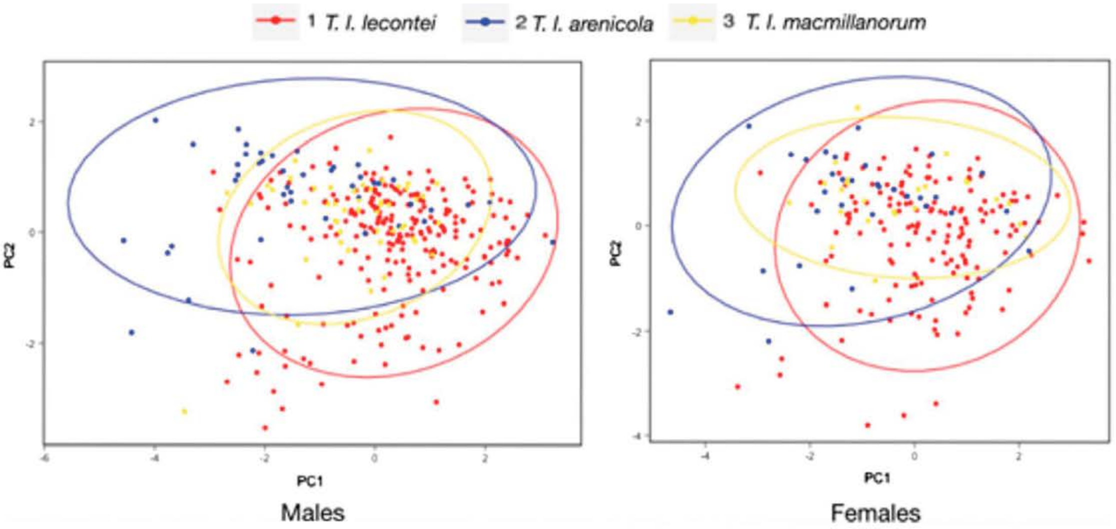

Figure 2: Principal components analysis of the full dataset of four morphological characters from three subspecies of T. lecontei*; circles represent 95% confidence ellipses. The plots show no distinct grouping of subspecies based on morphology.*

Vázquez-Miranda et al. (2017) also examined genetic variation among two of the three currently recognized subspecies: *T. l. lecontei* and *T. l. arenicola*. Vázquez-Miranda et al. (2017) sequenced ≥ 14 samples for both *T. l. lecontei* and *T. l. arenicola* for one mtDNA locus (ND2), 7 sex-linked loci, and 9 autosomal loci. They conducted both concatenated and species-tree phylogenetic analyses. Corroborating Zink et al. (1997), Vázquez-Miranda et al. (2017) found reciprocal monophyly in both mtDNA gene trees (Fig. 4A) and concatenated nuDNA phylogenies (Fig. 4B), although the node uniting all *T. l. arenicola* did not receive strong support (BP < 0.95). The species tree recapitulated the concatenated alignment with strong nodal support.

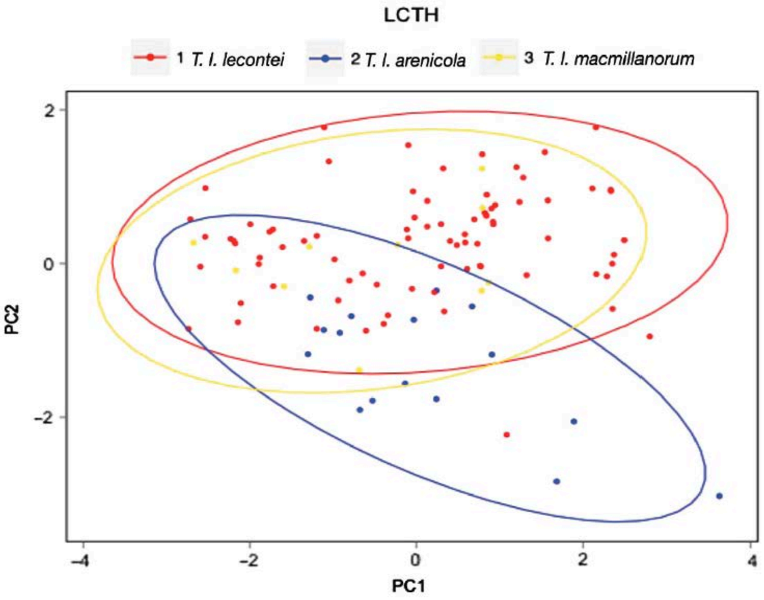

Figure 3: Principal components analysis of three coloration characters from subspecies of T. lecontei *showing overlap in principal components space. The circles show 95% confidence ellipses.*

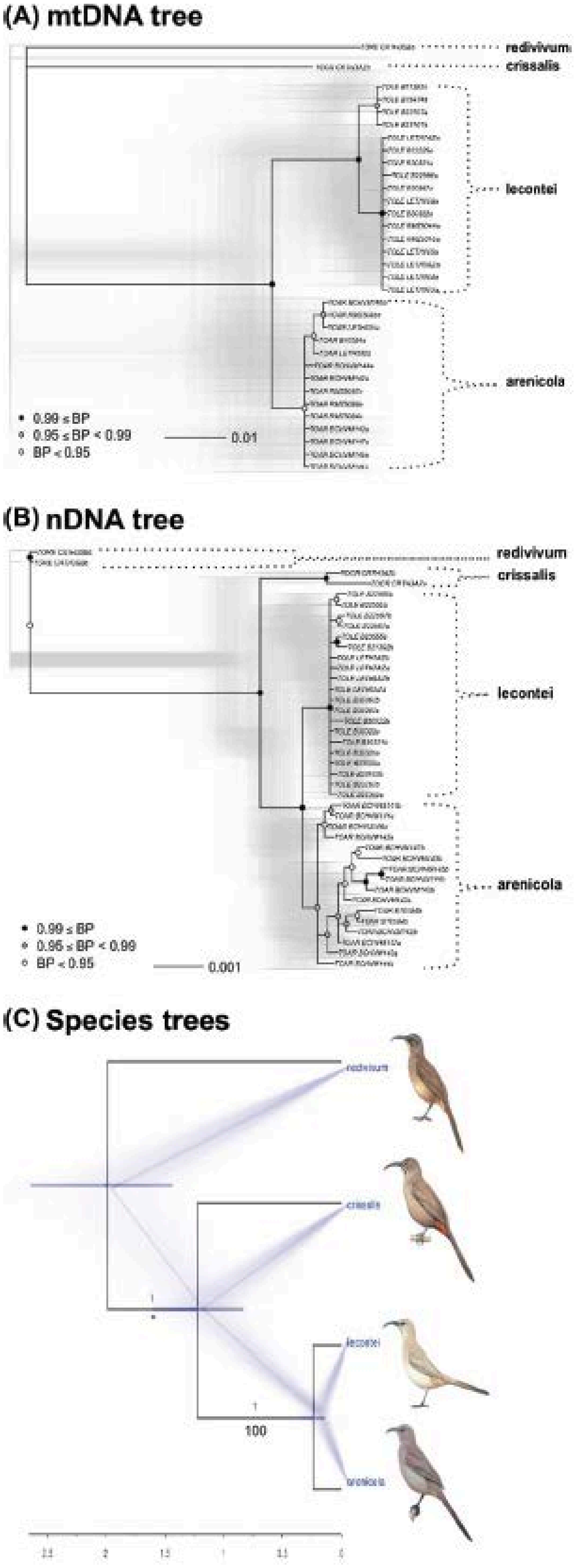

Figure 4: Speciation and lineage divergence between T. l. lecontei *and* T. l. arenicola*. (A) Single locus (mtDNA; ND2) Bayesian tree in black and cloudogram in grey. (B) Concatenated multilocus (16 nDNA loci) tree in black and cloudogram in grey. Legend indicates clade Bayesian posterior probability support (BP) and scale corresponds to branch lengths on substitutions/site units. Tip labels indicate sample voucher number and terminal taxon assignment for species tree analyses: TORE – California thrasher* T. redivivum*, TOCR – Crissal thrasher* T. crissale*, TOLE – Le Conte's thrasher* T. l. lecontei*, and TOAR – Vizcaíno thrasher* T. l. arenicola*. (C) Time calibrated species tree in black and cloudogram in blue. *BEAST posterior credibility support is depicted as above-branch values and SVDquartets bootstrap percentages as below-branch values (tree identical to *BEAST's, not shown). The asterisk (*) indicates a branch being a product of a posteriori quartet rooting (non-ultrametric) and, thus, has no bootstrap support value. The horizontal bars represent the 95% highest posterior density (HPD) time interval. Bottom scale represents time in millions of years. Images taken with permission from the Handbook of the Birds of the World (HBW Lynx Edicions). Note that the phenotypic differences between Le Conte's and Vizcaino thrashers represent extremes on a color gradient as many individuals show overlap in coloration.*

Haplotype networks of individual loci revealed varying degrees of lineage sorting between *T. l. arenicola* and *T. l. lecontei* that roughly corresponded to the effective population size of the locus in question (Fig. 5). Vázquez-Miranda et al. (2017) noted that the ND2 genetic distance between *T. l. lecontei* and *T. l. arenicola* is greater than that between Bendire's Thrasher (*T. bendirei*) and Gray Thrasher (*T. cinereum*) (2.08% vs 1.3%), suggesting that genetic differentiation observed between *T. l. lecontei* and *T. l. arenicola* is similar to interspecific differences among other thrashers. The addition of Z-linked and autosomal loci by Vázquez-Miranda et al. (2017) corroborates the mtDNA patterns recovered by Zink et al. (1997) and suggests little ongoing gene flow between *T. l. lecontei* and *T. l. arenicola*.

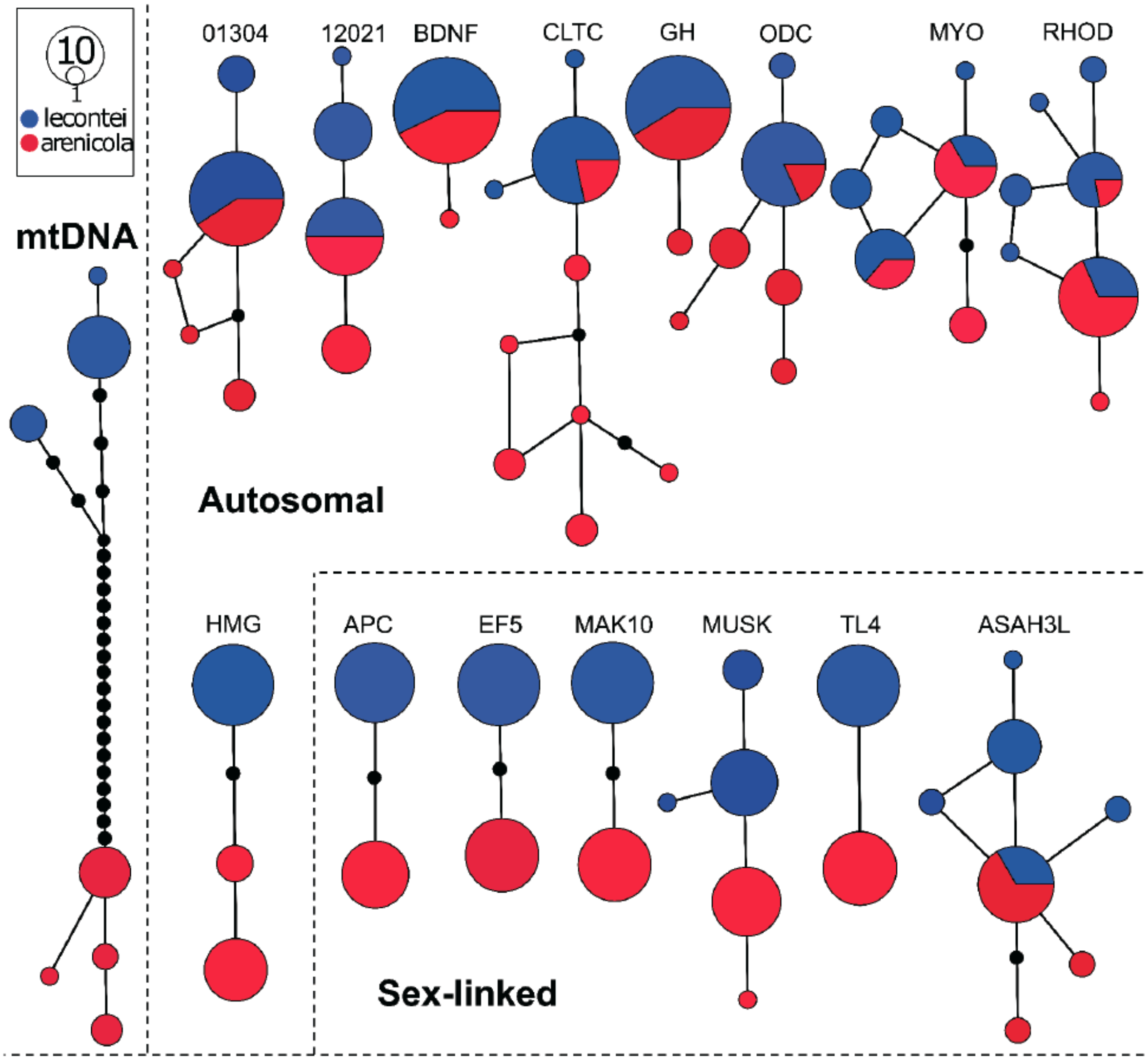

Figure 5: Median-joining (MJ; Bandelt et al. 1999) phased allele (haplotype in mtDNA) networks by locus from POPART (Leigh and Bryant 2015). Colors: Toxostoma lecontei lecontei *alleles in blue,* T. l. arenicola *alleles in red. Closed circles represent non-sampled alleles. Circle size corresponds to allele number (see legend). Dashed lines separate loci with different ploidy (see Table 2).*

Vázquez-Miranda et al. (2017) constructed ecological niche models and found no evidence for niche differentiation between *T. l. lecontei* and *T. l. arenicola*. They suggested that similarity in abiotic habitat combined with similarity in morphometric characters may be preventing the two lineages from co-occurring due to competitive exclusion (Hutchinson 1959, Zink 2014). Furthermore, Vázquez-Miranda et al. (2017) noted that the region that divides *T. l. lecontei* and *T. l. arenicola* is a common biogeographic barrier in other taxa, including fish, reptiles, mammals, amphibians, and various invertebrates.

One criticism of the earlier NACC proposal based solely on mtDNA data (Zink et al.

1997) was that vocal differences were not addressed and it was unknown what transpires in zones where the two lineages come into contact. Vázquez-Miranda et al. (2017) stated that *T. l. lecontei* and *T. l. arenicola* are essentially allopatric. Whereas previous work had suggested that a narrow contact zone may exist (Sheppard 1996), extensive fieldwork by Vázquez-Miranda et al. (2014) did not find any such contact zone. Vázquez-Miranda et al. (2014) did not analyze vocalizations in their study, but noted that individuals in the range of *T. l. arenicola* were attracted to a tape recording of an individual from southern California representing *T. l. lecontei* (RMZ in 1994; HVM in 2009). However, the authors noted that many *Toxostoma* species are attracted to tape recordings of *T. l. lecontei* (Reichard and Price 2008) and that other thrashers, such as LeConte's and Crissal thrashers readily respond to playback of each other's vocalizations. Thrashers often incorporate confamilial songs into repertoires that can exceed 1500 songs (Reichard and Price 2008). Vázquez-Miranda et al. (2017) subsequently suggested that vocal displays may not be a good indicator of pre-mating barriers to gene flow in *Toxostoma* thrashers and that other data should be considered to evaluate species limits.

Vázquez-Miranda et al. (2017) suggested Vizcaíno Thrasher (Brewer 2001) as the most appropriate English name for *T. arenicola*. This common name draws from the Vizcaíno Desert and highlights this taxon's area of endemism. Vázquez-Miranda et al. (2017) did not discuss English names for the other daughter taxon of this proposed split. I suggest that *T. l. lecontei* and *T. l. macmillanorum* retain the common name of LeConte's Thrasher because (1) this common name is already in wide use; (2) the geographic range of this proposed daughter taxon is much larger than *T. l. arenicola*; (3) the common name will match the specific epithet of the scientific name.

Recommendation:

Based largely on molecular divergence and lineage sorting in mtDNA and nuDNA markers, **I recommend** that *T. arenicola* be recognized as a separate species from *T. lecontei*. The level of genetic differentiation (mtDNA divergence ~ 2.1%; ~140,000 yrs divergence) is similar to interspecific comparisons between other widely recognized species of thrashers, and the relative degree of lineage sorting among markers that differ in ploidy (mtDNA; Z-linked; autosomal) reflect a neutral process of lineage sorting in the absence of gene flow. There seems to be little to no geographic overlap between *T. l. arenicola* and *T. l. lecontei* amid low population densities, which precludes a more detailed study of assortative mating. Vocal variation and playback responses have not been examined. However, mimids—and thrashers in particular—are prone to respond to both intraspecific and interspecific vocal signals, which may make vocal differentiation and playback responses less reliable as signals of premating reproductive isolation in these taxa. Vázquez-Miranda et al. (2017) documented similarity in morphometric characters, plumage, and ecological niches between the two lineages, suggesting these lineages may be conspecific, or may represent cryptic sister species that are developmentally or evolutionarily constrained to a particular phenotype and/or niche. To me, the molecular evidence presented by Vázquez-Miranda et al. (2017) depicts a scenario of prolonged reproductive isolation and evolutionary divergence that is deeper and more pronounced than many species currently recognized by the NACC, such as *Acanthis flammea* and *A. hornemanni*, or *Vermivora cyanoptera* and *V. chrysoptera*. Thus, to support consistency in taxonomic treatments, I recommend that *T. arenicola* and *T. lecontei* be recognized as species.

Regarding English names, I follow Vázquez-Miranda et al. (2017)'s recommendation of using Vizcaíno Thrasher for the daughter taxon that corresponds to *T. l. arenicola*. For the reasons stated above, I believe that *T. l. lecontei* and *T. l. macmillanorum* should retain LeConte's Thrasher as their English name.

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

Date of proposal: 27 February 2018

Revise generic assignments of New World “grassland” sparrows

Background:

Recent large-scale phylogenetic studies of the New World nine-primaried oscines have revealed extensive paraphyly at the family, genus, and species level, and have resulted in substantial shifts in the taxonomic treatment of the group. Some taxonomic issues are challenging, and may require creative solutions. One such problem is the paraphyly of the New World sparrow genus *Ammodramus* (Passerellidae). The genus, as currently recognized, consists of seven species of grassland and marsh sparrows found in open habitats in North America:

Ammodramus savannarum
Ammodramus bairdii
Ammodramus henslowii
Ammodramus leconteii
Ammodramus nelsoni
Ammodramus caudacutus
Ammodramus maritimus

Two additional species are found in South America:

Ammodramus aurifrons
Ammodramus humeralis

New Information:

Klicka *et al*. (2014) published the first comprehensive molecular phylogeny of the Passerellidae, which showed that the genus *Ammodramus*, as currently recognized, is paraphyletic, comprising at least three distinct groups that are not each other’s closest relatives. Two groups were relatively closely related within a largely North American clade of sparrows (the “grassland” sparrows), while the third was more distantly related, and sister to a group of largely South and Central American sparrows (Klicka *et al*. 2014, Barker *et al*. 2015). These results largely agree with earlier work by Klicka and Spellman (2007) who showed, using mtDNA sequence data from a smaller set of species, that *Ammodramus* was paraphyletic. *Ammodramus savannarum* fell well outside of a clade of “grassland” sparrows that included the remaining *Ammodramus* (which was found to be further paraphyletic), *Melospiza*, *Passerculus*, and *Xenospiza*. Additional work by Bryson *et al*. (2016), using ultraconserved element data (UCEs), also found strong support for a paraphyletic *Ammodramus*, though only two species were sampled (*A. savannarum* and *A. leconteii*).

In all analyses that sampled one or both South American species of *Ammodramus*, they consistently, and with strong support, grouped together with *A. savannarum* (DaCosta *et al*. 2009, Klicka *et al*. 2014, Barker *et al*. 2015). Together, these three species are part of a well-supported clade that includes *Peucaea, Arremonops*, and *Rhynchospiza*. Thus, without question, *A. aurifrons*, *A. humeralis* and *A. savannarum* should not be classified in the same genus as the remaining *Ammodramus*.

Within the "grassland" sparrow group, relationships have been more challenging to resolve, and the paraphyly of *Ammodramus* within this clade presents a complicated problem that cannot be addressed without considering changing the names of other passerellid genera. The "marsh" or "sharp-tailed" sparrows, consisting of *A. leconteii, A. nelsoni, A. caudacutus,* and *A. maritimus,* have consistently been found to form a well-supported clade within the larger "grassland" group, which includes *A. bairdii*, *A. henslowii* and the genera *Melospiza, Passerculus, Xenospiza, Pooecetes*, and *Artemisiospiza* (Klicka and Spellman 2007, Klicka *et al*. 2014, Barker *et al*. 2015). Thus, the quartet of "marsh" *Ammodramus* species deserves a distinct genus.

Resolving the relationships of *A. bairdii* and *A. henslowii* have been particularly challenging, with no published topology receiving strong support. Various analyses have alternatively suggested that *A. bairdii* and *A. henslowii* are sister taxa (though with weak support) that are in turn sister to *Passerculus* (mtDNA tree of Klicka *et al*. 2014; Fig. 1), or are separate from one another, either in a large polytomy with *Melospiza*, *Passerculus*, and *Xenospiza* (species tree of Klicka *et al*. 2014), or with *A. henslowii* sister to *Passerculus* and *A. bairdii* sister to *Xenospiza* (Barker *et al*. 2015; Fig. 2). It is clear from the present data that *A. henslowii* and *A. bairdii* are both closely related to *Melospiza, Passerculus* and *Xenospiza*, but relationships among these taxa are not well resolved.

Further complicating matters is an ambiguous issue concerning the type species of *Ammodramus*, due to an unfortunate mishap in the order of publication of two papers by Swainson in 1827 (later referred to as the infamous "Swainsonian genera"; Allen 1905). The short version of this story is that Swainson (1827b) clearly described *Ammodramus* with *A. caudacutus* as the type. However, due to publication delays, this publication apparently, and accidentally, came out a few months after he (Swainson 1827a) described the species *A. bimaculatus* (now a subspecies of *A. savannarum*) and assigned it to *Ammodramus* (whose genus description was supposed to have already been published, given the dates that he submitted the two manuscripts). Therefore, the name *Ammodramus* was accidentally first printed with the description of *A. bimaculatus*, not the formal intended description of the genus wherein *A. caudacutus* was designated as the type. This issue affected several other bird genera. Oberholser (1905) took a strict interpretation of priority based on the dates of publication (June versus September 1827), and, despite the clear intentions of Swainson, assigned *A. bimaculatus* as the type of *Ammodramus*. Allen (1905) objected on the basis of common sense, but in the Fifteenth Supplement to the A.O.U. Check-List (Allen et al. 1909), the committee sided with Oberholser after arbitration by the Nomenclature Committee of the International Zoological Congress.

Now, nearly two centuries later, this mishap continues to be consequential, as the two putative types are clearly in different genera and we must assign a type in order to split the genus. In this proposal, we reluctantly accept the AOU checklist committee's decision in the Fifteenth Supplement (1909) that the type of *Ammodramus* is *A. bimaculatus* (now *A. savannarum*), rather than the intended *A. caudacutus*.

Recommendations:

Here we present a three-part recommendation for changes that would resolve the taxonomy of this genus:

A. *Ammodramus savannarum*, *A. humeralis*, and *A. aurifrons* remain in *Ammodramus*. This follows the taxonomy of del Hoyo and Collar (2016). See Swainson (1827a, b), Allen (1905), and Allen et al. (1909) for a discussion of priority.

B. Place the four "marsh" sparrows, *A. leconteii, A. maritimus, A. nelsoni,* and *A. caudacutus*, in *Ammospiza*, originally described by Oberholser (1905) for *A. caudacutus*. The genus *Ammospiza* has been used previously for at least some of these species (Oberholser 1905, Murray 1968, Robins and Schnell 1971), and this classification is currently used by the Howard and Moore Checklist (Dickinson and Christidis 2014).

C. This part concerns the more difficult treatment of *A. bairdii* and *A. henslowii*. We describe three options before making a recommendation:

    1. Transfer *A. bairdii* and *A. henslowii* to *Passerculus* (the type species of which is *savanna*, now considered a subspecies of *sandwichensis*), following the results of Klicka *et al*. (2014). However, transferring *A. bairdii* and *A. henslowii* to *Passerculus* exclusive of any other taxa would not be recommended, as not all of the analyses of Klicka *et al*. (2014) support this, nor do the results of Barker *et al*. (2015). Nevertheless, this classification is used by del Hoyo and Collar (2016).

    2. Following the treatment of Dickinson and Christidis (2014), place *A. bairdii* and *A. henslowii* in the separate genus *Centronyx*, described by Baird in 1858 with the type species *A. bairdii*. Although this classification agrees with the mitochondrial trees recovered in Klicka and Spellman (2007) and

Klicka *et al*. (2014), and would result in the least change to other grassland sparrow genera, this may not be the best approach given the uncertainty in the nuclear sequence data in Klicka *et al*. (2014), the low-support this topology receives from the mtDNA trees, and the phylogeny in Barker *et al*. (2015). In short, although it is tempting to assume a sister relationship between *A. bairdii* and *A. henslowii* based on ecology and phenotype, molecular support for this relationship is not strong and the two species are very closely related to other members of the group.

3. Ultimately, we recommend that *A. bairdii* and *A. henslowii* be lumped in a single genus along with *Passerculus*, *Melospiza*, and *Xenospiza*. The genus *Passerculus* would have priority over *Melospiza* and *Xenospiza*, having been described in 1838 (*Melospiza* was described in 1858, *Xenospiza* in 1931). Due to the uncertainty in the relationships of *A. bairdii* and *A. henslowii* in relation to these three genera, and the poor resolution for members of this 'grassland' clade in all phylogenetic studies to date, we feel that lumping these genera into a single, inclusive *Passerculus* is the most reasonable approach. This approach was originally proposed by Klicka and Spellman (2007). Though this would eliminate two long-established genera (*Melospiza* and *Xenospiza*, the latter of which has itself been a controversial genus [Robins and Schnell 1971]), this solution would be the most stable and least likely to change with additional data.

At first glance, it may seem that lumping these species into *Passerculus* would create a genus that is older and more ecologically and phenotypically diverse than other passerellid genera. However, we suggest that this perspective is a result of the bias of long-standing familiarity with the present taxonomy, which likely distracts from similarities among the members of a more inclusive *Passerculus*. The size or age of a *Passerculus* that includes *Melospiza, Xenospiza*, and *A. bairdii* and *A. henslowii* would not be older or contain more species than several genera in Passerellidae.

Finally, although it may seem desirable to wait for more information before resolving the genus-level classification of this grassland clade, unfortunately this is not possible if we are to resolve the more obvious and conspicuous problems with *Ammodramus* paraphyly (parts A and B). The research group that has done the most work on passerellid systematics in recent years has no plans to continue working on these species (J. Klicka, in litt.).

In summary, we recommend Yes to part A and B. For part C, we propose that option #3 is the best approach, and recommend Yes to Part C option 3.

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Date of Proposal: 1 March 2018

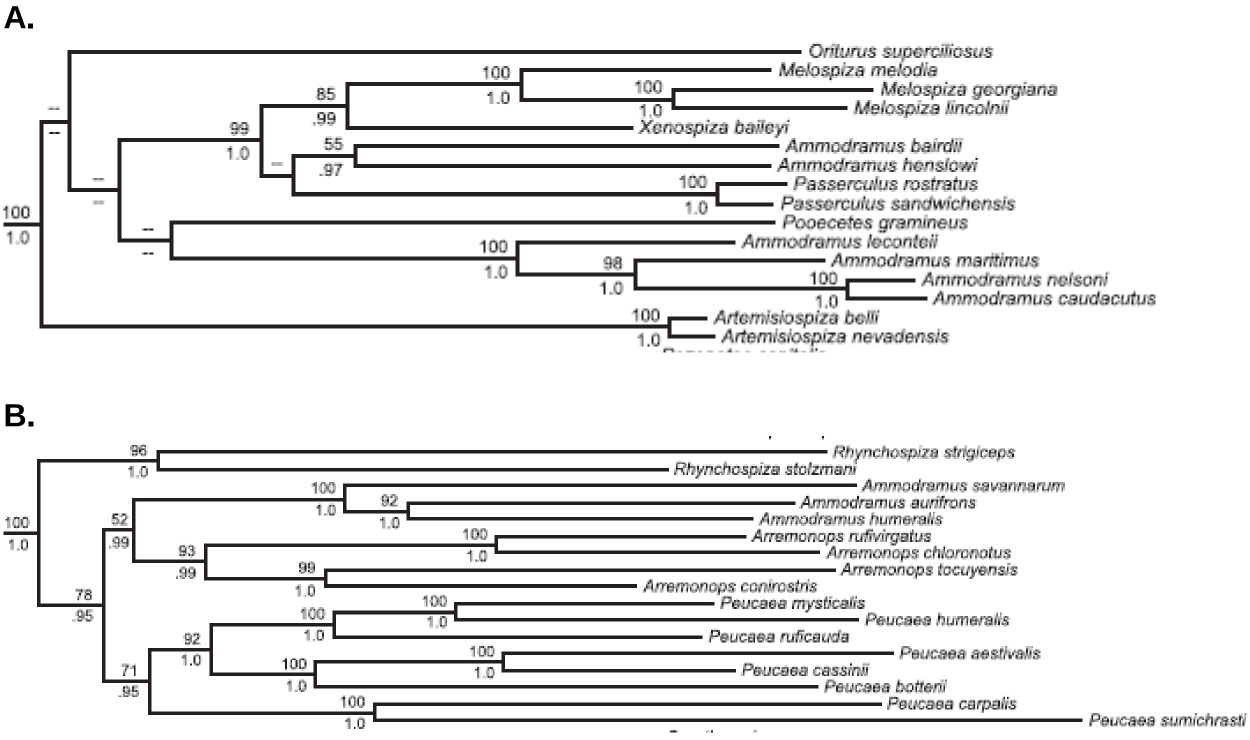

Figure 1. Part of Figure 1 from Klicka *et al*. (2014), showing the best maximum likelihood tree inferred from mtDNA sequence data. (A) shows the relationships among the "grassland" sparrow clade, which includes the genera *Melospiza*, *Passerculus*, and *Xenospiza*, as well as *Ammodramus bairdii*, *A. henslowi*, *A. leconteii*, *A. maritimus*, *A. nelsoni*, and *A. caudacutus*. (B) shows the relationships of *A. savannarum, A. aurifrons*, and *A. humeralis*, and their relationship to a clade that includes *Arremonops* and *Peucaea*.

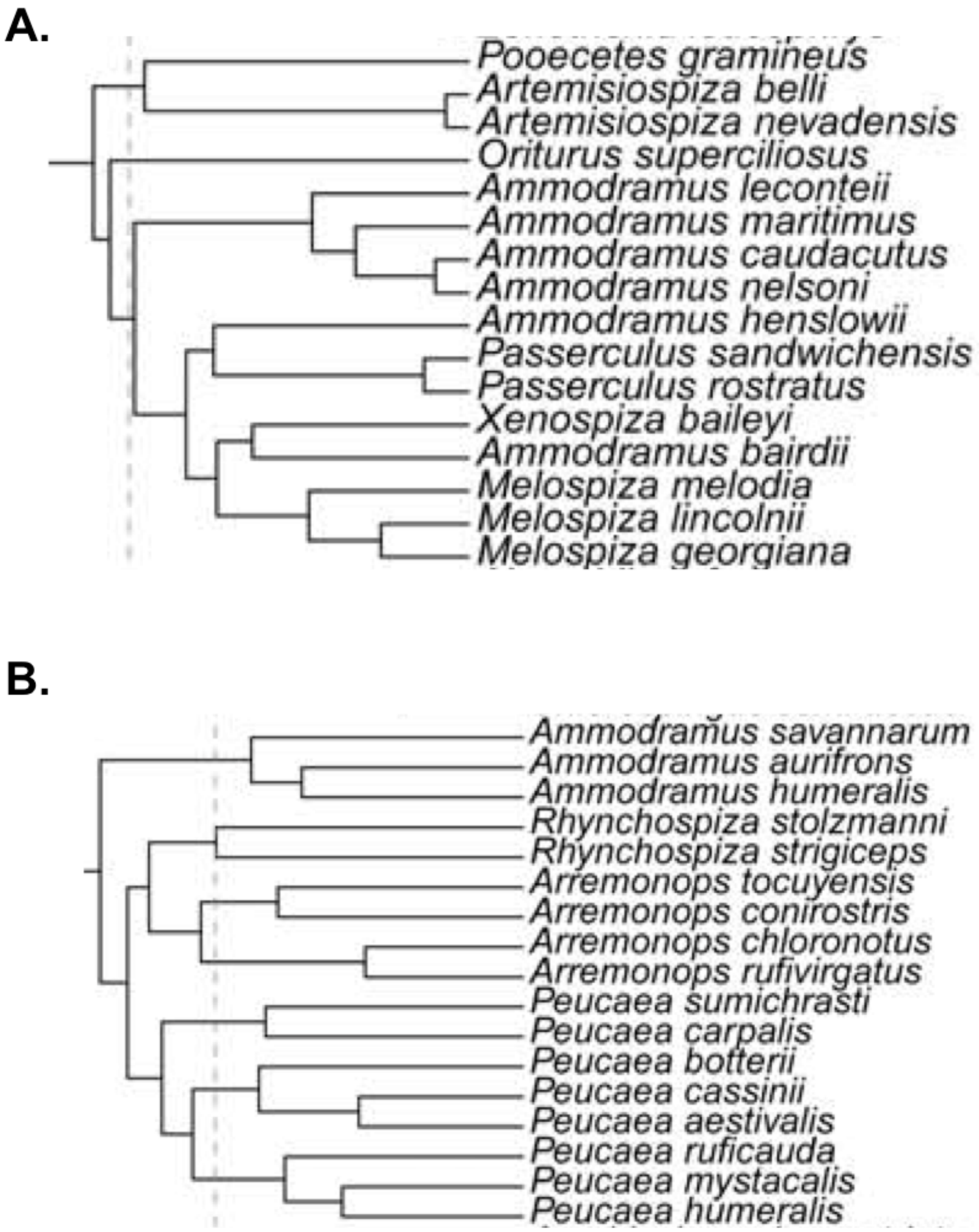

Figure 2. Part of Figure 1 from Barker *et al*. (2015), a time-scaled phylogeny of the entire New World nine-primaried oscine clade based on maximum clade credibility from various species trees assembled into a species tree backbone. (A) shows the relationships among the “grassland” sparrow clade, which includes the genera *Melospiza*, *Passerculus*, and *Xenospiza*, as well as *Ammodramus bairdii*, *A. henslowi*, *A. leconteii*, *A. maritimus*, *A. nelsoni*, and *A. caudacutus*. (B) shows the relationships of *A. savannarum, A. aurifrons*, and *A. humeralis*, and their inclusion in a clade that includes *Arremonops* and *Peucaea*.