

N&MA Classification Committee: Proposals 2010-A

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**Separate Snowy Plover *Charadrius nivosus* from
Kentish Plover *C. alexandrinus***

Description of the problem:

Despite their distinct geographic distributions, Palearctic and Nearctic populations of Snowy Plover *Charadrius alexandrinus* are currently considered to be a single species. Snowy Plovers in America were first described as *Aegialitis nivosus* by Cassin in 1858 (cited by Oberholser 1922), but the differences in adult plumage to Eastern Snowy Plovers were not deemed to be consistent enough to warrant full species status (Oberholser 1922).

New information:

Genetic differences between Eurasian and American populations of Snowy Plovers are substantial (Küpper et al. 2009). Mitochondrial DNA sequences of ND3 and ATPase differ by more than 6% between American and Eurasian populations. Φ_{st} values for North American and Eurasian populations are large (all population comparisons ≥ 0.95). Autosomal and sex chromosomal markers show distinct alleles for Eurasian and American Snowy Plovers. F_{st} values based on microsatellite analyses are above 0.25 for all population comparisons between Eurasian and North American Snowy Plovers. The American and Eurasian Snowy Plovers are more genetically differentiated than the Eurasian Snowy Plovers and African White-fronted Plovers *C. marginatus* (described by Vieillot 1818).

Genetic differences are also reflected in morphological and behavioural differences. Eurasian Snowy Plovers are larger than American Snowy Plovers. There are also differences in chick plumage and male advertisement calls (Küpper et al. 2009).

The North American subspecies *nivosus*, *tenuirostris* and *occidentalis* show genetic structuring, but mitochondrial sequence differences between subspecies are comparatively low (< 1%, Funk et al. 2007).

Recommendations:

1. Split Kentish Plover from Snowy Plover and adopt 'Kentish Plover' for Palearctic populations
2. Change scientific name of Snowy Plover to *Charadrius nivosus* (Cassin 1858) with three subspecies: *C. nivosus nivosus* (currently *C. alexandrinus nivosus*), *C. nivosus tenuirostris* (currently *C. alexandrinus nivosus*) and *C. nivosus occidentalis* (currently *C. alexandrinus occidentalis*)

3. Keep scientific name *Charadrius alexandrinus* (Linnaeus 1758) for Kentish Plover

Literature cited:

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Date of proposal: 23 Dec 2009

Modify the type locality of the Mountain Chickadee *Poecile gambeli***Description of the Problem:**

The type locality for *P. gambeli* has been somewhat confused in various editions of the AOU Checklist. Gambel's (1843) original statement, "This new and distinct species we first observed about a day's journey from Santa Fé, in New Mexico, and from thence in all the ranges of the Rocky Mountains nearly to California." was vague to begin with.

In the first (1886) edition of the Checklist, Ridgway quoted Gambel as to the locality but truncated that description. This was maintained in the second (1895) edition.

The third (1910) edition of the Checklist described the initial observation as: "about a-day's journey west from Santa Fé." There is no citation or justification for the addition of "west." The fourth (1931) edition repeated this description.

In the fifth (1957) edition, "west" appears in brackets. This bracketing continues through the sixth (1983) and seventh (1998) editions.

The presently recognized type specimen, USNM 175399, was collected in Albuquerque, Bernalillo Co., New Mexico, on 27 December 1900 by Francis Birtwell (1901) about 55 miles southwest of Santa Fé.

New information:

The eighteen-year-old William Gambel arrived in the Mexican provincial capital of Santa Fé on 2 July 1841, on the Santa Fé Trail. He remained in Santa Fé until 1 September 1841, collecting plant and animal specimens in the area. The preponderance of evidence suggests that he based his description of the chickadee on observations made *before* he arrived in Santa Fé and almost certainly not *west* of Santa Fé.

Gambel arrived in Santa Fé in the midst of a difficult political situation. Texas, which had won its independence from Mexico in 1836, was agitating to expand to the west. In June of 1841, while Gambel was still dodging Indians on the Santa Fé trail, President Lamar of the Republic of Texas had dispatched an expedition to try to annex New Mexico to Texas (Hyslop 2002:275-279). As a result of these activities, every Anglo in New Mexico was suspect. It is therefore likely that Gambel did not have freedom to travel much beyond Santa Fé.

The immediate vicinity of Santa Fé would have been pretty much denuded of piñon-juniper habitat due to firewood gathering. If he was looking for undisturbed habitat for new plants or animals, he would not have found it close to town or in more settled locales farther to the north or southwest along the Camino Real. He might well have ascended the mountains to the east of Santa Fé, but we have no other evidence that he did so. He seems to have been more interested in the lizards of the area than the birds. He collected three species of reptiles in the Santa Fé area that are in the National Museum collection.

From the specific descriptions of his plant collections, we know that Gambel explored along the Rio Grande. He found Gambel's Oak (*Quercus gambelii*) "on the banks of the Rio del Norte, but not abundant" and the Many-Flowered Gilia (*Gilia multiflora*), in "sandy hills along the borders of the Rio del Norte" (Nuttall 1848). To the northwest of Santa Fé there are sandy hills along the Rio Grande, about 20 miles by trail from Santa Fé, over hills close to town and down the Cañada Ancha to the Rio Grande. This is undoubtedly the type locality for these botanical collections and some of his reptile collections. Local topography (White Rock Canyon) precludes easy access to the Rio Grande to the west of Santa Fé and could hardly be described as "sandy hills."

Gambel spent two months in and around Santa Fé without commenting on the Mountain Chickadee, although he is known to have frequented areas where the bird would have been found. He also clearly identifies his locations along the Rio Grande—a likely place for him to find the chickadee—for his botanical collections but did not do so for the chickadee. These facts suggest that his first observation of the bird was not *after* his arrival in Santa Fé.

So what is the type locality for the Mountain Chickadee? As wagon trains approached Santa Fé on the trail, their final campsites prior to arrival in Santa Fé are known to have been near Glorieta in Santa Fé County (17 miles southeast of Santa Fé) and near Pecos in San Miguel County (27 miles southeast of Santa Fé), both about a-day's journey *southeast* of Santa Fé. The trains would have stopped at one or both of these places on 30 June and/or 1 July 1841. Both of these locales are likely habitat for *P. gambeli*. Gambel's statement that the bird was found "from thence" together with the bird's almost certain appearance during his time in Santa Fé reinforces the conclusion that the bird was "first observed about a day's journey" prior to his arrival in Santa Fé along the Santa Fé trail.

Gambel's specimen of the chickadee—if there ever was one—is lost, although other bird skins he collected later in California are deposited in the National Museum collection. Likewise a number of reptiles collected in the vicinity of Santa Fé survived his travel to California and return to Philadelphia. The circumstances of travel in 1841, either on the Santa Fé Trail or on the Old Spanish Trail to California, would not have been conducive to careful collection or preservation of specimens in any event.

Recommendation:

I recommend that the type locality for Mountain Chickadee be changed from “about a-day’s journey [west] from Santa Fé, New Mexico” to “on the Santa Fé Trail, about a-day’s journey southeast from Santa Fé in New Mexico.)

Literature cited:

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Date of proposal: 9 Mar 2010

Split Mountain Chickadee (*Poecile gambeli*) into two species

Description of the problem:

The 7th edition of the AOU Check-list recognizes one species of Mountain Chickadee (*Poecile gambeli*) with no groups, although multiple subspecies have been described. Grinnell (1918) was the first to undertake serious systematic revision of this species, in which he reviewed a series of 464 skins and found that Rocky Mountain birds were diagnosable from California birds (longer tail, cinnamon tinge of sides and back) and deserved subspecific status (*Penthestes gambeli gambeli*). Within California, Grinnell (1918) recognized 3 subspecies (*P. g. inyoensis*, *P. g. abbreviatus*, *P. g. baileyae*). Subsequently, several other authors (Oberholser 1919, Grinnell and Swarth 1926, van Rossem 1928, Linsdale 1936, Behle 1950) extended the geographic ranges of some subspecies or described additional forms based primarily on differences in plumage color, tail length, and bill morphology.

Behle (1956) followed up on this earlier work by conducting a second systematic review. His study included variation in morphological measurements of both breeding and wintering birds (species resident through range), as well as qualitative examination of color variation. Although much of the variation is clinal and intergradation occurs between subspecies, Behle (1956) recognized seven subspecies which he divided into three groups: Rocky Mountain "*gambeli*" group (subspecies *gambeli* and *grinnelli*); Great Basin "*inyoensis*" group (subspecies *inyoensis* and *wasatchensis*); Pacific "*abbreviatus*" group (subspecies *abbreviatus*, *baileyae*, *atratus*). The latter includes populations from the Cascade-Sierra Nevada mountains and disjunct mountains of southern California and northern Baja California. However, he noted that a more conservative approach might be to recognize the 4 most well-marked subspecies: *gambeli*, *abbreviatus*, *atratus*, *inyoensis* (although this "would not reveal the true picture of variation and subspeciation, Behle 1956).

Miller (1934:163) reported on song differences that he detected between Mountain Chickadees from southern Utah (*wasatchensis*) and from California (*abbreviatus* or *baileyae*): "I note repeatedly that the songs of this chickadee [*wasatchensis*] consists of two groups of notes separated by three or more half tones of pitch. In contrast to this type of song are those of the races *P. g. baileyae* and *abbreviatus* in which the greatest interval of pitch with rare exceptions is no larger than one whole tone."

The first molecular evidence for divergence of Pacific versus Rocky Mountain populations was provided by Gill and Mostrom (1993), who surveyed mtDNA restriction site variability within and between populations of 6 species of North American chickadees. In this study, they examined 5 individuals from each of two

populations of *P. gambeli* (*P. g. gambeli* from Arizona, *P. g. baileyae* from southern California). Divergence between these population was 3.1%. Similar results were obtained by Gill et al. (2005), who obtained cytochrome-b sequences for 2 individuals of *P. g. gambeli* from Arizona and 1 individual of *P. g. baileyae* from California. The two samples from Arizona had identical sequences but differed by 4.5% from the California sample.

New information:

Spellman et al. (2007) used mtDNA sequences (ND2) to investigate the phylogeography of Mountain Chickadee populations. This thorough study included 320 individuals from 31 locations representing all but one (*P. g. atratus*) subspecies. Sample sizes were generally 10 or more per location. Their results showed two well-supported clades that differed by 4.4%: a Western Clade (Sierra Nevada, Cascades, disjunct populations in southern California), and an Eastern Clade (Rocky Mountains, Great Basin). Only one site near Mono Lake and Mono Crater, California, contained haplotypes from both clades (only 3 individuals sampled). Genetic divergence within clades was shallow, although disjunct populations in the Transverse and Peninsular ranges of southern California contained unique haplotypes. Divergence time between clades was estimated to be 610,000-1,530,000 years ago. Preliminary analyses of multi-locus nuclear data (10 anonymous loci: 9 autosomal and 1 z-linked) corroborate the mtDNA results (Spellman et al. unpublished). The concordance of molecular data with morphological variation supports a hypothesis of long-term isolation of Mountain Chickadee populations in the Sierra Nevada and Rocky Mountains (Behle 1956, Spellman et al. 2007).

Recommendation:

The congruence of molecular, morphological, and vocal information – and the apparently very limited contact – provides a strong case for splitting the Mountain Chickadee into two species.

We recommend splitting, with the following English names that consider the history and discovery of the two species:

Gambel's Chickadee (*Poecile gambeli*) – includes the Rocky Mountain and Great Basin populations which Gambel (1843) would have first encountered in New Mexico (see separate proposal re type locality). Subspecies: *P. g. gambeli*, *P. g. grinnelli*, *P. g. inyoensis*, *P. g. wasatchensis*.

Bailey's Chickadee (*Poecile baileyae*) – includes the coastal California, Sierra Nevada, and Cascade populations, with the first description being *P. g. baileyae*. Grinnell (1908) described this southern California subspecies from specimens collected in 1903 on Mount Wilson in Los Angeles County, California. He named it *Parus gambeli baileyae* - note not *baileyi* – after Florence Merriam Bailey, a

pioneer ornithologist in her own right. Subspecies: *P. b. baileyae*, *P. b. abbreviatus*, *P. b. atratus*.

If accepted, replace the current account for *Poecile gambeli* with the following accounts:

***Poecile gambeli* (Ridgway). Gambel's Chickadee.**

Parus montanus (not Conrad von Baldenstein, 1827) Gambel, 1843, Proc. Acad. Nat. Sci. Philadelphia 1: 259. (on the Santa Fé Trail, about a-day's journey southeast from Santa Fé in New Mexico.)

Parus gambeli Ridgway, 1886, A.O.U. Check-list North American Birds, ed. 1: 335. New name for *Parus montanus* Gambel, preoccupied.

Habitat.—Montane coniferous forest, primarily pine, spruce-fir, and locally piñon-juniper and desert riparian woodland, also aspen; in nonbreeding season, also pine-oak association, riparian woodland, and suburbs (locally).

Distribution.—*Resident* from northwestern and central British Columbia, west-central Alberta, eastern Washington and Oregon, central Montana south through the Great Basin east of the Sierra Nevada, Wyoming, Colorado, central and southeastern Arizona (except mountains along the Mexican border), southern New Mexico, and extreme western Texas (Davis and Guadalupe mountains). Recorded in summer (and possibly breeding) in southeastern Alaska (Warm Pass Valley) and southern Yukon.

Casual (mostly in winter) elsewhere in southeastern Alaska, southwestern British Columbia, eastern Washington and Oregon, and east to southwestern Saskatchewan, southwestern South Dakota, southwestern Kansas, and the panhandles of northern Texas and western Oklahoma.

Notes—See comments under *P. atricapillus*. Formerly considered conspecific with *P. baileyae* but split on the basis of molecular (Spellman et al. 2007), morphological, and vocal differences.

***Poecile baileyae* (Grinnell). Bailey's Chickadee.**

Parus gambeli baileyae Grinnell, Condor, X, 1908, 29. (November 27, 1903, Mount Wilson, at 5500 feet, Los Angeles Co., California.)

Habitat.—Montane coniferous forest, primarily pine, spruce-fir, and locally piñon-juniper and desert riparian woodland, also aspen; in nonbreeding season, also pine-oak association, riparian woodland, and suburbs (locally).

Distribution.—*Resident* from Cascade Mountains of Washington south along the Sierra Nevada (except for most of the coast ranges) to northern Baja California (Sierra Juarez and Sierra San Pedro Martir).

Casual (mostly in winter) in central and coastal California.

Notes—See comments under *P. gambeli*.

Literature cited:

Behle, W. H. 1950. A new race of mountain chickadee of the Utah-Idaho area. *Condor* 52:273-274.

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Linsdale, J. M. 1936. The birds of Nevada. *Pacific Coast Avifauna* 23:1-145.

Miller, A. H. 1934. Field experience with mountain-dwelling birds of southern Utah. *Wilson Bull.* 46:156-168.

Oberholser, H. C. 1919. The range of the short-tailed mountain chickadee (*Penthestes gambeli abbreviatus* Grinnell). *Auk* 36:424.

Spellman, G. M., B. Riddle, and J. Klicka. 2007. Phylogeography of the mountain chickadee (*Poecile gambeli*): Diversification, introgression, and expansion in response to Quaternary climate change. *Molecular Ecology* 16:1055-1068.

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Submitted by: Carla Cicero, Thomas R. Jervis, Garth Spellman

Date of proposal: 9 Mar 2010

**Split the Yellow-rumped Warbler *Dendroica coronata* into
two, three, or four species**

Description of the problem:

The yellow-rumped warbler complex consists of four visually distinct forms originally described as distinct species: *Dendroica coronata coronata* (Linnaeus 1766), *D. c. auduboni* (Townsend 1837), *D. c. nigrifrons* (Brewster 1889), and *D. c. goldmani* (Nelson 1897). Oberholser (1921) considered *nigrifrons* and *goldmani* subspecies of *D. c. auduboni*. Discovery of a hybrid zone between *coronata* and *auduboni* in western Canada (Hubbard 1969) led the AOU to lump the entire complex into a single species, *Dendroica coronata* (AOU 1973). Previous studies of this hybrid zone have reached conflicting conclusions about the degree of reproductive isolation it represents. Hubbard (1969) found that nearly all individuals in the center of a 150-km-wide hybrid zone showed some evidence of admixture in plumage pattern, but speculated that the narrowness of the hybrid zone implied that it was maintained by selection. Barrowclough's (1980) analysis of Hubbard's data, pooled with additional samples he collected, concluded that the cline could be explained by neutral mixing since secondary contact 5-10 thousand years ago. However, this analysis was based on an assumed dispersal distance (1 km per generation) that subsequent research has demonstrated to be unreasonably low.

The contact zone between *auduboni* and *nigrifrons* is unstudied so far. Oberholser (1921), Moore (1946), and Hubbard (1970) noted that birds from southern Arizona appeared intermediate between *auduboni* and *nigrifrons* in size and the extent of black plumage, and suggested that some interbreeding may occur.

No published data exists on song and call variation in this group. Hubbard (1969) did not perceive a difference in song across the hybrid zone, although he did note a difference between allopatric *coronata* and *auduboni* from Michigan and New Mexico. Hubbard (1969) and others have noted that the call notes of these two forms are readily distinguishable.

Because of changing attitudes toward the effect of hybridization on species status, as well as two recently published studies and additional work in progress, it may be time to revisit the taxonomic status of this complex.

New information:

Mila et al. (2007) surveyed mitochondrial genetic variation across multiple populations of all four taxa (COI, ATPase 6 and 8, control region). This study

found three reciprocally monophyletic clades separated by substantial sequence divergence: one corresponding to *D. c. goldmani*, another for *nigrifrons*, and a third that included both *coronata* and *auduboni*. Mila et al. found slight but significant genetic differentiation between *coronata* and *auduboni* despite the lack of reciprocal monophyly. The deep mitochondrial divide between the northern and southern forms was unexpected, since *auduboni* had always been placed with the southern forms based on phenotype. Estimated divergence times between taxa were approximately 10,000 years (*coronata* from *auduboni*), 0.5 million years (*goldmani* from *nigrifrons*), and 1.7 million years (*coronata*+*auduboni* from *goldmani*+*nigrifrons*).

Brelsford and Irwin (2009) used measurements of linkage disequilibrium between two nuclear markers in the *coronata/auduboni* hybrid zone to estimate the strength of selection maintaining the cline. The two taxa were reciprocally monophyletic at two of 11 nuclear markers screened, and clines in both markers were concordant with the cline in plumage traits. The plumage cline sampled in 2005-2007 was nearly identical in position and width to Hubbard's 1965 sample in the same area. The authors estimated per-generation dispersal at 20 (13 to 25) km, and a cline width of 132 km. Estimated selection maintaining the cline was equivalent to a single-locus heterozygote disadvantage of 18% (8% to 28%). Based on analysis of 77 breeding pairs, mate choice was not significantly different from random; i.e. no significant assortative mating by phenotype or genotype was observed. The authors suggest that mitochondrial capture, rather than recent common ancestry, could account for the similarity in mtDNA between *coronata* and *auduboni*.

Brelsford, Irwin, and Mila (unpublished) are working on a survey of genetic variation throughout the species complex, with additional geographic and genomic sampling. Relevant to this study, they have found that most birds in Arizona (classified as *auduboni* based on phenotype) carry mitochondrial DNA from the *nigrifrons* clade. Analysis of over 300 AFLP markers (anonymous and presumably nuclear) identified three distinct clusters: *coronata*, *goldmani*, and *auduboni*+*nigrifrons*. At the two nuclear sequence loci that were reciprocally monophyletic between *coronata* and *auduboni* (Brelsford and Irwin 2009), both *nigrifrons* and *goldmani* grouped with *auduboni*. None of the 11 sequenced nuclear markers supported the deep north/south split found in mitochondrial DNA. (Notably, both mitochondrial DNA (Mila et al 2007) and AFLPs show very low within-population diversity in *goldmani* compared to the other three taxa, indicating a low effective population size.) Taken together, the evidence suggests that the oldest divergence within the complex is between *coronata* and the other three forms, and that mitochondrial DNA from *coronata* has introgressed and become fixed in northern populations of *auduboni* within the last 20,000 years.

Alternatives:

1. No action

D. coronata coronata
D. coronata auduboni
D. coronata nigrifrons
D. coronata goldmani

Reasoning: interbreeding occurs between *auduboni* and both adjacent forms, *coronata* and *nigrifrons*. In the *coronata-auduboni* hybrid zone, there is little if any assortative mating (Brelsford & Irwin 2009), and within the hybrid zone nearly all birds are admixed (Hubbard 1969, Brelsford & Irwin 2009). The contact zone between *auduboni* and *nigrifrons* is less well studied, but Oberholser (1921), Moore (1946), and Hubbard (1970) noted morphological intermediates in southern Arizona and suggested that intergradation was the cause. Although there is no indication of gene flow between the disjunct *goldmani* and the other subspecies, some gene flow is possible between the most divergent forms within this species complex, so it could be argued that they should not be considered biological species in the strictest sense. According to the AOU's (1998) criteria, taxa connected by a narrow, stable hybrid zone should be considered separate species; the hybrid zone between *coronata* and *auduboni* is stable (Brelsford and Irwin 2009), but whether a width of 132 km (~7 times per-generation dispersal) qualifies as narrow is open to interpretation.

2. Split all 4

D. coronata
D. auduboni
D. nigrifrons
D. goldmani

Mila et al. (2007) wrote that elevation of *goldmani* and *nigrifrons* to species status would be uncontroversial, based on reciprocal monophyly and substantial sequence divergence of mtDNA, as well as phenotypic differences. Brelsford and Irwin (2009) have shown substantial (albeit incomplete) reproductive isolation between *auduboni* and *coronata*. All four groups are distinguished by fixed differences in at least one genetic marker and are visually distinct, and these differences are maintained despite ongoing interbreeding between *auduboni* and its two neighboring forms.

3. Split *coronata* from the rest

D. coronata
D. auduboni auduboni
D. auduboni nigrifrons
D. auduboni goldmani

The *coronata* form is the most distinctive in appearance within the species complex, and its contact zone with *auduboni* has been well studied over a 40-

year period (Hubbard 1969, Barrowclough 1980, Brelsford and Irwin 2009). The most recent research demonstrates temporal stability of the hybrid zone, and its width (132 km) is narrow relative to the continent-spanning range of the species complex. To date, the zone of potential contact between *auduboni* and *nigrifrons* (near the Arizona/Mexico border) has been subject to very little study, and Mila (unpublished data) has encountered some evidence of discordant clines in phenotype and mtDNA in that region. The strength of reproductive isolation between the disjunct *goldmani* and other forms remains unstudied. As such, it may be best to split *coronata* and postpone a decision on any further splits within the "Audubon's group."

4. Split *coronata* and *goldmani*, leave *nigrifrons* a subspecies

D. coronata

D. auduboni auduboni

D. auduboni nigrifrons

D. goldmani

Several lines of evidence, including mtDNA (Mila et al. 2007), nuclear DNA (AFLPs, Brelsford, Irwin, and Mila unpublished), and morphology (Hubbard 1970), show clear distinctions between *goldmani* and the other taxa in this complex. Although reproductive isolation cannot be assessed directly because of the allopatric distribution of *goldmani*, it is a genetically and ecologically distinct population, and mtDNA suggests a reasonably long history of independent evolution (0.5 million years according to the 2% mitochondrial clock).

Despite the deep mitochondrial divide between *auduboni* and *nigrifrons* indicated by Mila et al (2007), unpublished data (Brelsford, Irwin, and Mila) do not support reproductive isolation between these taxa. Most birds in Arizona (classified phenotypically as *auduboni*) carried mtDNA from the *nigrifrons* clade, and morphology (Hubbard 1970) and nuclear DNA (Brelsford, Irwin, and Mila unpublished) show broad clinal variation between Mexico and the northern Rocky Mountains, suggesting substantial gene flow. Further study of the *nigrifrons/auduboni* contact zone is needed, and may uncover evidence for reproductive isolation between them, but elevation of *nigrifrons* to species status based on current data may be premature.

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Submitted by: Alan Brelsford, University of British Columbia

Date of Proposal: 26 Mar 2010

Remove *Schiffornis*, *Laniocera*, *Pachyramphus*, and *Tityra* from *incertae sedis* within the Tyrannidae, and place in the new family Tityridae

Description of the problem:

The relationships among the Cotingidae, Tyrannidae, and Pipridae have been notoriously difficult to resolve, and several genera have been moved back and forth among them. These troublesome genera have included *Schiffornis*, *Laniocera*, *Pachyramphus*, and *Tityra*, currently treated as genera *incertae sedis* in the Tyrannidae (AOU 1998). Prum and Lanyon (1989) were the first to hypothesize a close relationship of these genera, as well as several other genera (including *Laniisoma*, *Iodopleura*, and *Xenopsaris*), based on evidence from syringeal and cranial characters. Based on analyses of several morphological characters, McKittrick (1985) also found support for the close association of the becards, tityras, and mourners within the Tyrannidae.

Early genetic work on the Tyrannoidea similarly suggested a close relationship between the tityras and the becards. However, due to limited taxon sampling and limited phylogenetic resolution, further hypotheses as to the relationships of these troublesome genera could not be made (Lanyon 1985).

New information:

Recent studies based on DNA sequence data have improved our understanding of the relationships of tityras and their allies. Based on extensive taxon and gene sampling, it has been found that *Schiffornis*, *Laniocera*, *Pachyramphus*, and *Tityra* form part of a well supported monophyletic group that is far outside the Tyrannidae, and which is generally placed either as sister to the Cotingidae or the Pipridae (Chesser 2004, Ericson *et al.* 2006, Barber and Rice 2007, Ohlson *et al.* 2007, Tello *et al.* 2009). Based on these findings, authors have suggested adopting the name Tityridae for this well supported group, a measure that has been adopted by the SACC (Remsen *et al.* 2009), IOC (Gill *et al.* 2009), and Clements (2009) (Ericson *et al.* 2006, Barber and Rice 2007, Ohlson *et al.* 2007, Tello *et al.* 2009).

Recommendation:

The genera *Schiffornis*, *Laniocera*, *Pachyramphus*, and *Tityra* should be removed from *incertae sedis* within the Tyrannidae and elevated to family rank within the new family Tityridae (Ericson *et al.* 2006, Barber and Rice 2007, Ohlson *et al.* 2007, Tello *et al.* 2009). Numerous studies, both morphological and molecular, have confirmed the close relationships among these three genera, with recent genetic studies showing that they represent a well supported,

monophyletic group distinct from the Tyrannidae, Cotingidae, and Pipridae (Lanyon 1985, McKittrick 1985, Prum and Lanyon 1989, Chesser 2004, Ericson *et al.* 2006, Barber and Rice 2007, Ohlson *et al.* 2007, Tello *et al.* 2009). This leaves only *Piprites griseiceps* as *incertae sedis* within the Tyrannidae.

The sequence of affected taxa on the Check-list will be as follows (based on Tello *et al.* 2009):

Tyrannidae

Tityridae

Schiffornis turdina

Laniocera rufescens

Tityra spp.

Pachyramphus spp.

Cotingidae

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Submitted by: Shawn Billerman, Cornell Lab of Ornithology

Date of proposal: 29 Mar 2010

**Change English name of *Turdus nudigenis* from
Bare-eyed Thrush to Spectacled Thrush**

I'm sure you are all painfully aware that when we changed the English last names of various Neotropical *Turdus* from Robin to Thrush, this produced the name Bare-eyed Thrush, which is "preoccupied" by *Turdus tephronotus* of Africa, provoking an intercontinental crisis.

Fortunately for NACC, SACC has gone through the excruciatingly interesting exercise of solving this crisis and has adopted a new name, Spectacled Thrush. For all the details, see:

<http://www.museum.lsu.edu/~Remsen/SACCprop295.html>

and

<http://www.museum.lsu.edu/~Remsen/SACCprop295x.html>

Because this name is already in use now in the major portion of the species' range, I see no reason for NACC not to follow SACC on this, especially to maintain consistency between the lists.

Submitted by: Van Remsen, Intercontinental Crisis Mediator

Date of proposal: June 2010

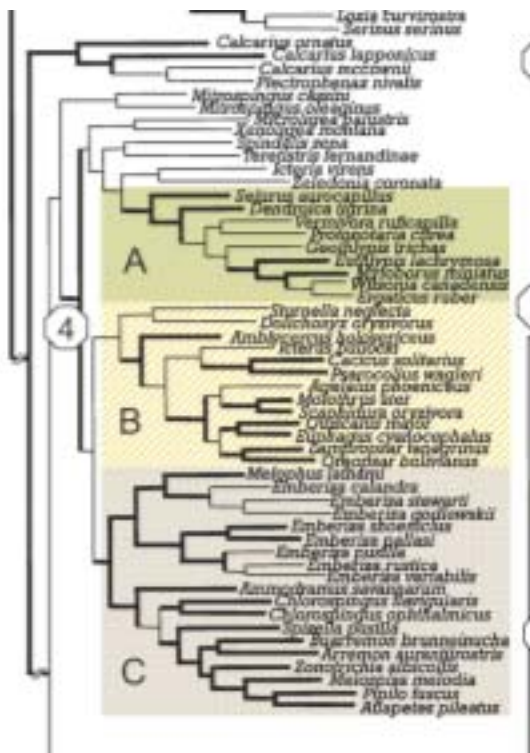
Transfer *Chlorospingus* from Thraupidae to Emberizidae

Description of the problem:

Chlorospingus has traditionally been placed in the Thraupidae but has always been recognized as peculiar. Recent papers by Kevin Burns and collaborators using mtDNA sequence data have failed to find support for placement of this genus in the Thraupidae.

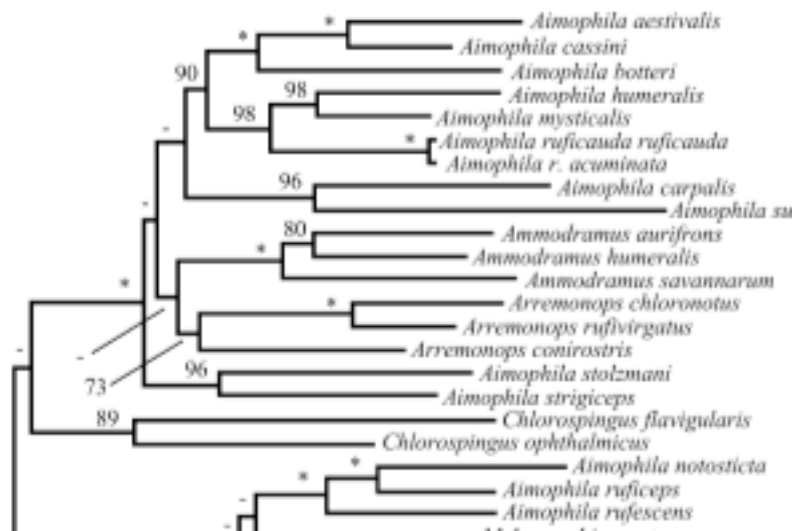
New information:

Klicka et al. (2007) presented the genetic data that show that *Chlorospingus* is embedded in the Emberizidae. Their tree is as follows:



What the tree shows is that even with the limited number of emberizine taxa sampled (Klicka et al. 2007 is focused on Cardinalidae), *Chlorospingus* is a member of a group that includes most of the W. Hemisphere emberizids, and that group is sister to E. Hemisphere *Emberiza*.

DaCosta et al. (2009) dramatically expanded sampling within the Emberizidae to include most genera; *Chlorospingus* remained nested within the Emberizidae and is the sister to a group of genera that consists of *Aimophila*, *Ammodramus*, and *Arremonops*. A portion of their tree is shown below:



Ongoing additional taxon- and gene-sampling by Klicka and colleagues will undoubtedly better resolve the placement of *Chlorospingus* as well as produce a refined tree for the Emberizidae, so for now, I would say there is no need to worry about where to place it other than at the of Emberizidae in the linear sequence, with a Note that explains that this is a tentative solution.

The South American Classification Committee recently unanimously passed this proposal (#426), and comments from committee members and others are pasted in below.

Recommendation:

The genetic data are solid for placement within our Emberizidae, as currently defined, so I recommend a YES.

Literature cited:

DaCOSTA, J. M., G. M. SPELLMAN, P. ESCALANTE, AND J. KLICKA. 2009. A molecular systematic revision of two historically problematic songbird clades: *Aimophila* and *Pipilo*. *J. Avian Biology* 40: 206-216.

KLICKA, J., K. BURNS, AND G. M. SPELLMAN. 2007. Defining a monophyletic Cardinalini: A molecular perspective. *Molecular Phylogenetics and Evolution* 45: 1014-1032.

Submitted by: Van Remsen

Comments solicited from John Klicka: “According to the available mtDNA data, the genus *Chlorospingus* is clearly a member of the emberizid clade, although, it's exact placement within this assemblage remains unclear.”

Comments from Thomas Donegan: “This comment is restricted to the issue of linear placement. We seek to avoid incertae sedis where possible in the Colombian checklist and hence placed *Chlorospingus* in the Emberizidae last year (Salaman et al. 2009) based on the papers referred to in this proposal. We concluded that the better linear placement was at the end of the Emberizidae. Thraupidae (and hence *Chlorospingus*) are currently listed before Emberizidae, so one could place *Chlorospingus* first for that reason. We placed them at the end for two other reasons. First, "unplaced" genera traditionally go at the end rather than the start of the order. Secondly, aesthetically, it would be a bit confusing to have a family that most people relate to finches and sparrows start off with a bunch of birds called (and for a long time thought of as) tanagers. The generic order of this family clearly needs some work, so this placement will obviously need to be revised in future.”

Comments from Stiles: “YES. Although the exact placement of *Chlorospingus* in the Emberizidae remains to be determined, their allocation to this family seems clear – and it is a relief to get *Chlorospingus* out of the onerous “incertae sedis”, at least at the family level!”

Comments from Nores: “YES, los análisis moleculares de Klicka et al. (2007) y de DaCosta et al (2009) muestran claramente que *Chlorospingus* no es un Thraupidae como era antes considerado sino un Emberizidae. Sin embargo, yo no veo que la opinión de Frank Pitelka citada por Tordoff 1954 de que *Chlorospingus* tiene comportamiento de Emberizidae, sea muy acertada. Son pequeños pájaros moviéndose activamente en las copas de los árboles, para mi recuerdan más a ciertos Tharupidae (por ejemplo *Tangara*) que a Emberizidae.”

Elevate *Chaetura andrei meridionalis* to species status**Description of the problem:**

We currently include the South American species Ashy-tailed Swift *Chaetura andrei* in the Check-list (AOU 1998) as an accidental species based on a record from Panama (Juan Díaz, western Panamá province, 4 August 1923; Rogers 1939). The Notes section to this species account states the following: "Also known as Andre's Swift. Although the nominate form may be a subspecies of *C. vauxi*, the subspecies *C. a. meridionalis*, the form recorded in Panama, may be a separate species, *C. meridionalis* Hellmayr, 1907 [Sick's Swift] (Marín 1997)."

New information:

In a review of species limits in New World swifts, Marín (1997) concluded that *Chaetura andrei* is actually a subspecies of *C. vauxi*. He recommended that *C. a. meridionalis* be separated from *C. andrei* and elevated to species status.

The SACC follows Marín (1997) in considering *C. meridionalis* to be a distinct species and uses the English name Sick's Swift. The SACC website includes the following comment for *C. meridionalis*:

Chaetura meridionalis was formerly (e.g., Cory 1918, Pinto 1937, Meyer de Schauensee 1970, Haverschmidt & Mees 1994) considered a subspecies of *C. andrei*; Marín (1997), however, showed that *andrei* was indistinguishable from *C. vauxi aphanes*, but that *meridionalis* warranted treatment as a separate species. This species is presumably closely related to *C. pelagica*; the two are nearly indistinguishable except by wing formula (Chantler 1999). Called "Ashy-tailed Swift" by Hilty (2003).

Recommendation:

I recommend that we adopt the SACC position on this and elevate *C. meridionalis* to species status. The species account for *Chaetura andrei* would be replaced by a proposed new account, as follows:

Chaetura meridionalis Hellmayr. Sick's Swift.

Chaetura andrei meridionalis Hellmayr, 1907, Bull. Brit. Orn. Cl. 19: 63. (state of Santiago del Estero, Argentina.)

Habitat and Distribution would remain the same. The current Notes would be replaced by the following:

Notes.—Formerly (e.g., Cory 1918, Pinto 1937, Meyer de Schauensee 1970, Haverschmidt and Mees 1994) considered a subspecies of *C. andrei*. Elevation to species status follows Marín (1997).

Submitted by: Terry Chesser

Date of proposal: 9 Sep 2010

Change English names of North American *Troglodytes* [*troglodytes*] wrens

I realize that there are few cases of perfect names, and that decisions about names are not necessarily easy ones to make. However, when a split into two species occurs in North America, to give one species a novel name, even a pleasant sounding name that agrees with the (equally inaccurate and thus inappropriate) scientific name, is not conducive to facilitating communication - and simply makes the AOU seem rather removed from the person in the street. The case of Winter Wrens is a case in point.

When two related species have ostensibly eastern and western distributions in North America, there is considerable benefit to using the modifiers Eastern and Western for their English names, to allow association, as in wood-pewees (or pewees, as the rest of the world calls them - but dropping the redundant "wood" is another subject), meadowlarks, or bluebirds (despite E Bluebirds in the Southwest). Anyone in the field in California, say, can simply say "pewee" or "meadowlark" and it's understood what species they're talking about - unless there's good reason to think another (much rarer) species is involved.

Hence we don't have simply Meadowlark and Yellow-breasted Grassbird, or even Common Meadowlark and Neglected Meadowlark - I think Neglected Meadowlark is a great name: who wouldn't want to see a bird with that name? But useful? Not really.

To the best of my knowledge (and that of the Oxford English Dictionary as well), Pacific refers to either 1) peaceful or 2) an Ocean; not to shady groves of redwood trees or mossy thickets. I don't think *Troglodytes* [*troglodytes*] *pacificus* is any more peaceful than other wrens, and it certainly doesn't inhabit the ocean, unlike, say, *Ardenna pacifica* [= *Puffinus pacificus*]. Pacific-slope, although clunky, might have been more accurate. But as it stands, Pacific Wren is about as "meaningful" as Kansas Shearwater.

Yet it is only one of two (at present) *Troglodytes* wrens in North America that have long (always?) been known collectively as Winter Wren. If House Wrens were split, it would be a little like keeping simply "House Wren" for North American *aedon* and calling the widespread Neotropical *musculus* the Mouse-like Wren, or Murine Wren.

By simply adding the modifiers Eastern and Western (or Northern and Southern, as usually done with house wrens), however:

- 1) Some information is conveyed about distribution.
- 2) An idea is conveyed that the two wrens are related. Right now one could think Carolina Wren and Pacific Wren might be related; yes, I know that's what

scientific names are for, and thus there's even more argument to have English names that also facilitate parallel communication.

3) The old and universally (well, in North America at least) name of Winter Wren is maintained for both species and can be used coast-to-coast in the vernacular.

4) A novel name is not introduced to confound people, and the AOU comes across as thoughtful and considerate. A lot more people in the West live year-round in the range of "Winter Wren" than in the East, and so the change to Pacific Wren is even more invidious for westerners who have always called it "Winter Wren" (despite the inappropriateness of the name; but two wrongs don't make a right).

5) And no, I wouldn't use hyphens as with Western Winter-Wren (I assume everyone read the fairly recent discussion in Wilson about hyphenation? Egos and personal differences aside, I think their rationale makes objective sense).

6) The name Pacific Wren hasn't caught on, and there is still time to change it before a whole generation of literature adopts it.

Submitted by: Steve N G Howell

Date of proposal: 5 Oct 2010

**Split Common Gallinule (*Gallinula galeata*) from
Common Moorhen (*G. chloropus*)**

Description of the problem:

Gallinula chloropus is one of these cosmopolitan species that shows only minor morphological differences over a huge range. There has been little controversy regarding this arrangement, all controversy seems to have been focused on the English name of this bird.

Plumage differences between Old World and New World birds are slight, although bill morphology differs. Old World forms have an elliptical shaped bill shield that is rounded at top, whereas New World forms have a truncated topped shield that is widest at the top.

New information:

Recently Constantine et al. (2006) used *Gallinula chloropus* as an example (p. 139) of how paying attention to sound may “uncover biodiversity.” They illustrate the shield and head shape differences of American and European birds, as well as the longer bill of New World gallinules. But they also describe rather extreme differences in voice between the two populations, publish sonograms and provide examples (on CD) of these differences. What appears to be the primary vocalization in the New World population is a rich nasal “laughter” whereas the homologous call in the Old World populations is a rather short, simple quavering note lasting less than half a second “kruuuk”. A secondary call type with paired notes is similar in note structure between the two populations, but not in tempo, in which differences are apparent. These vocal differences can be heard on xeno-canto, making sure to include examples from outside of the Americas, here is the link that will do this for you:

http://www.xeno-canto.org/browse.php?query=Common%20Moorhen&pagenumber=&order=taxonomy&global_filter=0

Groenenberg et al. (2008) recently published molecular data that addresses some species of *Gallinula*. They were interested in unraveling the relationship of *Gallinula* on two South Atlantic Islands (Gough and Tristan da Cunha), but also sampled New World and Old World representatives of *Gallinula chloropus* as well as *Fulica*. They analyzed molecular data from the D-loop, tRNA-Lysine/ATP8 and cytochrome b. Their result shows *Gallinula chloropus* to be polyphyletic. They confirm that two separate taxa once inhabited Gough (*G. comeri*) and Tristan da Cunha (*G. nesiotis*), and this pair is sister to an Old World group of populations of

G. chloropus. Their samples came from Europe, Africa, and Asia. Two samples from the New World (Suriname) are basal to the Old World and Atlantic Island clades. The paper is open access and available here:

<http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0001835>

In several *Gallinula* species plumage is conservative, and much of the difference is in the shield shape and color, or in body size. This is parallel to the situation in coots (*Fulica*). *Gallinula chloropus*, *G. nesiotis*, and *G. tenebrosa* show similar bill coloration of a yellow-tipped red bill with a red shield, although shield shape and size differs. *Gallinula angulata* is small and has much more extensive yellow on the bill than the other three. Otherwise body plumages are similar, although *angulata* and *chloropus* show the white flank stripe, whereas *nesiotis* and *tenebrosa* do not. Leg color varies among species. In essence the bill shape differences between Old World and New World populations of *G. chloropus*, as well as body size differences (OW birds are smaller), are small, but not that different from currently accepted species within the group.

On the other hand, the vocal differences between OW and NW Common Gallinules are quite extreme, and it does not surprise me that OW populations are sister to the small and flightless Tristan Moorhens, rather than to NW birds. If a wider sample of *Gallinula* had been looked at in the molecular paper, it is quite possible that other OW *Gallinula* taxa (*tenebrosa* and *angulata*) may also be closer to OW *G. chloropus* than are the NW birds.

Notes – Galapagos populations sound essentially like mainland South American birds, and respond to playback from Eastern North American birds (Jaramillo pers. obs.). Hawaiian populations are more distinct, and need to be looked at in more detail, particularly with respect to voice. I may have recordings but they are currently not accessible. But overall, they are squarely in the NW population based on shield type. The very large and dark highland (Titicaca Basin) form *garmani* bears future attention too; again it is clearly a NW form.

Recommendation:

I recommend a YES vote, to split *Gallinula chloropus*. The oldest name for a New World population appears to be *galeata* (Lichtenstein 1818).

I think we could keep using the English Name Common Gallinule for *Gallinula galeata*, but note that Constantine et al. (2006) suggest the English Name “Laughing Moorhen” based on its distinctive voice as well as the name *cachinnans* (Laughing) for the widespread North American subspecies.

Literature Cited:

Constantine, M. & The Sound Approach (2006). *The Sound Approach to Birding: A guide to understanding bird sound*. Sound Approach, Dorset.

Groenenberg DSJ, Beintema AJ, Dekker RWRJ, Gittenberger E, 2008 Ancient DNA Elucidates the Controversy about the Flightless Island Hens (*Gallinula* sp.) of Tristan da Cunha. PLoS ONE 3(3): e1835. doi:10.1371/journal.pone.0001835

Submitted by: Alvaro Jaramillo

Date of proposal: Sep 2009

Comments from Robbins: “YES. Given that I don’t have access to the Constantine et al. CD, I’m taking at face value that the vocal differences that Alvaro points out on xeno-canto are indeed analogous (there are no on line examples available on MLNS). Having said that, the few examples on xeno-canto demonstrate that Old and New World birds sound nothing alike. Groenenberg et al. (2008) genetic data support this split.”

Comments from Stiles: “YES, at least tentatively. The genetic data for a basal split between New and Old World *Gallinula chloropus* are convincing, with high bootstrap and Bayesian support; the analysis of vocalizations by Constantine et al. also show strong differentiation between these groups. The morphological differences are not great, but would be in keeping with species-level distinctions in *Gallinula* and *Fulica*. Although sampling from the New World was quite limited in the Gough-Tristan da Cunha study, at least in my experience with birds from North, Central and South America sound quite similar and nothing like the Old World birds. I note in passing that this would lay to rest the burning English name controversy over whether to call our birds gallinules or moorhens.”

Comments from Zimmer: “YES. This is one of those groups where plumage characters are evolutionarily conservative, and voice (plus frontal shield color/morphology) is a much better indicator of relationship. And yes, this would finally give us the perfect rationale for getting rid of “Common Moorhen” as the English name for New World birds!”

Comments from Remsen: “YES. All data point towards a minimum of two species within *chloropus*.”

Comments from Pacheco: “YES. Os dados disponíveis no momento apontam objetivamente para a interdependência, ao menos, dos táxons presentes no Velho e no Novo Mundo.”

Comments from Nores: “YES. La propuesta hecha por Alvaro es muy convincente ya que muestra que existen diferencias en vocalizaciones (basado en Constantine et al. y xeno-canto) y genéticas (en Groenenberg et al.). Como

Gallinula chloropus era un ejemplo siempre citado de especie cosmopolita, resulta un poco desilusionante esta separación, pero ya hay varios ejemplos similares sobre la relación de especies del nuevo mundo con las del viejo mundo. Por ejemplo *Larus maculipennis* era considerada una subespecie de *L. ridibundus*, *Larus dominicanus* de *L. marinus*, *Himantopus mexicanus* de *H. himantopus*, *Phoenicopterus chilensis* de *P. ruber*, *Plegadis chihi* de *P. falcinellus*, etc. Otras especies, por el contrario, tales como *Sarkidiornis melanotos*, *Nycticorax nycticorax*, *Chroicocephalus cirrocephalus*, etc. se mantienen y sería bueno ver también si no son diferentes las del Nuevo Mundo del las del Viejo Mundo.”

Place *Sapayoa aenigma* in its own family, Sapayoidae

Description of the problem:

The NACC currently places the Sapayoa (*Sapayoa aenigma*) in the Eurylaimidae (Banks *et al.* 2008). However, the taxonomic position of the Sapayoa has only recently been resolved. This species was long considered an aberrant member of the Pipridae (manakins), as evidenced by the old common name Broad-billed Manakin (Snow 2004). Peculiarities in its morphology precluded definitive placement in any group of the suboscines, although work by Prum (1990) placed it near the Tyrannidae.

Early genetic studies were unable to place the Sapayoa in a specific group. Lanyon (1985), in a study of tyrannoids using protein electrophoresis, found that the Sapayoa did not belong with any of the sampled species, which included representatives of the Pipridae, Tyrannidae, Cotingidae, and Tityridae. Instead, the Sapayoa was found to be sister to the other tyrannoids sampled (Lanyon 1985). Sibley and Ahlquist (1990) considered the Sapayoa as *incertae cedis*; however, they suggested that it might be closely related to the Old World suboscines (Sibley 1994).

New information:

It was not until the use of DNA sequence data that the taxonomic position of the Sapayoa became clear. Based on several studies, the Sapayoa has been found to be closely related to the Old World suboscines, specifically the Eurylaimidae (Fjeldså *et al.* 2003, Chesser 2004, Irestedt *et al.* 2006, Moyle *et al.* 2006). Two primary hypotheses as to its relationships have emerged. The first hypothesis has the Sapayoa as sister to the asities (*Philepitta* and *Neodrepanis*) and several broadbill genera (*Cymbirhynchus*, *Psarisomus*, *Serilophus*, *Eurylaimus*, *Corydon*, and *Pseudocalyptomena*), hereafter referred to as the Asian and Grauer's Broadbills (Moyle *et al.* 2006). The second hypothesis places the Sapayoa as sister to the *Calyptomena* and *Smithornis* broadbills, hereafter referred to as the green and African broadbills (Fjeldså *et al.* 2003, Irestedt *et al.* 2006).

Based on these findings, two taxonomic treatments have been proposed. The first is the taxonomy already adopted by the NACC and the SACC, which involves the recognition of a single large Eurylaimidae, within which are placed the Sapayoa, the green and African broadbills, and the asities (Clements 2007, Gill *et al.* 2009). The second option involves the recognition of four "broadbill" families, including a monotypic Sapayoidae (Dickinson 2003).

Based on the available genetic data, the morphological evidence, and the biogeographic patterns, we propose the recognition of a monotypic Sapayoidae, which would necessitate the elevation of the green and African broadbills to family status as the Calyptomenidae (Fjeldså *et al.* 2003, Chesser 2004, Irestedt *et al.* 2006, Moyle *et al.* 2006). Irestedt *et al.* (2006) proposed this action based on the Sapayoa's morphological and biogeographical distinctness. In addition, the Sapayoa has undoubtedly been isolated from the rest of the broadbill taxa for quite some time (estimated at 52 million years by Moyle *et al.* 2006), and its syringeal morphology is quite distinct from that of the other broadbills (Prum 1990).

The inclusion of Sapayoa within the Eurylaimidae also renders the family paraphyletic with respect to the asities (Philepittidae). The asities, a distinctive group of birds endemic to Madagascar, are recognized by most authorities as deserving family rank, and the placement of Sapayoa within the Eurylaimidae requires this family to be included in the larger Eurylaimidae (Dickinson 2003, Irestedt *et al.* 2006).

The correct name for the family is Sapayoidae, formed by adding the family ending -idae to the stem of the type genus, Sapayo-. Although Dickinson (2003) incorrectly used the name Sapayoaidae, and the code does provide for priority in such cases (ICZN 1999), this name was not formally proposed and the appropriate citation for the correct family name (Sapayoidae) is instead Irestedt *et al.* (2006).

Recommendation:

Vote yes to recognize the monotypic family Sapayoidae. The Sapayoa is genetically, morphologically, and biogeographically distinct from the rest of the Old World suboscines. In the Check-list, Family **EURLAIMIDAE**: Broadbills would be replaced by Family **SAPAYOIDAE**: Sapayoa. The sequence of species would not change.

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