

AOU Classification Committee – North and Middle America

Proposal Set 2016-C

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Change the English name of *Alauda arvensis* to Eurasian Skylark

There are a dizzying number of larks (Alaudidae) worldwide and a first-time visitor to Africa or Mongolia might confront 10 or more species across several genera. Within North America, we have but two taxa: Horned Lark *Eremophila alpestris* and Sky Lark *Alauda arvensis*. The latter occurs both as a rare migrant and vagrant in the West (especially Alaska) and as an introduced species (Hawaii, Pacific Northwest).

English name stability is generally a good thing, but in some cases changes are warranted. Pertinent to this proposal, I believe the following philosophies are worth applying when possible:

Prevailing Usage:

When an English name used by NACC differs from the name being used widely elsewhere in the world, it is preferable to follow prevailing usage and change the name [except for "diver", "skua", etc. which are in roughly equal usage on different continents].

Use of Local Names:

Many of the species on the North American list are vagrants from the Palearctic. In those cases, I believe it is preferable to defer to the nomenclature being used in the core of the species range rather than implementing a novel name.

Consistency Within Genera:

Although it would be impossible to apply this rule consistently, when clear opportunities arise to use a unique English name for a monophyletic group, these names help birdwatchers understand relationships between species and even help with bird identification. Although not all *Tyrannus* are called "kingbird", it is nice to know that all kingbirds are *Tyrannus*. Consistent use of Gerygone for species in the genus *Gerygone* and of Wheatear for *Oenanthe* do help to convey that those are monophyletic groups and make it easy to remember the genera (especially so for Gerygone!).

History and Prevailing Usage:

From the first (1886) to the 34th supplement of the 5th edition, the AOU (NACC) had used the name "Skylark". With the 34th supplement, the name "Eurasian Skylark" was adopted and continued up through the 40th Supplement of the 6th edition (1995). The name was then changed to "Sky lark" (40th and 41st) and then to "Sky Lark" with the publication of the 7th edition (1998). It has remained "Sky Lark" for NACC ever since, even though no other major taxonomies use this name currently.

The change from Eurasian Skylark to Sky Lark was proposed in the Fortieth supplement: <https://sora.unm.edu/sites/default/files/journals/auk/v112n03/p0819-p0830.pdf>. The text of that supplement reads only: "p. 488. Change the English name of *Alauda arvensis* from EURASIAN SKYLARK to SKY LARK, following BOU (1992)."

Notably, the BOU (7th ed., including Jan 2009 supplement) has since reverted to the use of “Skylark”. The nomenclature of the BOU has always been very focused on the British Isles without much concern for nomenclatural conflicts or inconsistencies outside the U.K. Few species names contain geographical modifiers, even with genera or groups of species that have other representatives that occur outside the United Kingdom (e.g., Wigeon *Anas penelope*, Wren *Troglodytes troglodytes*, Jay *Garrulus glandarius*, etc.). I would certainly not recommend strict concordance with BOU for nomenclature outside the United Kingdom, since many conflicts and confusions would arise. NACC does not attempt to follow BOU names in most other cases except where the name is applicable globally.

<http://onlinelibrary.wiley.com/doi/10.1111/ibi.12069/full>

Globally, the name Sky Lark has been followed by the eBird/Clements taxonomy because of our deference to the AOU whenever possible. As a global taxonomy, this currently creates unnecessary issues with both prevailing usage and with inconsistency within the genus *Alauda* (see below “Consistency within *Alauda*”).

Avibase provides an easy way to check on the nomenclature of other major taxonomies; the Avibase page for *Alauda arvensis* is here:

<http://avibase.bsc-eoc.org/species.jsp?lang=EN&avibaseid=ED2AC04E&sec=summary&ssver=1>

According to Avibase, other taxonomies have used the following names (asterisks indicate current usage):

- *Eurasian Skylark: African Bird Club (versions from 2004 to 2010)
- *Eurasian Skylark: Handbook of Birds of the World (print and HBW Alive versions)
- Eurasian Skylark: Howard and Moore (3rd edition)
- *Eurasian Sky Lark: Howard and Moore (2nd and 4th editions)
- *Eurasian Skylark: IOC World Bird Names (v 1.0 to v5.04)
- *Eurasian Skylark: Oriental Bird Club

Furthermore, according to Avibase, Christidis and Boles (2008) recognize Japanese Skylark (see below) but also use Eurasian Skylark as well for the *alauda* group.

Thus, among major global and regional taxonomies, Eurasian Skylark is *clearly* the prevailing usage and only Howard and Moore has the slight variation of breaking “Sky Lark” into two words.

Changing to Eurasian Skylark would reduce confusion and bring NACC into alignment with most other major taxonomies used by birders and ornithologists worldwide. It would also take a name unique to NACC—“Sky Lark”—out of circulation.

Consistency within *Alauda*:

Using the name “Skylark” would provide two additional advantages:

1. One distinctive genus within larks would consistently use a different English name from “Lark”.
2. All members of *Alauda* would use a regionally modified version of the name “Skylark” that would thus correctly reflect their close relationship within the same genus.

Elsewhere in the world it is widely recognized that there are three species

- Sky Lark or Eurasian Skylark *Alauda arvensis*
- Razo Skylark *Alauda razae* - Endemic to Razo I. (Cape Verde Islands)

<http://avibase.bsc-eoc.org/species.jsp?lang=EN&avibaseid=359C16F5B8631E8D>

- Oriental Skylark - *Alauda gulgula* - Widespread in east Asia

<http://avibase.bsc-eoc.org/species.jsp?lang=EN&avibaseid=E988F1D549A6773D>

Range of subspecies as follows is from the Clements Checklist:

- *Alauda gulgula inconspicua* Transcaspia to Turkmenistan, e. Iran, Afghanistan and nw. India
- *Alauda gulgula lhamarum* Pamir Mts. and w. Himalayas (Kashmir to n. Punjab)
- *Alauda gulgula weigoldi* E. China (Shandong to s. Shaanxi and c. Sichuan)
- *Alauda gulgula inopinata* Tibetan plateau, e. Qinghai, Gansu and sw. Inner Mongolia
- *Alauda gulgula vernayi* E. Himalayas and adjacent China (se. Xizang and w. Yunnan)
- *Alauda gulgula gulgula* E. India to Sri Lanka and Indochina
- *Alauda gulgula coelivox* Se. and s. China to n. Vietnam; Hainan I.
- *Alauda gulgula wattersi* Taiwan and the Philippines

Changing from “Sky Lark” to “Eurasian Skylark” would thus be consistent with the names Razo Skylark and Oriental Skylark used by eBird/Clements. Notably, however, whereas Oriental Skylark is used by all major taxonomies (IOC, HBW, Birdlife, ABC, OBC, eBird/Clements), other major global taxonomies use the names Razo Skylark (eBird/Clements), Raso Lark (ABC, IOC, HBW, Birdlife), and Raso Island Lark (Howard and Moore) for *Alauda razae*. We will be sending separate proposals to those

committees to ensure consistency on both the spelling of Raso and the usage of Skylark.

In addition, Sibley and Monroe (1993, 1996) and Birdlife International (v00 to v07, through 2014) have recognized the *japonica* group as specifically distinct using the name Japanese Skylark: <http://avibase.bsc-eoc.org/species.jsp?lang=EN&avibaseid=0F6AE02E&sec=summary&ssver=1>

When split, the name “Japanese Skylark” has been consistently applied and the name Eurasian Skylark would still be appropriate for the remainder of the species range for the *arvensis* group.

Summary:

Four reasons to support the English name change of *Alauda arvensis* from Sky Lark to Eurasian Skylark:

1. Consistencies with other major global taxonomies and regional taxonomies within the species' range
2. Removal of a unique name (Sky Lark) not used elsewhere
3. Consistent usage of “Skylark” for closely related species
4. Consistent usage of “Skylark” across an entire genus within Alaudidae

Recommendation:

I recommend this name change for NACC.

Submitted by: Marshall Iliff

Date of Proposal: 2 February 2016

**Recognize Lilian's Meadowlark *Sturnella lilianae* as a
separate species from *S. magna***

Background:

Species limits between Eastern Meadowlark (*Sturnella magna*) and Western Meadowlark (*Sturnella neglecta*) have been studied in depth, and hybrid pairings are apparently very rare, even in areas of sympatry (Szijj 1963, Szijj 1966, Rohwer 1976). Lanyon (1979) found hybrid eggs 90% fertile (comparable to those produced by pure matings) and hybrid young to be viable, but found that when F1 hybrids paired just 10% of their eggs were fertile. This supported observations from the contact zone by Szijj (1963) and Rohwer (1976) that suggested strong selection against hybrid young and minimal signs of hybridization. Mayden (1997) considered the species status of Western Meadowlark to be firmly established under evolutionary, phylogenetic, and biological species criteria.

Within *S. magna*, the *lilianae* group (Lilian's Meadowlark) has long been considered distinctive and has been split as a species by some (Sibley and Monroe 1993, Fraga 2011). In a morphological comparison of *lilianae* and the *magna* group, Rohwer (1976) found *lilianae* to be 100% diagnosable and also suggested that it may warrant species status. Jaramillo and Burke (1999) and others have also suggested full species status for *lilianae*, and Barker et al. (2008) provided genetic evidence that augments the previously documented differences in habitat, plumage, and voice.

Sturnella magna, as currently defined, is broadly distributed in grasslands, marshes, and agricultural areas from Canada to northern South America. Lilian's Meadowlark appears to include three named subspecies ranging from the southwestern United States to Oaxaca. *Sturnella m. lilianae* is restricted to desert grasslands of the southwestern United States and northwestern Mexico. *Sturnella m. auropectoralis* is similar in plumage and morphology and occurs in the desert grasslands of central Mexico from Durango south to Oaxaca. Genetic material from *S. m. saundersi*, of coastal Pacific grasslands in Oaxaca, was not available to Barker et al. (2008) but its inclusion within Lilian's Meadowlark is strongly suggested by morphology, plumage, and biogeography.

New Genetic Data:

Barker et al. (2008) collected and analyzed sequence data from mitochondrial cytochrome *b*, ND2, cytochrome *b* + ND2, and from an intron of the sex-linked gene aconitase 1 across the ranges of *S. magna* and *S. neglecta*. This yielded four analyses with progressively more restricted taxon sampling. The data were analyzed with equally

weighted maximum parsimony, maximum likelihood and Bayesian inferences; the aconitase 1 data were analyzed with Bayesian methods alone. Support was assessed with non-parametric bootstrap for maximum parsimony and maximum likelihood (1000 and 200 replicates, respectively).

They found three deep and strongly supported clades within the yellow-breasted *Sturnella* of North America, pertaining respectively to the *magna* group, *neglecta* group, and *lilianae* group. This result was strongly supported by both mitochondrial (Fig. 2) and nuclear (Fig. 3) data.

The *lilianae* group was found to be sister to the *magna* group in all analyses, but the support for this sister relationship was not strong. However, the branch lengths and inferred divergence times between the *lilianae* group and the *magna* group were similar to those between *S. magna* and *S. neglecta*.

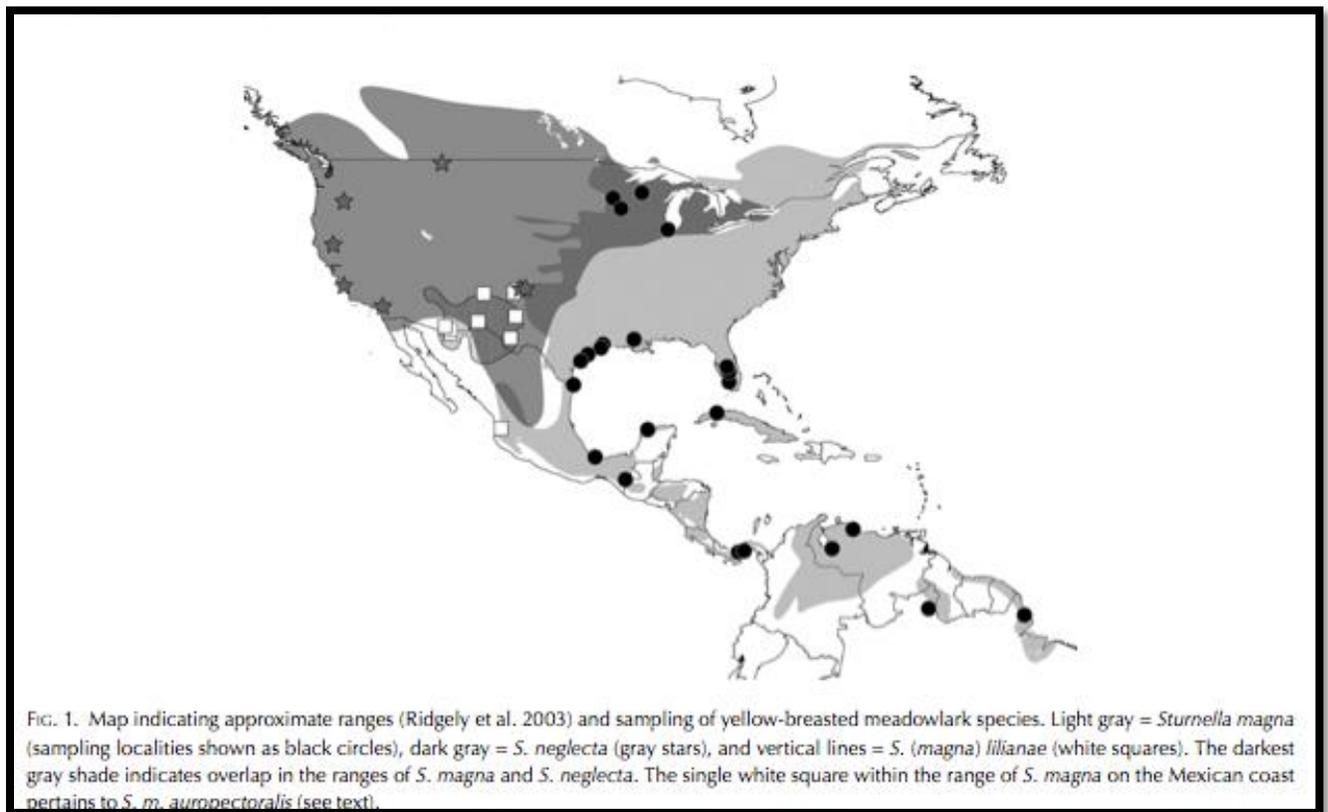


Fig. 1. From Barker et al. (2008). Map showing the distribution of Eastern, Western, and Lilian's Meadowlarks. Locations of sampling from each clade are shown: dark circles = *magna* group; gray stars = *neglecta* group; and white squares = *lilianae* group. The white square on the Pacific coast of Mexico represents the sample of two *auropectoralis*.

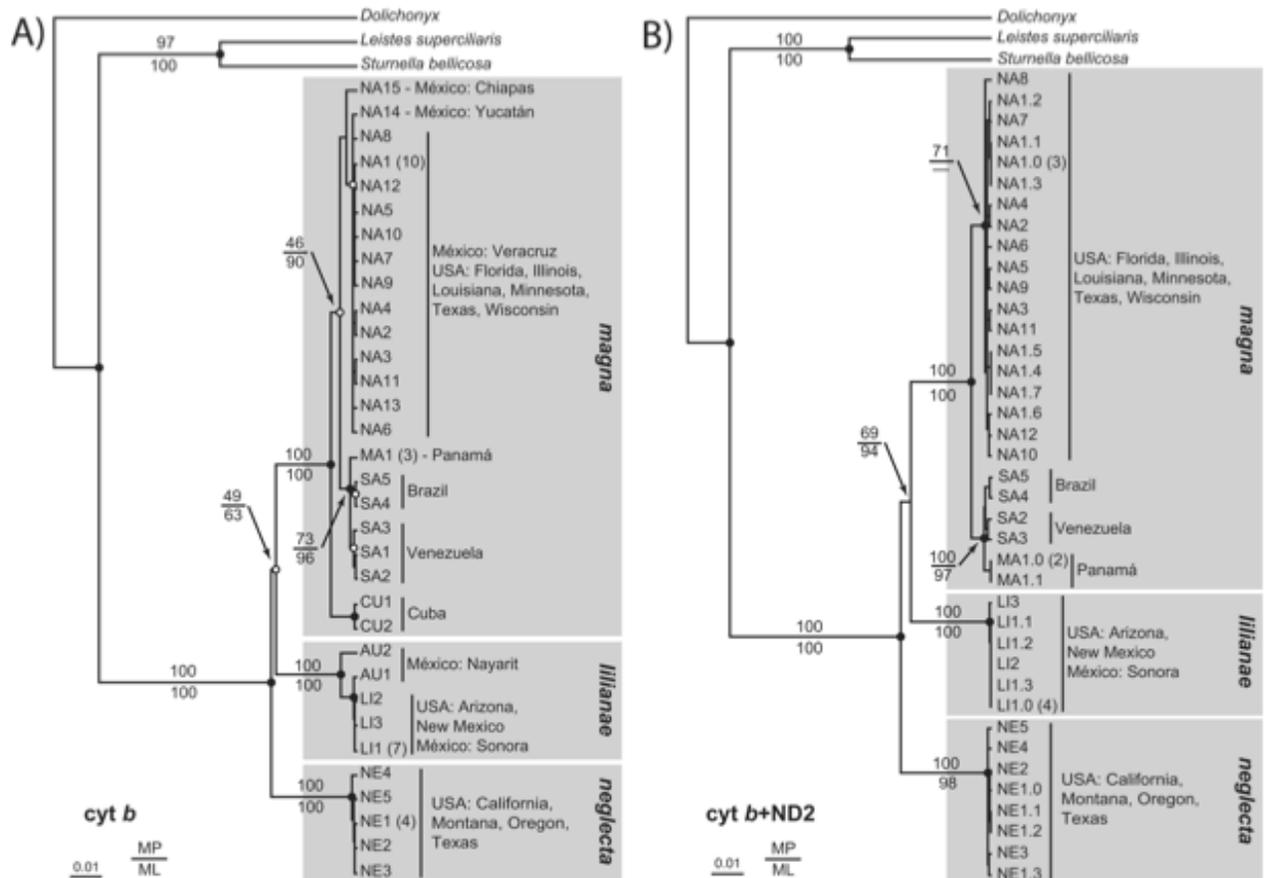


FIG. 2. (A) Phylogenetic analysis of unique cytochrome-*b* haplotypes of yellow-breasted meadowlarks (numbers in parentheses indicate frequencies of occurrence > 1; see Table 1 for assignments to individuals). Shown is the maximum-likelihood (ML) tree of relationships (see Table 3 for parameterization), with branch lengths proportional to expected divergence. The shaded boxes indicate Eastern (*magna*), Lillian's (*liliana*, *sensu lato*), and Western (*neglecta*) meadowlarks, and localities where given haplotypes were found are indicated. Recovery of given relationships as indicated by nonparametric bootstrapping is shown at each node (parsimony above, likelihood below). All nodes with estimated Bayesian posterior probabilities ≥ 0.95 for the combined mtDNA and nuclear data set are marked by circles: the subset of nodes with estimated probabilities ≥ 0.95 with the cytochrome-*b* data alone are indicated by solid black circles. (B) Phylogenetic analysis of unique cytochrome *b* + ND2 haplotypes of yellow-breasted meadowlarks (see Table 1 for assignments to individuals). Shown is the ML tree of relationships (see Table 3 for parameterization), with branch lengths proportional to expected divergence. Shading is as in Figure 2A. Recovery of given relationships as indicated by nonparametric bootstrapping is shown at each node (parsimony above, likelihood below), and estimated Bayesian posterior probabilities ≥ 0.95 are indicated by closed circles.

Figure 2. From Barker et al. (2008). Phylogenetic analysis of mitochondrial genes from cytochrome *b* and cytochrome *b* + ND2 resolve similar structure within the *Sturnella* meadowlarks, with three strongly supported clades and with *liliana* sister to *magna* group. Divergence of the *liliana* group from the *magna* group was comparable to the divergence between the *magna* and *neglecta* groups.

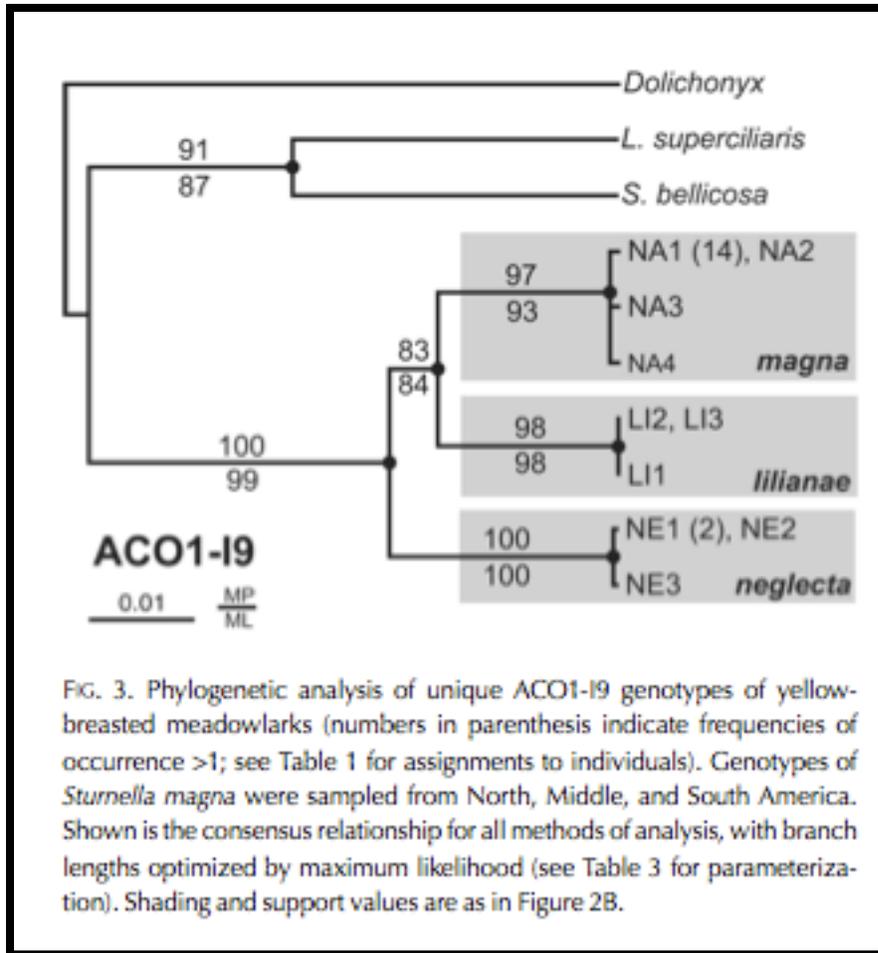


FIG. 3. Phylogenetic analysis of unique ACO1-I9 genotypes of yellow-breasted meadowlarks (numbers in parenthesis indicate frequencies of occurrence >1; see Table 1 for assignments to individuals). Genotypes of *Sturnella magna* were sampled from North, Middle, and South America. Shown is the consensus relationship for all methods of analysis, with branch lengths optimized by maximum likelihood (see Table 3 for parameterization). Shading and support values are as in Figure 2B.

Figure 3. From Barker et al. (2008). Independent tree from analysis of sex-linked nuclear gene aconitase 1. This tree yielded a structure similar to the mitochondrial genes, showing three strongly supported clades with the *lillianae* group sister to the *magna* group.

The well-understood species limits between *S. magna* and *S. neglecta* provide an important anchor when assessing the species status of Lilian's Meadowlark. Hybridization in *S. magna* and *S. neglecta* is not common (Szijj 1963, Szijj 1966, Rohwer 1976), and Lanyon (1979) found that F1 hybrids had very low egg fertility, strongly selecting against hybrids. Despite similarity in plumage and some vocalizations, studies of genetics and hybridization have strongly supported the treatment of Eastern and Western Meadowlark as distinct species, and indeed the species-pair is often cited as an example when discussing species concepts (Mayden 1997). Although data are not available on hybrid pairings between the *lillianae* group and the *magna* group, the similar divergence times suggest that if the *magna* groups and *neglecta* groups are granted species status, the *lillianae* group should also be split.

Note also that Powell et al. (2014) include samples from all *Sturnella*; these data were used by SACC to revise the sequence in *Sturnella*
<http://www.museum.lsu.edu/~Remsen/SACCprop612.htm>.

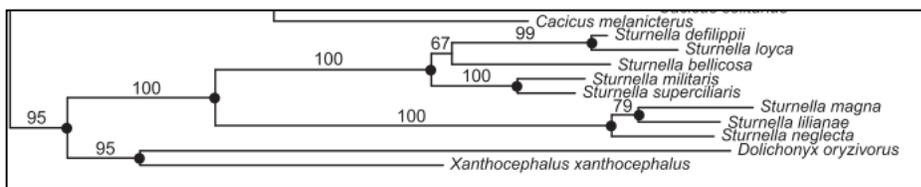
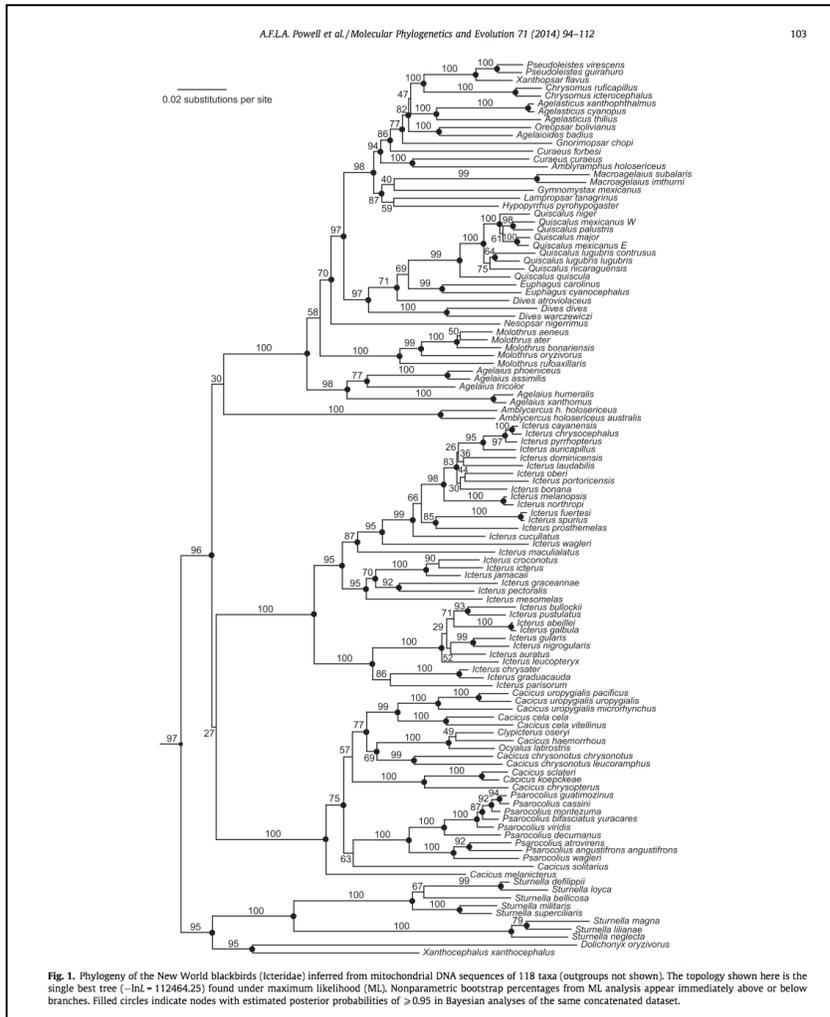


Fig. 4. Phylogeny of the Icteridae from Powell et al. (2014), with inset of the *Sturnella* from the bottom of the tree.

As in that proposal, I'll quote from their abstract: "Using mitochondrial gene sequences from all ~108 currently recognized species 7 and six additional distinct lineages, together with strategic sampling of four nuclear loci and 8 whole mitochondrial

genomes, we were able to resolve most relationships with high confidence. Our phylogeny is consistent with the strongly-supported results of past studies, but it also contains many novel inferences of relationship, including unexpected placement of some newly sampled taxa, resolution of relationships among major clades within Icteridae, and resolution of genus-level relationships within the largest of those clades, the grackles and allies”. Although they did not discuss the species-level relationships in depth, they did write: “The nuclear data recovered the following relationships... *Sturnella lilianae* and *S. magna* together (73, 98), and that pair sister to *S. neglecta* (99, 100), thus supporting monophyly of the yellow-breasted meadowlarks.” Regardless, their work treated *lilianae* at the species level, using samples from Texas and Sonora, and found that relationship comparable to others in *Sturnella*.

Vocal Data:

Eastern Meadowlark and Western Meadowlark have marked differences in both songs and calls, especially the primary contact call, which is a buzzy *dzrrt* in *magna* and a grackle-like *chuck* in *neglecta*. However, *S. l. lilianae* vocalizations are much more similar to those of *S. magna*, and although some average differences have been reported in the songs, even those, in many cases, may be indistinguishable.

Both *magna* and *lilianae* have similar whistled, melodic songs. Cassell (2002) and others (Sibley 2000) have pointed out the lower pitch of the songs of *lilianae* as compared to *S. m. magna*. Follow up analysis by Pieplow (2009), elaborated upon by Leukering and Pieplow (2009), reveals more complexity to the songs, although average differences are upheld, with *lilianae* having a lower pitched song and a usually down-slurred final note.

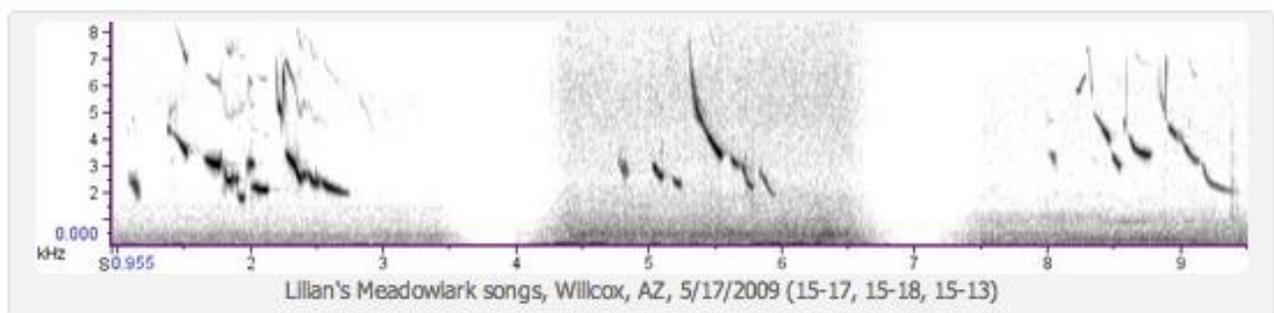


Fig. 3. From Pieplow (2009). Sonograms of songs from *lilianae*. Note the lowest pitch is about 2 kHz and the down-slurred ending typical to all songs. See Pieplow (2009) to hear the recordings and read a more complete analysis.

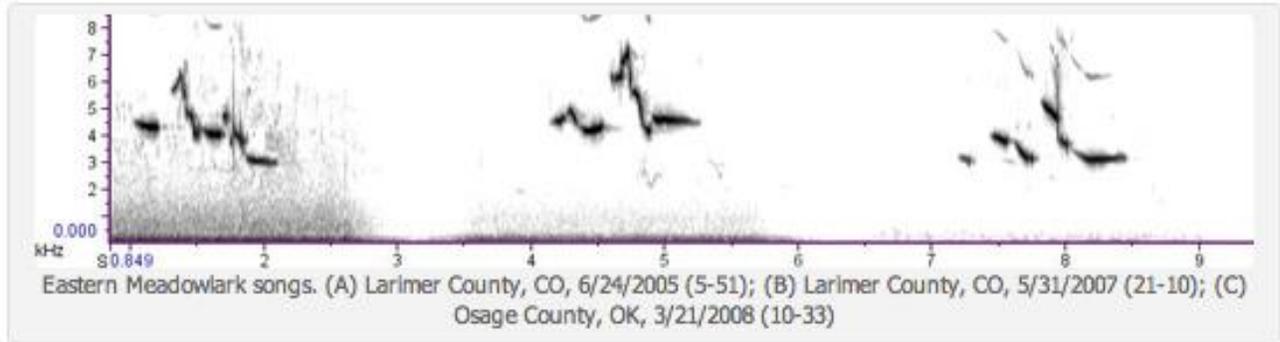


Fig. 4. From Pieplow (2009). Sonograms of songs from *magna*. Note the lowest pitch is about 3 kHz and the ending is more of a monotone. See Pieplow (2009) to hear the recordings and read a more complete analysis.

Because meadowlark songs are learned, the average differences may not be as meaningful as differences in call notes, especially given the stark differences between Eastern and Western meadowlarks in typical song and contact call. The calls of *S. m. lillianae* are certainly very close to those of the rest of the *magna* group and may be indistinguishable. Pieplow (2009) discusses the *bzert* note, considering it possibly distinctive in Lillian's but pointing out that a more complete study is needed. No differences have been reported in the *wink* flight call or the metallic rattle.

Vocalizations of *S. m. auropectoralis* and *S. m. saundersi* have not been studied. Xeno-canto has one recording of a singing bird from the Valley of Oaxaca, a reported intergrade zone between *auropectoralis* and *saundersi*. That recording sounds low pitched and truncated, perhaps consistent with traits discussed above for *lillianae*: <http://www.xeno-canto.org/67073>.

In addition, Nathan Pieplow wrote me the following in August 2015: "This past spring I was in west Mexico with Andrew Spencer and got some recordings of song and call from *auropectoralis*. There are also a few recordings on xeno-canto from within the range of *auropectoralis*. My subjective impression, without having looked into it closely, is that *auropectoralis* shares the low pitch of *lillianae*. However, the same seems to be true of some of the "Eastern" Meadowlarks from elsewhere in Mexico -- e.g., <http://www.xeno-canto.org/127730>. And I think the biogeographic/ecological differences between northern "Eastern" and "Lilian's" may well become much blurrier in Mexico. That's all I can tell you, but hopefully it's useful." I don't have more information on this, but thought the comments on *auropectoralis* and general comments about meadowlark songs in Mexico should be mentioned. Clearly more study is needed.

Morphological Data:

Upperparts coloration and size vary significantly across the 14 subspecies of the *magna* group and within the three proposed subspecies of the *liliana* group. Upperparts coloration can be expected to vary widely, because this is likely governed by substrate and vegetation and is a trait that varies substantially in other widely distributed open-country species such as Savannah Sparrow (*Passerculus sandwichensis*) and Horned Lark (*Eremophila alpestris*).

Most taxa in the *magna* group identified by Barker et al. (2008) vary in size, key morphometrics (wing, bill, tail, tarsus), and upperparts coloration. On the other hand, the two taxa within their *liliana* group (*auropectoralis* and *liliana*), as well as *saundersi*, do have several additional traits in common. All three have entirely white outer three rectrices (r4 to r6) and the third rectrix (r3) mostly white, while all other taxa have one fewer white rectrix (only r4 to r6 largely white). In addition, the cheek of *liliana*, *auropectoralis*, and *saundersi* is markedly whitish as compared to taxa within the *magna* group, which all have grayish or brownish cheeks. Finally, while *magna* is large, of the forms in the southern U.S., Mexico, Central America, and South America, *liliana* and *auropectoralis* are the two largest taxa, followed by *saundersi*, which is also large in addition to being comparatively short-billed.

Rohwer (1976) compared *liliana* to *hoopesi* and “demonstrated that this taxon was morphologically as distinct from other forms of *S. magna* as both were from *S. neglecta*.”

Subspecies Characters

<i>S. m. hoopesi</i>	Medium-sized; 2 entirely white rectrices; grayish-white cheeks; pale upperparts with narrow bars on tail (note that Jaramillo and Burke illustrate 4 white rectrices, presumably an error?)
<i>S. l. liliana</i>	Large; 3 entirely white rectrices; pale whitish cheek; short tarsometatarsus and tail; rich orange or yellow breast; very pale above with narrow tail barring on central rectrices
<i>S. l. auropectoralis</i>	Large; 3 entirely white rectrices; pale whitish cheek; like <i>liliana</i> , but darker above, more heavily marked central tail feathers, and more orange tone to breast; shorter-winged than <i>liliana</i>
<i>S. l. saundersi</i>	Large; 3 entirely white rectrices; pale whitish cheek; paler than <i>auropectoralis</i> on upperparts and more yellow (less orange) below; short-billed and shorter-winged than <i>auropectoralis</i> and slightly longer-winged than <i>alticola</i>

S. l. alticola Medium-sized; 2 entirely white rectrices; grayish-white cheeks; Similar to *auropectoralis* in upperparts coloration, but tail w/ less white (r4 usu. partly or mostly dark); breast more yellow and less orange; longer wing, shorter tail and tarsometatarsus, and slightly shorter culmen

Jaramillo and Burke (1999:301) note that “According to J. Barlow . . . the Mexican taxa [sic] *auropectoralis* is clearly more closely related to ‘Lilian’s,’ while the very similar appearing *hoopesi* belong[s] in Eastern Meadowlark. Saunders (1934) also hypothesized that *liliana* was most closely related to *auropectoralis*, and that the more southern *alticola* also fit in this group.”

Although the conclusion regarding *alticola* appears to be refuted by genetic data, the phenotypic group of large, pale-cheeked meadowlarks with one extra white feather in the tail appears to match a biogeographic grouping from the southwestern United States to Pacific west Mexico. Notably, this also largely matches the *liliana* group identified by Barker et al. (2008).

Table 2. Using data from multiple sources, the appearance of five meadowlark taxa, each of which has at times been considered similar to *liliana* or part of a *liliana* group, is summarized here. Note that *liliana*, *auropectoralis*, and *saundersi* often have four largely white rectrices, but the above summary focuses on the number of entirely white rectrices.

Subspecies of *liliana* group: Fifteen of seventeen subspecies of *S. magna* (Clements et al. 2015) were sampled by Barker et al. (2008) across most of the range of the two species (Fig. 1); for some taxa only mitochondrial genes were available. Among the two unsampled subspecies was *S. m. praticola* of the northern South American llanos, but Blake (1968) considered *S. m. monticola* (which was sampled) synonymous. The samples of *S. m. monticola* fell within a shallow South American clade among the deeper *magna* clade and it seems safe to presume that *S. m. praticola* also falls within the *magna* clade.

The range and component subspecies of Lilian’s Meadowlark have been confused, and the incomplete sampling by Barker et al. (2008) leaves some questions as to the limits of the *liliana* group.

Authors that have recognized a *liliana* group, either as a species (Sibley and Monroe 1993, Fraga 2011) or distinctive subspecies group (Jaramillo and Burke 1999, Jaster et al. 2012, Clements et al. 2013) have been quite inconsistent in the component subspecies of the group. Some authors (Sibley and Monroe 1993, Jaramillo and Burke 1999, del Hoyo et al. 2011, Clements et al. 2013) have considered the *liliana* group monotypic, but genetic data from Barker et al. (2008) show that at least *auropectoralis* also should be included. In his original description, Saunders (1934) found

auropectoralis to be so morphologically similar to *liliana* that he considered *liliana* as its “nearest relative”. Jaramillo and Burke (1999) included only *liliana* in their account of Lilian’s Meadowlark, but discuss the possibility that *S. m. auropectoralis*, *S. m. saundersi*, and *S. m. alticola* also pertain to this group; apparently deferring to this suggestion by Jaramillo and Burke (1999), this arrangement is followed by Jaster et al. (2012) who include these four subspecies in their *liliana* group.

Subspecies	Range
<i>S. m. hippocrepis</i> (Wagler, 1832)	Cuba and Isle of Pines
<i>S. m. magna</i> (Linnaeus, 1758)	S Ontario east to Quebec and south to n Texas and ne Georgia
<i>S. m. argutula</i> Bangs, 1899	SE Kansas and Oklahoma to e US (Carolinas to Florida)
<i>S. m. hoopesi</i> Stone, 1897	S Texas (Eagle Pass to n Coahuila, Nuevo León and n Tamaulipas)
<i>S. m. alticola</i> Nelson, 1900	Highlands of s Mexico (Guerrero, s Puebla, Veracruz to Costa Rica)
<i>S. m. mexicana</i> Sclater, PL, 1861	Caribbean slope of se Mexico (Veracruz and Tabasco to Chiapas)
<i>S. m. griscomi</i> van Tyne & Trautman, 1941	SE Mexico (arid coastal n Yucatán Peninsula)
<i>S. m. inexpectata</i> Ridgway, 1888	Pine savanna of Belize, Petén of Guatemala, Honduras, Nicaragua
<i>S. m. subulata</i> Griscom, 1934	Pacific slope of Panama
<i>S. m. meridionalis</i> Sclater, PL, 1861	Eastern Andes of Colombia to Andes of nw. Venezuela
<i>S. m. parali</i> Bangs, 1901	N. Colombia and savannas of w. Venezuela
<i>S. m. monticola</i> Chubb, 1921	Tepuis of s. Venezuela (Mt. Roraima)
* <i>S. m. praticola</i> Chubb, 1921	Llanos of e. Colombia to s. Venezuela and n. Guyana
<i>S. m. quinta</i> Dickerman, 1989	Suriname and ne. Amazonian Brazil
<i>S. [l.] liliana</i> Oberholser, 1930	N. Arizona to e. New Mexico, sw. Texas, s. Sonora and nw. Chihuahua

<i>S. [l.] auropectoralis</i> Saunders, GB, 1934	Mexico (Durango and Sinaloa to Michoacán, México, and n. Puebla)
* <i>S. [l.] saundersi</i> Dickerman & Phillips 1970	S. Mexico (Oaxaca)
<i>S. n. confluenta</i> Rathbun, 1917	Sw. and c. British Columbia to w. Idaho and s. California
<i>S. n. neglecta</i> Audubon, 1844	SE British Columbia to n Baja, Texas

Table 1. Subspecies of Eastern Meadowlark and Western Meadowlark according to Clements et al. (2013) with citations from Avibase (<http://avibase.bsc-eoc.org/species.jsp?lang=EN&avibaseid=4A11480B216EBB80&sec=summary&ssver=1>). The two subspecies marked with an asterisk (*) were not sampled by Barker et al. (2008).

Barker et al. (2008) included two samples from *S. m. auropectoralis*, but both were January specimens from the Pacific slope (Nayarit), and not from the breeding grounds. Both *auropectoralis* fell clearly within the *liliana* clade without obvious divergence. Although samples from the breeding grounds would have been preferable, this provides strong support for the suggestion by Saunders (1934) that *auropectoralis* and *liliana* are each other's closest relatives.

Barker et al. (2008) also sampled at least one *S. m. alticola* (from Chiapas, Mexico, in January) and this highland form clustered with the *magna* clade, although, again, samples from the breeding season would have been preferable. These limited genetic data suggest that Jaster et al. (2012) may be in error in including *alticola* in the *liliana* group.

More problematically, *S. m. saundersi* of Oaxaca was not sampled by Barker et al. (2008). This recently described form (Dickerman and Phillips 1970) occurs in the Isthmus of Tehuantepec region on the Pacific slope of Oaxaca. Intergrades with *S. m. auropectoralis* in the Valley of Oaxaca are also reported (Dickerman and Phillips 1970). Dickerman and Phillips (1970) describe *saundersi* as similar to *auropectoralis*, being sandy brown above and rather bright. Compared to *auropectoralis*, they describe it as short-billed, paler and less rufescent dorsally and on the flanks, as well as paler and less ochraceous yellow on the breast. Dickerman and Phillips (1970) do not describe tail pattern but apparently it is similar to *auropectoralis* and *liliana*, as it is not listed as one of the characters distinguishing it from those taxa. In the absence of genetic data, it would seem that the close plumage and structural similarity of *saundersi* to *auropectoralis*, combined with the apparent interbreeding with *auropectoralis*, is sufficient evidence to provisionally place this subspecies within the *liliana* group.

Some authors have discussed the similarity of *hoopesi* and *liliana*, although Rohwer (1976) found both to be 100% diagnosable in Texas. Barker et al. (2008) found that samples of *hoopesi* fell in the *magna* clade, despite the superficial similarity of that form to *liliana*, especially in upperparts coloration.

Contact Zones:

Areas of contact between *S. m. hoopesi* and *S. m. liliana* are reported in the semiarid plains of Tlaxcala, Puebla, and adjacent areas of Veracruz by Jaster et al. (2012), but the source of this information is not mentioned. Detailed studies from this reported zone of introgression appear to be lacking. Similarly, *S. m. auropectoralis* is reported to hybridize with the "*liliana*-*hoopesi* complex" in Distrito Federal and eastwards in Volcanic Belt (Jaster et al. 2012), but if so, this contact zone has not been studied in detail, nor, to my knowledge, has this report of hybridization been confirmed. The extent to which *hoopesi* interacts with the *liliana* group from Barker et al. (2008) appears to be lacking detailed study.

Dickerman and Phillips (1970) suggested that intermediate specimens between *S. m. saundersi* and *S. m. auropectoralis* in the Valley of Oaxaca are evidence of introgression between those two subspecies. Furthermore, they report two male specimens collected 4 km S of Sarabia, Oaxaca, that matched *S. m. mexicana* in coloration but had long wings, "indicating an approach to the larger Pacific coastal form in size." It is not clear if these represent intergrades or simply larger specimens of *S. m. mexicana*. Clearly the extent and significance of introgression among the various taxa in the *liliana* and *magna* groups in Mexico is a topic in need of further study; these reports do not necessarily suggest that the *liliana* group is not a valid biological species. Note especially that of four contact zones above, only two (*hoopesi*-*liliana* and the possible contact zone in Oaxaca between *S. m. mexicana* and *S. l. saundersi*) would cross species boundaries if Lillian's Meadowlark is split.

Although studies characterizing the possible hybrid zones of the *liliana* group have not been conducted, the studies by Lanyon (1979) showing hybrid sterility in *magna* x *neglecta* hybrids may suggest that hybrids between the *magna* and *liliana* groups might be similarly sterile.

English Names:

Using the same common name for both a parent and daughter taxon is generally poor practice, as it creates significant confusion in literature and databases as to whether the name is *sensu stricto* or *sensu lato*. However, in some cases a vernacular name is well-enough entrenched and not a source of major confusion. Where taxa are largely allopatric, these nomenclatural changes are less problematical. In this instance,

retaining Eastern Meadowlark for *S. magna* is appropriate and Lillian's Meadowlark is the obvious choice for *S. lillianae*, as it is a name already well entrenched in popular usage.

Taxonomic possibilities: There are three potential treatments for *Sturnella*:

- 1) Maintain the status quo, with a single widely distributed *S. magna*
- 2) Split *S. lillianae* from *S. magna*.
- 3) Lump *magna*, *neglecta*, and *lillianae* under a single species

If #2 is accepted, I recommend that *lillianae* be considered to consist of three subspecies: *lillianae*, *auropectoralis*, and *saundersi*. In the absence of genetic material, evidence for *saundersi* as part of this group is based on morphological, plumage, and biogeographic grounds.

Recommendation:

I recommend a yes vote on option 2, which would split *S. lillianae* from *S. magna*. The well-established species status of *magna* and *neglecta* provides strong logic for this treatment (and strong evidence against option #3). If *neglecta* and *magna* are to be recognized as species, the genetic evidence strongly suggests that *lillianae* should be as well. Plumage differences between the *lillianae* group and the *magna* group are comparable to those between the *magna* and *neglecta* groups. Although vocal differences are more subtle than those between *magna* and *neglecta*, song differences do exist and may even be important near potential contact zones. As mentioned above, Lillian's Meadowlark was previously recognized as a species by Sibley and Monroe (1993) and Handbook of the Birds of the World (del Hoyo et al. 2011).

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Submitted by: Marshall Iliff

Date of Proposal: 20 February 2016

Change the English name of *Euplectes franciscanus* to Northern Red Bishop

Euplectes franciscanus is an introduced species in the AOU Area, occurring in southern California and various Caribbean islands, and occasionally elsewhere. The eBird map (<http://ebird.org/ebird/map/orabis1>) shows the concentration of reports in southern California along with scattered others north to the San Francisco Bay area, in Texas, Florida, Puerto Rico, Guadeloupe, Martinique, and possibly Jamaica (one validated record currently). This is an introduced species that is likely to persist for a while, so resolving this English name discrepancy seems worthwhile.

English name stability is generally a good thing, but in some cases changes are warranted. Pertinent to this proposal, I believe the following philosophies are worth applying when possible:

Prevailing Usage:

When a common name used by NACC differs from the name being used widely elsewhere in the world, it is preferable to follow prevailing usage and change the name.

Use of Local Names:

Many of the species on the North American list are vagrants or introduced species from the Old World. In those cases, I believe it is preferable to defer to the nomenclature being used in the core of the species range rather than implementing a novel name.

History and Prevailing Usage:

The AOU first used the name Red Bishop to refer to *Euplectes orix sensu lato*: it split *E. orix* and *E. franciscanus* with its 41st supplement (<https://sora.unm.edu/sites/default/files/journals/auk/v114n03/p0542-p0552.pdf>) using the name Orange Bishop for the latter. This would have been a great time to opt for Northern Red Bishop for continuity with the previous name, especially if Southern Red Bishop was used for *E. orix*. Alas, the text for that supplement reads:

p. 766. *Euplectes franciscanus* (Isert), Orange Bishop, is separated from *E. orix*, Red Bishop, following Hall and Moreau (1970). The birds established in Puerto Rico and southern California, and presumably those in Hawaii and Bermuda, are *E. franciscanus*, and an account for that species replaces the present account for *E. orix*.

Avibase provides an easy way to check on the nomenclature of other major taxonomies; the Avibase page for *Euplectes franciscanus* is here:

<http://avibase.bsc-eoc.org/species.jsp?lang=EN&avibaseid=3D12284957400BDC>

According to Avibase, other taxonomies have used the following names:

- African Bird Club Checklist (2004-2010) have all used Northern Red Bishop. Because this species is native to Africa, this name choice should carry special weight.
- Howard and Moore 3rd and 4th editions have both used Northern Red Bishop
- Handbook of Birds of the World (vol. 1-16) and HBW Alive have both used Northern Red Bishop
- The IOC World Bird Names checklist has unchangingly used Northern Red Bishop from v1.0 to the current v.6.1.
- The eBird/Clements Checklist used Orange Bishop from the 4th edition of the Clements Checklist through 2014, but changed to Northern Red Bishop in the 2014 update.
- Since the 41st supplement, the AOU Checklist has used Orange Bishop.
- Birdlife International has similarly used Orange Bishop in all their checklists (v00-v07 in July 2014), but as they are now aligning taxonomies with HBW, this name is likely to change to Northern Red Bishop for them too.
- Sibley and Monroe used Orange Bishop in their first and second editions, 1993 and 1996 respectively.
- Prominent African field guides (Zimmerman et al. 1999, Stevenson and Fanshawe 2002, Sinclair et al. 2003) all use Northern Red Bishop.

According to Avibase <http://avibase.bsc-eoc.org/species.jsp?lang=EN&avibaseid=95F08BC3&sec=summary&ssver=1>, the same authorities that use Orange Bishop above (Birdlife, NACC, and Sibley and Monroe) have also used Red Bishop for *E. orix*, whereas those that use Northern Red Bishop have consistently used Southern Red Bishop for *E. orix*.

Thus, among major global and regional taxonomies, Northern Red Bishop is *clearly* the prevailing usage and no other major taxonomy (other than Birdlife) departs from this usage.

English names within *Euplectes*

The eBird/Clements Checklist (Clements et al. 2015) lists these species in the genus *Euplectes*, matching closely the taxonomy of other taxonomies (e.g., IOC):

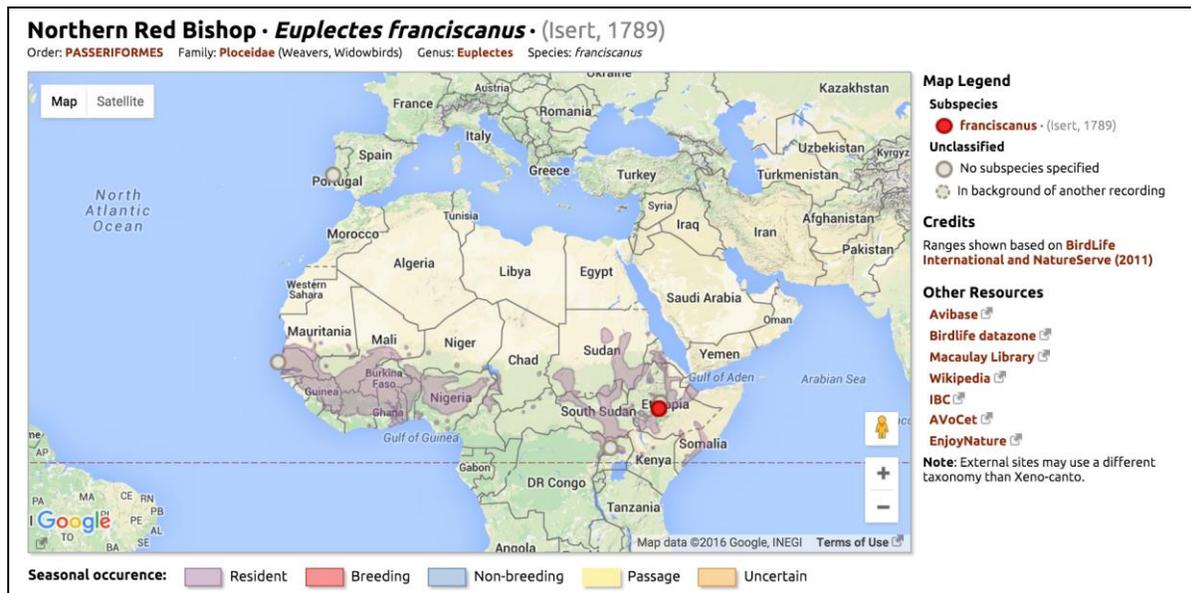
Northern Red Bishop	<i>Euplectes franciscanus</i>
Southern Red Bishop	<i>Euplectes orix</i>
Zanzibar Red Bishop	<i>Euplectes nigroventris</i>
Black-winged Bishop	<i>Euplectes hordeaceus</i>
Black Bishop	<i>Euplectes gierowii</i>

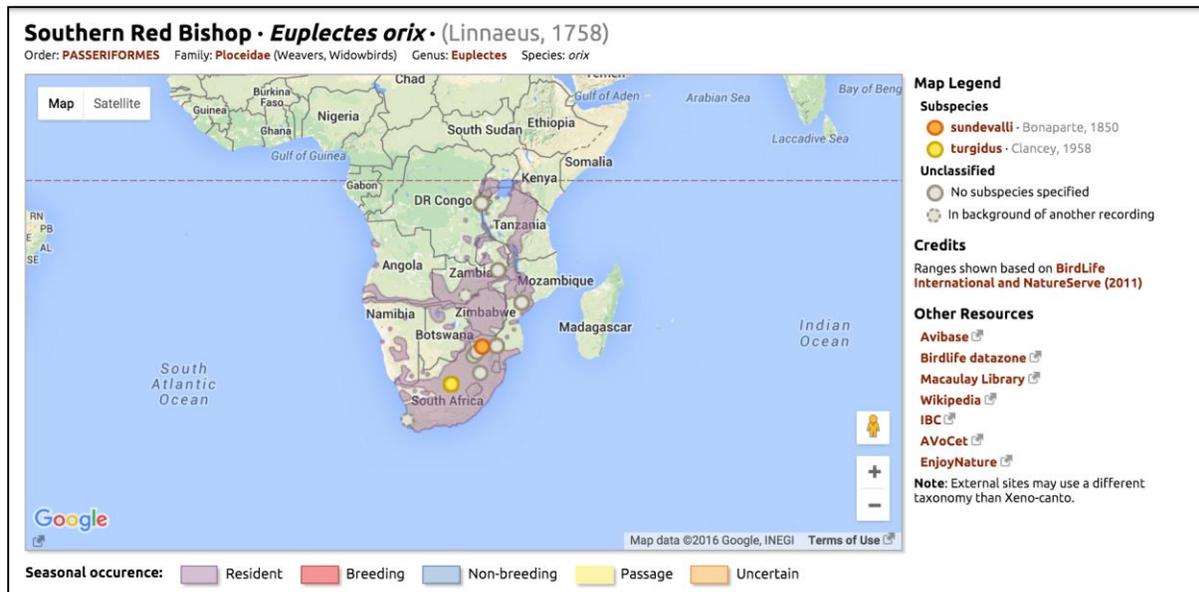
Yellow-crowned Bishop	<i>Euplectes afer</i>
Fire-fronted Bishop	<i>Euplectes diadematus</i>
Golden-backed Bishop	<i>Euplectes aureus</i>
Yellow Bishop	<i>Euplectes capensis</i>
White-winged Widowbird	<i>Euplectes albonotatus</i>
Yellow-shouldered Widowbird	<i>Euplectes macroura</i>
Red-collared Widowbird	<i>Euplectes ardens</i>
Fan-tailed Widowbird	<i>Euplectes axillaris</i>
Marsh Widowbird	<i>Euplectes hartlaubi</i>
Buff-shouldered Widowbird	<i>Euplectes psammocromius</i>
Long-tailed Widowbird	<i>Euplectes progne</i>
Jackson's Widowbird	<i>Euplectes jacksoni</i>

Notably the eight bishops are all named for the breeding colors of the males and the first three, including *E. franciscanus*, *E. orix*, and *E. nigroventris* are all variations of _____ Red Bishop. Since *E. orix* is known as Southern Red Bishop, it makes sense to also have a companion Northern Red Bishop.

Accuracy of the Name Northern Red Bishop:

Xeno-canto maps show that these names are appropriate, given the world ranges of these two species:





Stevenson and Fanshawe (2002) described the only useful field marks to distinguish adult males in breeding plumage as the extent of black on the crown (more extensive in *franciscanus*, restricted to forehead in *orix*) and the extent of the brown tail past the uppertail coverts (obvious in *orix*, hidden by coverts in *franciscanus*). Of *orix* they say “plumage is either bright red and black, or **orange and black**” (emphasis mine). Of *franciscanus*, they say “plumage is bright red and black, except in extreme [Northeastern Kenya] where race *pusillus* **may be** orange and black” (emphasis mine again). Thus, if anything, *franciscanus* is less red than *orix*.

Online photos show color of *E. franciscanus* ranging from scarlet-red:

[https://commons.wikimedia.org/wiki/File%3AEuplectes_franciscanus_-
Kotu Creek%2C Western Division%2C The Gambia -male-8.jpg](https://commons.wikimedia.org/wiki/File%3AEuplectes_franciscanus_-_Kotu_Creek%2C_Western_Division%2C_The_Gambia_-male-8.jpg)

to reddish-orange:

https://commons.wikimedia.org/wiki/File%3AEuplectes_orix_5_Luc_Viatour.jpg

or roughly in between: <https://www.flickr.com/photos/96759203@N06/8904737109/>

Importantly though, Southern Red Bishop is no less red and actually appears closer to orange in color:

https://commons.wikimedia.org/wiki/File%3AEuplectes_sp_PLW_crop.jpg

[https://commons.wikimedia.org/wiki/File:Euplectes_orix_-_Pretoria,_South_Africa_-
male_weaving_nest-8_\(1\).jpg](https://commons.wikimedia.org/wiki/File:Euplectes_orix_-_Pretoria,_South_Africa_-_male_weaving_nest-8_(1).jpg)

http://ibc.lynxeds.com/files/pictures/MG_7313_Southern_Red_Bishop.jpg

Overall these two species appear very similar in color and in the variability in appearance. Neither species is clearly orange, and using red in the name is just as appropriate. It certainly is misleading to retain the NACC status quo, referring to *E. orix* as Red Bishop and *E. franciscanus* as Orange Bishop.

Summary:

Four reasons to support the common name change of *Euplectes franciscanus* from Orange Bishop to Northern Red Bishop:

1. Consistencies with other major global taxonomies and regional taxonomies within the species' range
2. Provides a measure of consistency within the names of *E. orix*, *E. nigroventris*, and *E. franciscanus*.
3. Geographically appropriate names
4. Avoiding the misleading suggestion that color is a useful field mark to distinguish *E. orix* from *E. franciscanus*.

Recommendation:

I recommend this name change for NACC.

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Submitted by: Marshall Iliff

Date of Proposal: 20 February 2016

Transfer Sandhill Crane *Grus canadensis* to *Antigone*

Background:

The family Gruidae consists of 15 extant species of crane. These species have traditionally been placed in 4-5 genera: *Grus*, *Anthropoides*, *Bugeranus*, *Leucogeranus* (sometimes subsumed in *Grus*; e.g., Peters 1934), and *Balearicus*. Three cranes are included in our main list, all currently placed in *Grus* (Sandhill Crane *G. canadensis*, Whooping Crane *G. americana*, and the accidental species Common Crane *G. grus*), and two additional species (Demoiselle Crane *Anthropoides virgo* and Hooded Crane *Grus monacha*) are listed in the Appendix.

New Information:

Krajewski et al. (2010) sequenced mitochondrial genomes for all extant species of crane and produced a Bayesian phylogenetic tree for the group (their Fig. 2 below, also see Fig. 3). The crowned cranes (subfamily Balearicinae) were sister to the rest of the family (subfamily Gruinae), as expected, and within the Gruinae *Leucogeranus leucogeranus* was sister to the other species. Two main clades, each in turn containing two major subclades, were identified from the remaining group of 12 species. *Grus grus* (the type species of *Grus*), *G. americana*, and *G. monacha* were part of a subclade consisting of five species currently placed in *Grus*. Sister to this subclade was a subclade consisting of *Bugeranus carunculatus* and the two species of *Anthropoides*. The other main clade consisted entirely of species currently placed in *Grus*: *G. canadensis* formed one subclade, whereas *G. vipio*, *G. rubicunda*, and *G. antigone* formed the other subclade. Posterior probabilities for all nodes in the phylogeny were 1.0, except for the node uniting the *Grus grus* group with the *Bugeranus-Anthropoides* group, for which the posterior probability was 0.94 (no bootstrap values were published). This node was supported in none of the analyses of individual mtDNA genes, other than the control region, and it received noticeably lower support in analyses of the control region data than did other nodes.



FIG. 2. Crane phylogeny based on complete mtDNA (without the control region). Branch lengths are derived from Bayesian analyses of combined mtDNA sequences partitioned by codon position. All nodes have Bayesian posterior probability (BPP) values of 1.00, except node 11 (BPP = 0.94, shown in *italics*). Support values from other analyses are given in Table 4.

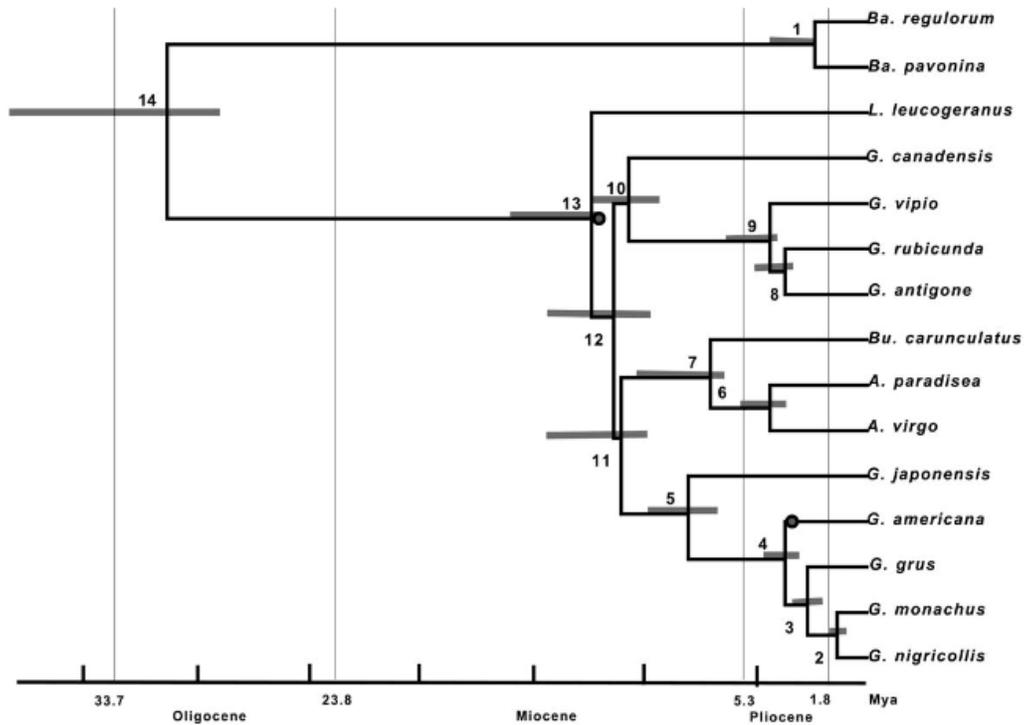


FIG. 3. Time-calibrated tree obtained using BEAST based on complete mtDNA sequences without control region and gap sites, partitioned by codon position. The analysis assumed lognormal prior distributions (mean = 0, standard deviation = 1.0) and fossil calibration points for the most recent common ancestor of Gruinae (12 Ma) and the minimum age of *Grus americana* (3.5 Ma). Tick marks on the time axis represent 5-Ma intervals. Calibration points are indicated by circles. Node numbers refer to Table 7. Bars on nodes are 95% confidence intervals on node heights.

In light of this phylogeny, we clearly need to make one or more changes in generic assignment. I see two viable options. The first would be to place all non-*Leucogeranus* gruines in the genus *Grus*. This classification has been adopted by the IOC World Bird List (Gill and Donsker 2016); in fact, they also transferred *Leucogeranus* to *Grus*. The effect of this arrangement on the AOU Checklist would be to transfer *Anthropoides virgo* to *Grus*. However, this classification is *contra* the traditional splitting of the Gruinae into several genera based on phenotypic differences and may be excessive given the deep divergences between the various clades and subclades, the lineages of which all extend well back into the Miocene and are > 10 million years old (Fig. 3):

The second option would be to continue to recognize >1 genus for the non-*Leucogeranus* gruines. At a minimum, for AOU Checklist purposes, *G. canadensis* would have to be transferred to a different genus. One classification based on this phylogeny would place the two major clades designated by nodes 10 and 11 above in different genera – this arrangement, which would place all species in clade 10 in *Antigone* and all species in clade 11 in *Grus*, has been adopted by the new Howard and Moore checklist (Dickinson and Remsen 2013). Arguing against this classification is the less than stellar support for node 11, which unites the *Bugeranus-Anthropoides* group with the *Grus grus* group. The bootstrap value for this node is unknown, but the 0.94 posterior probability leads one to suspect that it would be lower than 70%, quite possibly much lower; moreover, as mentioned above, this node was not present in analyses of most genes. It probably makes more sense to treat the subclades within this clade as lineages of currently unknown relationship rather than as sister groups. What we have, then, is three clades with uncertain relationships among them – they essentially form a polytomy. In this case, it seems to me, they should either all be lumped into the genus *Grus* or they should be considered 3 genera: *Grus*, *Anthropoides* (which has priority over *Bugeranus*), and *Antigone*. This latter arrangement would necessitate no change in genus for *A. virgo*, while also retaining *grus*, *americana*, and *monacha* in *Grus*, and would therefore be a conservative option in terms of continuity of names. This is similar to the classification adopted by HBW (del Hoyo et al. 2014), except that they retained both *Anthropoides* and *Bugeranus*, which seems untenable if *G. canadensis* is placed in *Antigone* along with *vipio*, *rubicunda*, and *antigone* (see below).

The remaining question for us concerns the new genus for *G. canadensis*. As noted above, this species would be transferred to *Antigone* if all species in clade 10 above are placed in a single genus. If the two subclades within this clade were considered separate genera, then *vipio*, *rubicunda*, and *antigone* would be placed in *Antigone*, requiring a monotypic genus for *canadensis*. I'm not aware of an available genus name for *canadensis*; thus, at this point our only reasonable option would seem to be transfer of *canadensis* to *Antigone*.

Recommendation:

I recommend that we transfer *G. canadensis* to *Antigone* and retain our other main list and appendix species in *Grus* (three species) and *Anthropoides* (one species), respectively. Until a better-supported tree with nuclear data becomes available, this seems like the best option.

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Submitted by: Terry Chesser

Date of Proposal: 22 February 2016

Add Rufous-necked Wood-Rail *Aramides axillaris* to the U.S. list**Background:**

A Rufous-necked Wood-Rail was present at Bosque del Apache National Wildlife Refuge, south of Socorro, New Mexico, 7-18 July 2013, during which time it was seen well and photographed by many. Publications to date include details of the record accompanied by a black-and-white photo (Williams 2014) and a color photo accompanying the ABA CLC report (Pranty et al. 2015).

No one disagreed with the identification, but the bird's origin was questioned by some, notably by Barry Zimmer who voted against it when the report circulated through the New Mexico Bird Records Committee. Basically, he found it nearly unfathomable that such a resident, coastal species could appear far away at an interior locality. That a Sungrebe *Heliornis fulica* had turned up at the same locality five years earlier (Williams et al. 2009, Chesser et al. 2011) Zimmer thought even more reason to doubt the natural occurrence of the wood-rail. In the end, though, the New Mexico Committee voted 7-1 to accept. The record was then voted on by the ABA CLC, where two members questioned origin on the first round but the record passed unanimously on a second (Pranty et al. 2015).

We think that questions about origin, while important, cannot be persuasive when the subject is a member of the Rallidae, because rails are notorious for their wanderings, with many quite amazing extralimital records, of numerous species, around the globe. Indeed, in recent years within the AOU area there have been numerous records of Corn Crake *Crex crex* (see North American Birds 58[1]: cover and its caption, 2004), two of Spotted Rail *Pardirallus maculatus*, in Texas and Pennsylvania (AOU 1998), and two of Paint-billed Crake *Neocrex erythrops*, in Texas and Virginia (AOU 1998). And a short-billed rail that eluded photographers at Attu Island, Aleutian Islands, Alaska (see Tobish 2001), was tentatively identified as a Baillon's Crake (*Porzana pusilla*).

Effect on Check-List:

On page 133 of 7th edition after the paragraph on Resident distribution, **we recommend** adding the following new paragraph:

Accidental in New Mexico (one bird observed at Bosque del Apache National Wildlife Refuge, south of Socorro, 7-18 July 2013, N. Am. Birds 67: 631-632).

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- Williams, S. O. III. 2014. New Mexico region (summer 2013). *North American Birds* 67:631-632.
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Submitted by: Jon L. Dunn and Daniel D. Gibson

Date of Proposal: 22 February 2016

Revise our Higher-level Linear sequence as Follows:

- (a) Move Strigiformes to precede Trogoniformes**
- (b) Move Accipitriformes to precede Strigiformes**
- (c) Move Gaviiformes to precede Procellariiformes**
- (d) Move Eurypygiformes and Phaethontiformes to precede Gaviiformes**
- (e) Reverse the linear sequence of Podicipediformes and Phoenicopteriformes**
- (f) Move Pterocliiformes and Columbiformes to follow Podicipediformes**
- (g) Move Cuculiformes, Caprimulgiformes, and Apodiformes to follow Columbiformes**
- (h) Move Charadriiformes and Gruiformes to precede Eurypygiformes**

Background:

The higher-level phylogeny of birds has been addressed over the past 25 years by genetic studies using various types of data and taxon sampling (e.g., Sibley and Ahlquist 1990, Groth and Barrowclough 1999, Fain and Houde 2004, Hackett et al 2008, McCormack et al. 2013, Kimball et al. 2013, Jarvis et al. 2014, Burleigh et al. 2015, Suh et al. 2015, Prum et al. 2015). The trees produced by these studies have been at odds with traditional ideas of avian phylogeny in a variety of ways, some of which have been widely adopted. For example, it is now generally recognized that the Galliformes and Anseriformes are sister taxa and together (as Galloanseres) are the sister group to all other extant non-paleognath birds, or Neoaves (Sibley and Ahlquist 1990, Groth and Barrowclough 1999, et al.). Non-traditional results among the Neoaves have been slower to gain acceptance, primarily because they had been found in only a single study (e.g., in Hackett et al. 2008; Fig. 1) or had been weakly supported. However, recent phylogenomic studies, especially Jarvis et al. (2014; Fig. 2) and Prum et al. (2015; Figs. 3 and 4), have provided strong support for several non-traditional results obtained in one or more previous studies. Several clades in the higher-level phylogeny of Neoaves are now reasonably well supported, including large core waterbird and core landbird clades. The core waterbird clade consists of the Gaviiformes, Sphenisciformes, Procellariiformes, Ciconiiformes, Suliformes, and Pelecaniformes, and the core landbird clade consists of the Accipitriformes, Strigiformes, Coliiformes, Leptosomiformes, Trogoniformes, Upupiformes, Bucerotiformes, Coraciiformes, Piciformes, Cariamiformes, Falconiformes, Psittaciformes, and Passeriformes.

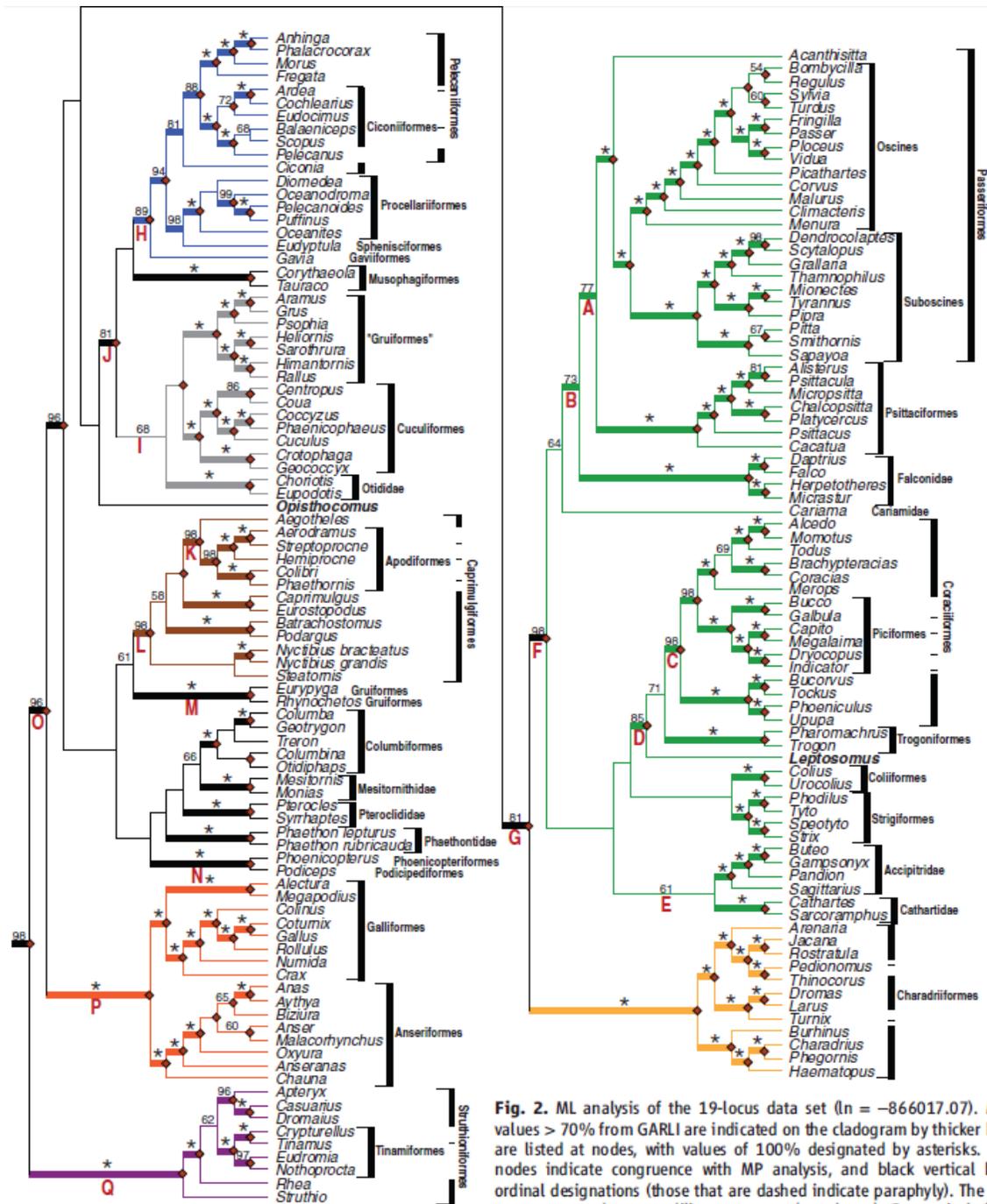


Fig. 2. ML analysis of the 19-locus data set ($\ln = -866017.07$). ML bootstrap values > 70% from GARLI are indicated on the cladogram by thicker branches and are listed at nodes, with values of 100% designated by asterisks. Diamonds at nodes indicate congruence with MP analysis, and black vertical bars refer to ordinal designations (those that are dashed indicate paraphyly). The phylogenetic tree was rooted to crocodylian outgroups (not shown). Genera in bold are icterae and cuckoos (gray), apodiforms and caprimulgiforms (brown), galloanserae (orange), and paleognaths (purple). Large capital letters indicate groups discussed in the text and Fig. 1.

sedis. Branch colors represent major clades supported in this study: land birds (green), charadriiforms (yellow), water birds (blue), core gruiforms and cuckoos (gray), apodiforms and caprimulgiforms (brown), galloanserae (orange), and paleognaths (purple). Large capital letters indicate groups discussed in the text and Fig. 1.

Figure 1. Maximum-likelihood phylogeny from Hackett et al. (2008).

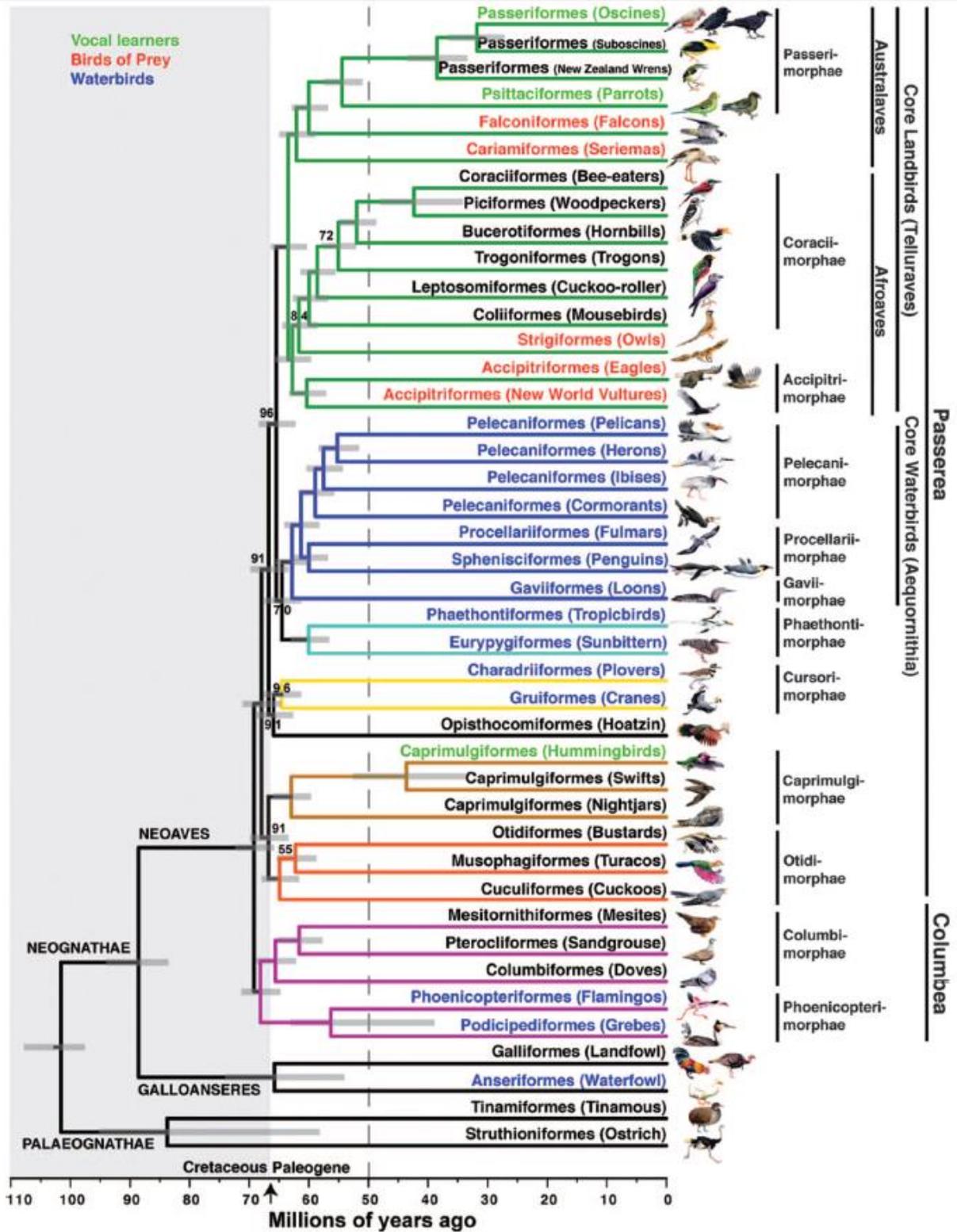


Figure 2. Maximum-likelihood phylogeny from Jarvis et al. (2014).

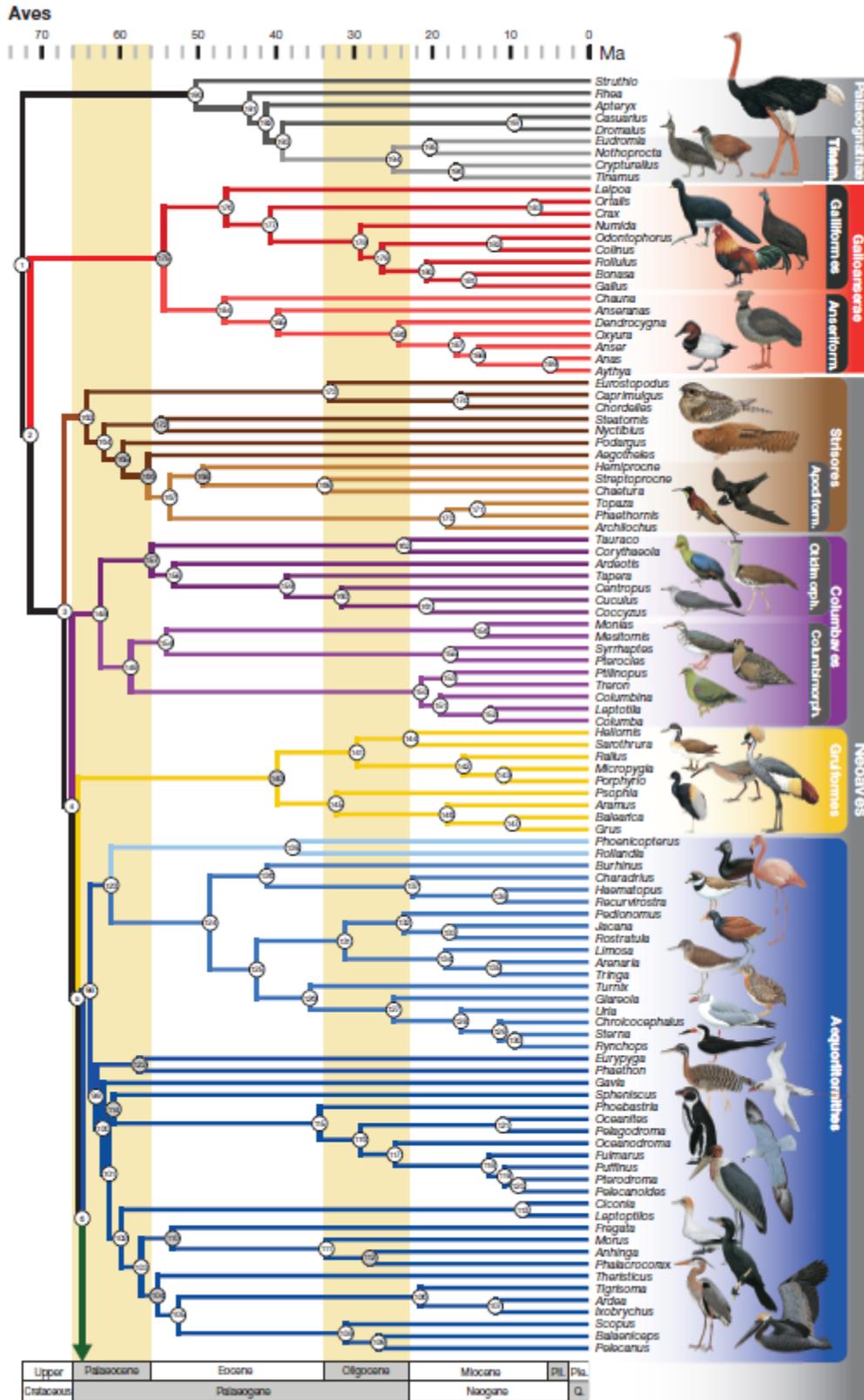


Figure 3a. First part of Bayesian phylogeny from Prum et al. (2015).

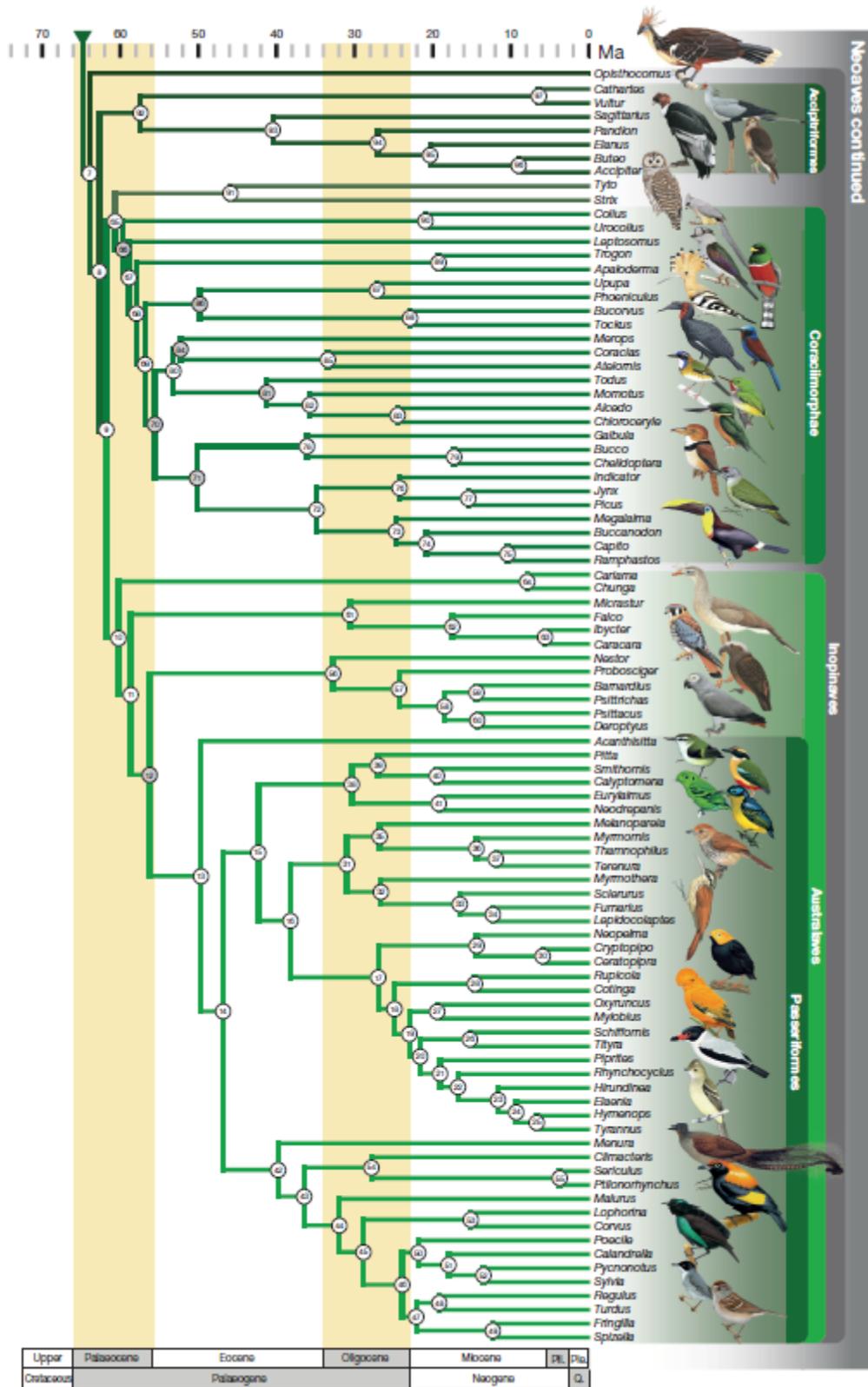


Figure 3b. Second part of Bayesian phylogeny from Prum et al. (2015).

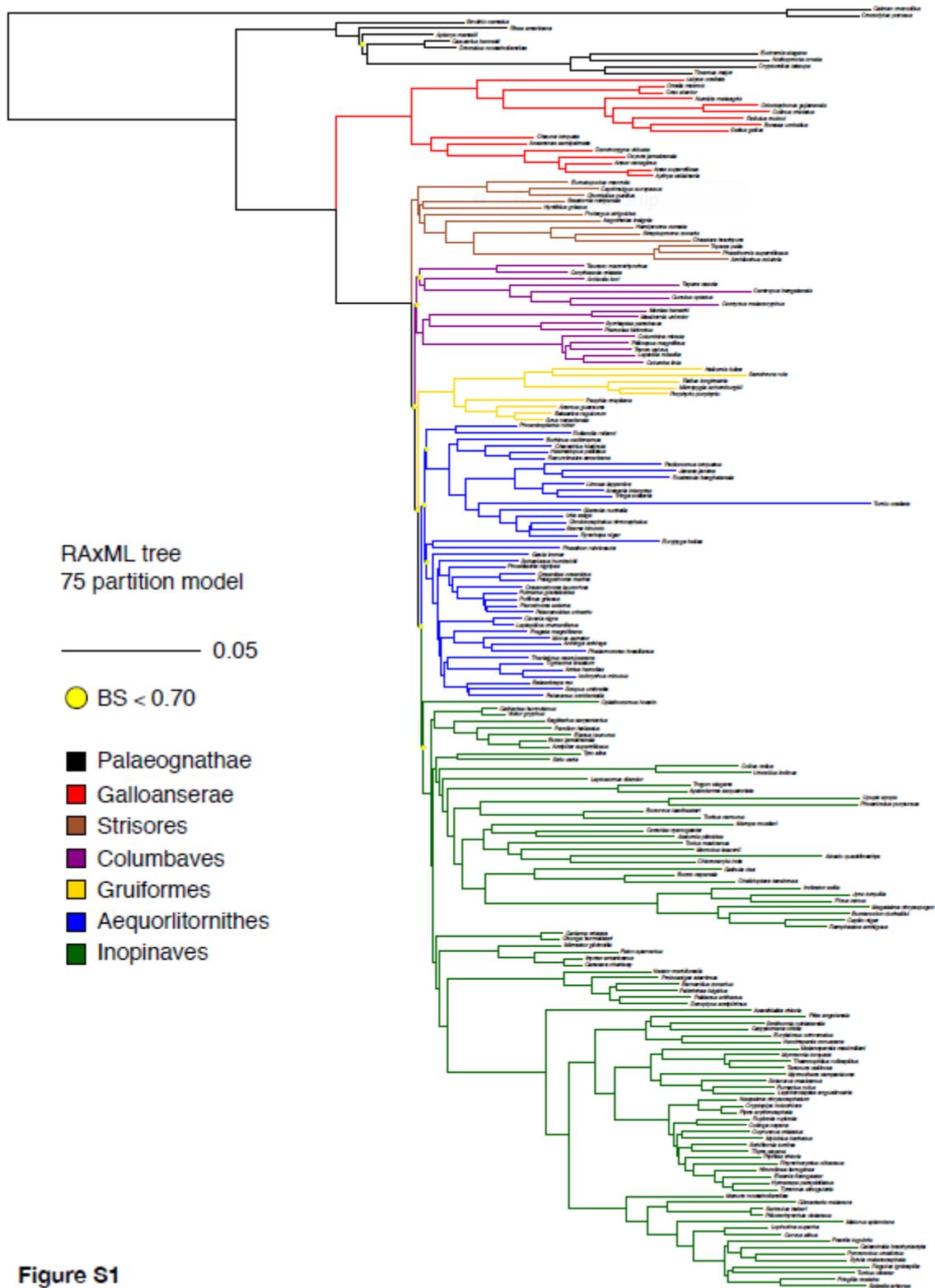


Figure S1

Figure 4. Maximum likelihood phylogeny in the supplemental material from Prum et al. (2015). Yellow dots indicate nodes with <70% bootstrap support.

As noted by Suh et al. (2015), the diversification of Neoaves seems to consist largely of three radiations: a poorly resolved initial radiation at the base of the Neoaves (consisting of Podicipediformes, Phoenicopteriformes, Columbiformes, Pteroclidiformes, Mesitornithiformes, Cuculiformes, Musophagiformes, Otidiformes, Caprimulgiformes, Apodiformes, Opisthocomiformes, Gruiformes, Charadriiformes, and perhaps Eurypygiformes and Phaethontiformes, although these latter two are likely the sister group to the core waterbirds) followed by the better resolved radiations of the core waterbirds and core landbirds. Thus, we have relatively strong support for the makeup and placement of the core waterbirds and landbirds, but only poor to moderate support for the placement of most other avian groups.

The following motions propose to change our higher-level linear sequence based on the new phylogenetic studies, relying more heavily on the most data-rich studies, those of Jarvis et al. (2014) and Prum et al. (2015). Subproposals (a)-(b) would place together in the linear sequence all orders that constitute the core landbirds, and subproposal (c) would do the same for the core waterbirds. Subproposal (d) would place the Eurypygiformes and Phaethontiformes so as to precede the core waterbirds, and (e) is a bookkeeping change that should have been made some time ago. Subproposals (f)-(h) would: (1) place together in the linear sequence all other orders that appear to constitute the initial radiation of Neoaves, and (2) place these orders in a linear sequence that seems to best represent the bulk of the evidence. Given the uncertainty at the base of the tree, the placements of these latter orders differ somewhat in the various studies, but many of these different placements can be accommodated in a linear sequence.

An appendix detailing our current linear sequence, the linear sequence that would result from approval of proposals (a)-(e), the linear sequence that would result from approval of all proposals, and the linear sequence that would result from following the Bayesian tree in Prum et al. (2015) appears at the end of this proposal.

(a) Move Strigiformes to precede Trogoniformes, and (b) move Accipitriformes to precede Strigiformes. One of the most striking results of the recent DNA sequence studies, such as the intron-based study of 169 species (Hackett et al 2008), the whole-genome study of 48 species (Jarvis et al 2014), and the target-enrichment study of 198 species (Prum et al. 2015), and not found in Sibley and Ahlquist, was the lack of a sister relationship between the falcons and caracaras on the one hand and the hawks, eagles, kites, and vultures on the other. We recently removed the Falconiformes *sensu stricto* from the Accipitriformes and placed them towards the end of the linear sequence as sister to a Passeriformes/Psittaciformes clade, but the Accipitriformes were left in their former position between the core waterbirds and the Gruiformes *sensu lato*. Likewise, we have maintained the Strigiformes in their traditional placement between the Cuculiformes and the Caprimulgiformes.

These new moves would reflect the phylogenetic relationships of the core landbird clade mentioned above and would result in the following sequence at the end of our classification: Accipitriformes, Strigiformes, Trogoniformes, Upupiformes, Coraciiformes, Piciformes, Falconiformes, Psittaciformes, and Passeriformes. This sequence is in agreement with the phylogenetic trees in Hackett et al. (2008), Jarvis et al. (2014), and Prum et al. (2015), among others.

According to Hackett et al. (2008), the Strigiformes are sister to the Coliiformes, and this clade is sister to a clade consisting of the Leptosomiformes, Trogoniformes, Upupiformes, Coraciiformes, and Piciformes. The Accipitriformes *sensu lato* (incl. Cathartidae) are sister to this entire clade. Although these results received poor bootstrap support (< 50%), all of the more recent studies support this result, some with strong support.

For example, Jarvis et al. (2014), in their whole genome study, recovered a clade consisting of the Coliiformes, Leptosomiformes, Trogoniformes, Bucerotiformes, Coraciiformes, and Piciformes (Coraciimorphae, *sensu* Jarvis et al.), with the Strigiformes sister to this clade, and the Accipitriformes *sensu lato* sister to this larger clade. Bootstrap support for the entire clade (“Afroaves” *sensu* Jarvis et al.) was 100%, support for the Accipitriformes as sister to all other taxa was 100%, and support for the Strigiformes as sister to the rest (except for the Accipitriformes) was 84%. Prum et al. (2015) also recovered this arrangement, except that the Accipitriformes were sister to a clade consisting of the Strigiformes and Coraciimorphae + Cariamiformes, Falconiformes, Psittaciformes, and Passeriformes (these four orders constituting the Australaves), making “Afroaves” paraphyletic. Posterior probabilities for their results were all 1.0 and ML bootstraps were all >70% (finer resolution was not provided for the bootstraps).

Our current linear sequence has a monophyletic Coraciimorphae but, as noted above, places the Accipitriformes far from the Coraciimorphae and also separates the Strigiformes from these two groups. By moving the Strigiformes to precede the Trogoniformes, and then moving the Accipitriformes to precede the Strigiformes, we achieve the following: (1) we make the core landbird clade monophyletic; (2) we place the Strigiformes in the correct position as sister to the Coraciimorphae; and (3) we position Accipitriformes in the linear sequence to reflect a sister relationship with the rest of “Afroaves” (as in Jarvis et al. 2014) or to reflect a sister relationship with the Strigiformes+Coraciimorphae+Australaves clade (as in Prum et al. 2015).

(c) Move Gaviiformes to precede Procellariiformes, and (d) move Eurypygiformes and Phaethontiformes to precede Gaviiformes. We currently maintain the Gaviiformes more-or-less in their traditional placement near the beginning of the linear sequence, at the beginning of the Neoaves. Numerous studies suggest that they do not

belong in this position, but instead should be placed near several other orders of waterbirds, namely the Procellariiformes, Sphenisciformes, Pelecaniformes, Suliformes, and Ciconiiformes. Sibley and Ahlquist (1990), using DNA-DNA hybridization, found that their representatives of these orders (the five listed above plus Gaviiformes) formed a monophyletic group, that this group of waterbirds was embedded deep within the Neoaves, that the Phaethontiformes were the sister group to this waterbird clade, and that within the clade the Gaviiformes and Procellariiformes were sister groups. Hackett et al. (2008) also found that the Gaviiformes, Procellariiformes, Sphenisciformes, Pelecaniformes, Suliformes, and Ciconiiformes formed a clade, with reasonably strong support (89% bootstrap), and that this clade was embedded within the Neoaves. However, the Gaviiformes were sister to the rest of this group (94% bootstrap).

The presence of a core waterbird clade that includes Gaviiformes, generally as sister to the rest, has been remarkably consistent in the recent studies. The UCE-based study of McCormack et al. (2013) found strong support for loons as sister to the waterbird clade, and Kimball et al. (2013) also recovered a waterbird clade that includes loons, although not as sister to the rest. Jarvis et al. (2014) found that the Gaviiformes, Procellariiformes, Sphenisciformes, Pelecaniformes, and Suliformes formed a clade, and presumably the Ciconiiformes would have formed part of this group had a representative been included in the study. As in Hackett et al. (2008) and McCormack et al. (2013), the Gaviiformes were sister to the rest of the group. Burleigh et al. (2015) and Prum et al. (2015) found Gaviiformes to be sister to a waterbird clade of the same composition but including Ciconiiformes, with moderate to strong support: 73% bootstrap in Burleigh et al., 1.0 pp and >70% bootstrap in Prum et al.

Three of the recent studies provided support for Sibley's result of the Phaethontiformes as sister to the waterbird clade. In Jarvis et al. (2014) and Prum et al. (2015), the Phaethontiformes and the Eurypygiformes formed a clade that was sister to the waterbird clade, with moderate to strong support (70% bootstrap in Jarvis et al., 1.0 pp and >70% bootstrap in Prum et al.), and this clade was also sister to the waterbird clade in at least one of the trees in Kimball et al. (2013), although with poor support.

The Eurypygiformes have generally been difficult to place, and the results of Jarvis et al. and Prum et al. provide some of the only reasonable support for placement of this order. Hackett et al. (2008), for example, had them as sister to the Caprimulgiformes-Apodiformes clade, but support was not strong (61% bootstrap). Several trees in Kimball et al. (2013) placed them as sister to the Phaethontiformes, as did McCormack et al. (2013), although their placement beyond this was uncertain.

All studies provide strong support for the monophyly of the Gaviiformes, Procellariiformes, Sphenisciformes, Pelecaniformes, Suliformes, and Ciconiiformes as a "core waterbirds" group, generally with the Gaviiformes as sister to the rest, with

reasonable support for the Phaethontiformes and Eurypygiformes as sisters to this group. Our current linear sequence places the Gaviiformes directly after the Galloanseres; the Podicipediformes and Phoenicopteriformes follow the Gaviiformes. Next in the linear sequence are the Procellariiformes, Phaethontiformes, Ciconiiformes, Suliformes, and Pelecaniformes; this is the core waterbird group identified by the genetic studies except for the presence of the Phaethontiformes and the absence of the Gaviiformes. By moving the Gaviiformes to precede the Procellariiformes, and then moving the Eurypygiformes and Phaethontiformes to precede the Gaviiformes, we achieve the following: (1) we make the core waterbird group monophyletic, (2) we place Gaviiformes in the correct position within the group (as sister to the rest), (3) we place Eurypygiformes and Phaethontiformes in the correct position as indicated by Jarvis et al. and Prum et al., as sister group to the core waterbirds, and (4) we move the Gaviiformes away from the Podicipediformes, breaking up a discredited traditional grouping that could be inferred as valid given our current linear sequence.

(e) Reverse the linear sequence of Podicipediformes and Phoenicopteriformes.

We have long recognized Podicipediformes + Phoenicopteriformes as a clade, but for some reason the order with more species (Podicipediformes = 22 species) precedes the one with fewer species (Phoenicopteriformes = 6) in our classification, in contradiction to our conventions for linear sequencing. Perhaps this was an attempt to retain an aspect of the traditional sequence by keeping the grebes near the loons. With the approval of subproposal (c), the Gaviiformes would be moved to the core waterbird clade, making moot even this poor rationale for placing Podicipediformes before Phoenicopteriformes.

(f) Move Pterocliiformes and Columbiformes to follow Podicipediformes, and (g) move Cuculiformes, Caprimulgiformes and Apodiformes to follow Columbiformes.

In our current linear sequence, the Pterocliiformes, Columbiformes, and Cuculiformes precede the Strigiformes, and the Caprimulgiformes and Apodiformes follow the Strigiformes. If subproposal (a) above passes, these groups will occur together in the linear sequence. The Columbiformes and Pterocliiformes have long been considered closely related, and they are placed together in our current linear sequence following the Charadriiformes. A surprising result of several of the DNA sequence studies is that the Mesitornithidae, considered part of the Gruiformes in Peters, were closely related to the Columbiformes and Pterocliiformes. In Hackett et al (2008), these groups formed a clade, and the Phaethontidae and Phoenicopteriformes/Podicipediformes were successive sisters to the clade, although there was generally weak support for these relationships. Jarvis et al. (2014) recovered similar relationships, except for the absence of the Phaethontidae, with 100% bootstrap support. Burleigh et al. (2015) recovered the same clade as Hackett et al. (2008), although relationships within the clade differed somewhat, but with poor support (< 50%). Fain and Houde

(2004), using sequences of a fibrinogen intron later used by Hackett et al., had previously identified a clade (dubbed Metaves) that included the Columbidae, Pteroclididae, Mesitornithidae, Phoenicopteridae, Podicipedidae, (along with the Caprimulgidae, Apodiformes, Phaethontidae, Eurypygidae, and several extralimital groups), but relationships among these groups had been poorly resolved. The study of Prum et al. (2015) recovered a Columbidae-Pteroclididae-Mesitornithidae clade, but their Phoenicopteridae + Podicipedidae clade was sister to the Charadriiformes and much further back in the linear sequence, and was not closely related to the Columbidae-Pteroclididae-Mesitornithidae clade.

Hackett et al. (2008), Jarvis et al. (2014), and Burleigh et al. (2015) found close relationships among the Columbiformes, Pterocliiformes, Mesitornithiformes, Phoenicopteriformes, and Podicipediformes, Jarvis et al. with strong support. The relevant discrepancy in their respective results was the addition of the Phaethontiformes to the clade in Hackett et al (2008) and Burleigh et al. (2015), although with poor support. The position of the Phaethontiformes well outside of this clade (as or in the sister group to the core waterbird clade) in the studies of Sibley and Ahlquist (1990), Kimball et al. (2013), Jarvis et al (2014), and Prum et al. (2015) along with the poor support for this clade in Hackett et al. (2008) and Burleigh et al. (2015), suggests that the placement as sister to the waterbirds, as above in (c), is likely more appropriate.

Other orders that have consistently shown up near the base of the Neoaves are the Cuculiformes, Caprimulgiformes, and Apodiformes. In Jarvis et al. (2014), representatives of these orders were placed in the clade that is sister to all other Passerea (which encompasses all Neoaves except for the Columbea), with reasonably strong bootstrap support (91%). In Hackett et al (2008), the Caprimulgiformes formed part of the clade that includes most of the orders in the Columbea of Jarvis et al., mirroring in part the Metaves of Fain and Houde (2004), although bootstrap support was weak (< 50%), whereas the Cuculiformes, Gruiformes, and Otidiformes formed a clade that was sister to the Musophagiformes + the core waterbird clade – a result that received reasonable support (81%) although this support was much reduced (<50%) in the extended dataset of Kimball et al. (2013). There was little support for relationships of these orders in McCormack et al. (2013) and Burleigh et al. (2015). Prum et al. (2015) found the Caprimulgiformes + Apodiformes to be sister to all other Neoaves, with their Columbaves (including Cuculiformes, Otidiformes, Musophagiformes, Columbiformes, Pterocliiformes, and Mesitornithiformes) the next successive sister, thus reversing the linear sequence proposed here.

By moving the Pterocliiformes and Columbiformes to follow the Podicipediformes, we achieve the following: (1) we place them in linear sequence to reflect a monophyletic “Columbea” *sensu* Jarvis et al., a group that also has strong support (although with the addition of Phaethontidae) in Hackett et al.; and (2) we place the Columbea in linear

sequence directly following the Galloanseres, in keeping with their position as sister to the rest of Neoaves (Jarvis et al. 2014), a position also consistent with that in Hackett et al., although at odds with Prum et al.

By moving the Cuculiformes, Caprimulgiformes and Apodiformes to follow the Columbiformes (and Columbimorphae), we position these orders to: (1) reflect their sister relationship (along with the extralimital Musophagiformes and Otidiformes) with the rest of the Passerea (according to Jarvis et al 2014), and (2) reflect their position as successive sisters (although in reverse order) at or near the base of the Neoaves (as in Prum et al. 2015).

(h) Move the Charadriiformes and Gruiformes to precede the Eurypygiformes.

These are groups for which many of the phylogenies rather profoundly disagree; this motion generally follows the results of Jarvis et al. (2014) and Prum et al. (2015). Jarvis et al. (2014) placed the Charadriiformes and Gruiformes (along with the hoatzin) as sisters to a clade consisting of the core waterbirds + Phaethontiformes + Eurypygiformes + the core landbirds. Prum et al. (2015) placed the Charadriiformes (along with the Phoenicopteriformes + Podicipediformes) as sister to the core waterbird clade + Phaethontiformes + Eurypygiformes, and the Gruiformes as sister to this large clade.

Recommendation:

I strongly recommend voting in favor of some of these proposals (a-e), and I endorse the others as well. A new linear sequence that includes some or all of these changes would reflect the best data on higher-level avian relationships much better than does our current sequence. The alternative would be to wait until phylogenomic studies with better taxon sampling and tree-wide consistent support are available, but consistent resolution of the initial radiation of Neoaves may be difficult to achieve, and I would say that some of these changes need to be made now.

If we approve only (a)-(e), then we have to decide whether the remaining orders fit in their “new” positions (see the appendix below). Approval of all proposals (a)-(h) would generally follow the bulk of the phylogenetic evidence currently available. An alternative would be to follow the published tree of the most recent major study, that of Prum et al. (2015). Their published Bayesian tree received strong support at almost all nodes, but most deeper nodes were poorly supported in the maximum likelihood tree in their supplementary material. The differences between the (a)-(h) linear sequence and that derived from Prum et al. are in the placement of the Phoenicopteriformes + Podicipediformes (early in the a-h sequence, somewhat later in Prum et al.) and the relative placement of the Pteroclitiformes + Columbiformes, Cuculiformes, and Caprimulgiformes + Apodiformes (in this sequence in (a)-(h), in the sequence

Caprimulgiformes + Apodiformes, Cuculiformes, and Pterocliiformes + Columbiformes in Prum et al.). Prum et al. placed all of the “initial radiation waterbirds” together preceding the core waterbirds, and this has some intuitive appeal in that all the waterbirds are together in the linear sequence. However, the (a)-(h) sequence causes less disruption to our current linear sequence, leaving Phoenicopteriformes + Podicipediformes near the beginning of the sequence, and leaving intact the linear sequence of Pterocliiformes + Columbiformes, Cuculiformes, Caprimulgiformes + Apodiformes. To me, this seems like the slightly better course until we get more definitive data on the initial Neoavian radiation.

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Submitted by: Terry Chesser

Date of proposal: 7 March 2016

Appendix to Proposal 2016-C-6: Our current linear sequence of orders, the linear sequence that would result from approval of proposals a-e above, the linear sequence that would result from approval of all proposals above, and the linear sequence that would result from following the Bayesian tree in Prum et al. (2015). Orders that form part of the poorly resolved initial radiation of Neoaves are in bold, those in the core waterbird clade are highlighted in blue, and those in the core landbird clade are highlighted in green.

current sequence	w/ approval of a-e:	w/ approval of a-h:	Prum Bayesian tree:
Tinamiformes	Tinamiformes	Tinamiformes	Tinamiformes
Anseriformes	Anseriformes	Anseriformes	Anseriformes
Galliformes	Galliformes	Galliformes	Galliformes
Gaviiformes	Phoenicopteriformes	Phoenicopteriformes	Caprimulgiformes
Podicipediformes	Podicipediformes	Podicipediformes	Apodiformes
Phoenicopteriformes	Eurypygiformes	Pterocliiformes	Cuculiformes
Procellariiformes	Phaethontiformes	Columbiformes	Pterocliiformes
Phaethontiformes	Gaviiformes	Cuculiformes	Columbiformes
Ciconiiformes	Procellariiformes	Caprimulgiformes	Gruiformes
Suliformes	Ciconiiformes	Apodiformes	Phoenicopteriformes
Pelecaniformes	Suliformes	Gruiformes	Podicipediformes
Accipitriformes	Pelecaniformes	Charadriiformes	Charadriiformes
Eurypygiformes	Gruiformes	Eurypygiformes	Eurypygiformes
Gruiformes	Charadriiformes	Phaethontiformes	Phaethontiformes
Charadriiformes	Pterocliiformes	Gaviiformes	Gaviiformes
Pterocliiformes	Columbiformes	Procellariiformes	Procellariiformes
Columbiformes	Cuculiformes	Ciconiiformes	Ciconiiformes
Cuculiformes	Caprimulgiformes	Suliformes	Suliformes
Strigiformes	Apodiformes	Pelecaniformes	Pelecaniformes
Caprimulgiformes	Accipitriformes	Accipitriformes	Accipitriformes
Apodiformes	Strigiformes	Strigiformes	Strigiformes
Trogoniformes	Trogoniformes	Trogoniformes	Trogoniformes
Upupiformes	Upupiformes	Upupiformes	Upupiformes
Coraciiformes	Coraciiformes	Coraciiformes	Coraciiformes
Piciformes	Piciformes	Piciformes	Piciformes
Falconiformes	Falconiformes	Falconiformes	Falconiformes
Psittaciformes	Psittaciformes	Psittaciformes	Psittaciformes
Passeriformes	Passeriformes	Passeriformes	Passeriformes

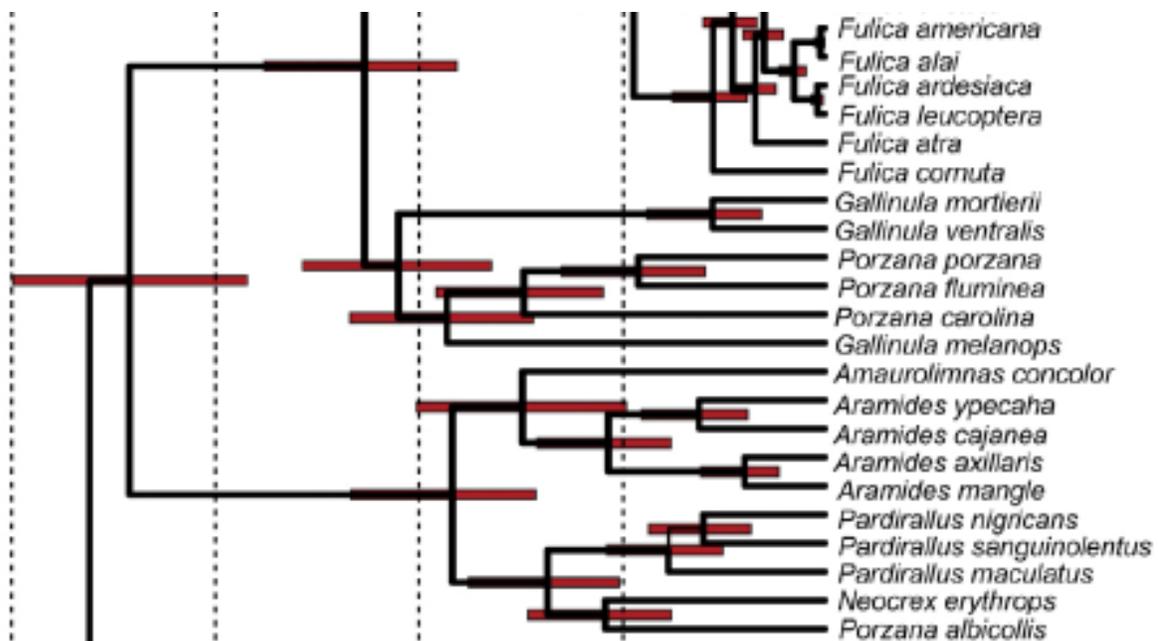
Transfer *Neocrex* to *Mustelirallus*

Note: This is a revision of [SACC proposal 650](#); A passed 9-0, B passed barely, 7-3; see the SACC proposal for extensive comments, especially on B, especially Dan Lane's.

Background:

Extralimital *Porzana albicollis* (Ash-throated Crake) has remained in *Porzana* for most of its history, starting in 1868 with Sclater and Salvin, although Bonaparte in 1858 had described a new monotypic genus, *Mustelirallus*, for what was then *Rallus albicollis*. It basically “looks like” a Sora, so no surprise (to me) that its placement has been uncontroversial. The only contrary opinion that I can find is that of Benson and Winterbottom (1968), who proposed that it was the sister to African *Crecopsis egregia*.

Garcia-R. et al. (2014) produced a phylogeny for the Rallidae based on a fairly large analysis of DNA sequence data, both mitochondrial and nuclear, largely compiled from GenBank etc. Their taxon sampling was fairly good for a family that is cosmopolitan and difficult to collect: 70 species in 22 of 33 extant genera. They found that *Porzana albicollis* was not particularly closely related to true *Porzana* (of which our *P. carolina* is a member; type species = *P. porzana*) but rather was the sister to *Neocrex*. A section of their tree is pasted in below – see the original paper for other trees and the full data set; let me know if you need a pdf.



The genetic data require removal of *albicollis* from *Porzana*. That *Porzana albicollis* has an antiphonal duet has been reported in the literature, and is unlike anything I associate with *Porzana carolina* or can find for *P. porzana*. Check out this amazing recording by Roger Ahlman on [xeno-canto](#). Also, true *Porzana* also have greenish or yellowish legs, whereas those of *albicollis* are a purplish brown. *Mustelirallus* Bonaparte, 1856, is available; as noted above, Bonaparte described this genus to remove the species from *Rallus*, which at that time was broadly defined.

SACC voted unanimously to resurrect *Mustelirallus* for *albicollis*. They also voted by the narrowest of margins to also include *Neocrex* (two species in NACC area) in *Mustelirallus*.

From the figure above, based just on branch lengths, this would be consistent with the genetic data. The right-most dashed line in the figure segment above is 10 mya. The two species of *Neocrex* share with *albicollis* a Neotropical distribution, general similarity in size and bill shape, and a tendency to occur in habitats besides marshes, such as grassy areas. Obviously, this is not evidence for congener status, but the point is that treating *albicollis* and the two *Neocrex* as congeners does not violate any important morphological or habitat themes. The two *Neocrex* have red legs, matching their red bill bases. Tangentially, red-legged *Cyanolimnas* of Cuba with its red bill base is almost certainly a *Neocrex*-derivative, and I see no reason to maintain that monotypic genus ... but there are no data that I know of to use in a proposal.

Mustelirallus Bonaparte 1858 has priority over *Neocrex* Sclater & Salvin 1868. Thus, a merger would cause some unfortunate taxonomic instability. *Neocrex* is feminine whereas I assume *Mustelirallus* is masculine (because *Rallus* is). *Neocrex colombiana* would thus become *Mustelirallus colombianus*, but *erythroptera* is invariable.

Images:

<http://www.hbw.com/species/colombian-crake-neocrex-colombiana>

<http://www.hbw.com/species/paint-billed-crake-neocrex-erythroptera>

<http://www.hbw.com/species/ash-throated-crake-porzana-albicollis>

Recommendation: I recommend a YES. without strong conviction, because until we have objective ways of defining genera, this is a matter of taste. In my opinion, treating *albicollis* and the two *Neocrex* as congeners is preferable, in my opinion, because (1) they do share characters as outlined above, although none of these defines the node that unites them, and (2) although the N is small for genes and taxa, the degree of divergence in this group is more similar to that shown in taxa treated as congeneric than as two or more genera; for example, as you can see in the figure above the node that

unites the species of *Aramides* is of similar age to that uniting *albicollis* with the two *Neocrex*. The “comparable lineage age” definition of generic boundaries is the only one that I can see that has any hope of being objective, although in this case a much more thorough sample of taxa and genes is obviously highly desirable. Reasons to vote NO would be (1) to wait for those additional better data that would permit family-wide comparisons, or (2) *Neocrex* and *Mustelirallus* differ sufficiently in phenotypic characters that treatment as separate genera fits your concept of “genus” better (see SACC comments) and also maintains taxonomic stability.

Literature Cited:

Benson, C. W. and J. M. Winterbottom. 1968. The relationship of the Striped Crake *Crecopsis egregia* (Peters) and the White-throated Crake *Porzana albicollis* (Vieillot). Ostrich 39: 177-179.

Garcia-R, J. C., G. C. Gibb, AND S. A. Trewick. 2014. Deep global evolutionary radiation in birds: diversification and trait evolution in the cosmopolitan bird family Rallidae. Molecular Phylogenetics and Evolution 81: 96–108.

Submitted by: Van Remsen

Date of Proposal: 8 March 2016

**(a) Split *Ardenna* from *Puffinus*, and
(b) revise the linear sequence of species of *Ardenna***

Note: This is a revision of [SACC proposal 647](#), to split *Ardenna* from *Puffinus*, which passed unanimously; see that proposal for SACC comments.

Background:

Based on a deep division in their mtDNA tree within broadly defined *Puffinus*, Penhallurick & Wink (2004) proposed that *Puffinus* be subdivided into two genera: (1) *Ardenna*, resurrected for *creatopus/carneipes*, *gravis*, *griseus*, *tenuirostris*, *pacifica*, and *bulleri*; and (2) *Puffinus* for all other taxa. Other genetic data (Austin et al. 2004, Pyle et al. 2011) have confirmed that these two groups are distinct, monophyletic lineages, and Dickinson & Remsen (2013), del Hoyo & Collar (2014), and SACC adopted this classification. Pyle et al.'s (2011) cytochrome b tree indicated that *Calonectris* was actually sister to true *Puffinus*, not *Ardenna*, but the support for that node is weak and is based on a single locus.

Analysis and Recommendation:

If the support for *Calonectris-Puffinus sensu stricto* were solid, then there would be no controversy in recognizing *Ardenna* as separate from *Puffinus*. As it stands, the decision is subjective. The three published trees are all based on the same mitochondrial gene. Nonetheless, I favor a YES on this one – we adopted the split in Dickinson & Remsen (2013), and HBW also did this independently. Our rationale was that the degree of genetic divergence, at least in cyt b, is fairly deep, and regardless of sister relationships, if we recognized *Calonectris*, then we also ought to recognize *Ardenna* as an equally divergent group. These two groups of shearwaters differ in general biogeography. Except for Wedge-tailed (*pacifica*), the *Ardenna* shearwaters (Buller's *bulleri*, Slender-billed *tenuirostris*, Sooty *grisea*, Great *gravis*, Pale-footed *carneipes*, Pink-footed *creatopus*) breed in cold-water islands in the Southern Hemisphere, mainly in the Pacific), whereas *Puffinus* shearwaters are more widespread, especially at tropical latitudes, and several species breed in the Atlantic and Mediterranean (e.g. Manx *puffinus* and Audubon's *Iherminieri*). True *Puffinus* are largely black or dark brownish above and white below, whereas species in the *Ardenna* group show much greater variation in plumage (and none are truly solid blackish above). These are all weak differences, with overlap.

Nonetheless, Peters (1931) recognized the two groups as subgenera, but placed Wedge-tailed in its own, third subgenus *Thyellodroma*. Oberholser (1917; <https://sora.unm.edu/sites/default/files/journals/auk/v034n04/p0471-p0475.pdf>) evaluated all the shearwaters on morphological grounds, including the four genera mentioned above plus *Hemipuffinus* (for *carneipes* and *creatopus*), *Alphapuffinus* (for *assimilis*, *Iherminieri*, *persicus*), and *Neonectris* (for *tenuirostris* and *griseus*). He concluded that *Calonectris*, *Ardenna*, *Thyellodroma*, and *Puffinus* should all be recognized based on morphological differences (but not the other three genera). This classification would match that in the proposal and in the classification of Penhallurick and Wink except for inclusion of *Thyellodroma* in *Ardenna*. Oberholser's *Thyellodroma* does form a monophyletic group (*pacifica* and *bulleri*) that is sister to the rest of *Ardenna* (and might be the topic of some future proposal if a new phylogeny emerges with many additional loci that would allow a broader view of degrees of divergence).

A YES vote, to recognize *Ardenna*, would produce the follow changes in our classification, with no changes to the linear sequence.

Ardenna creatopus (Pink-footed Shearwater)
Ardenna carneipes (Flesh-footed Shearwater)
Ardenna gravis (Great Shearwater)
Ardenna pacifica (Wedge-tailed Shearwater)
Ardenna bulleri (Buller's Shearwater)
Ardenna grisea (Sooty Shearwater)
Ardenna tenuirostris (Short-tailed Shearwater)

Puffinus nativitatis (Christmas Shearwater)
Puffinus subalaris (Galapagos Shearwater)
Puffinus puffinus (Manx Shearwater)
Puffinus auricularis (Townsend's Shearwater)
Puffinus newelli (Newell's Shearwater)
Puffinus bryani (Bryan's Shearwater)
Puffinus opisthomelas (Black-vented Shearwater)
Puffinus Iherminieri (Audubon's Shearwater)
Puffinus baroli (Barolo Shearwater)

Note the changes to the variable endings of *A. pacifica* and *A. grisea*.

A minor bookkeeping change in linear sequence is needed regardless of the vote on *A.* Following the convention of linear sequencing in which the least-diverse branch is listed first, the sequence should be (using the topology in Pyle et al., in which all the nodes

have reasonable support), with indentations used to signal nodes:

pacifica

bulleri

tenuirostris

grisea

gravis

creatopus

carneipes

I recommend a YES on this minor sequence change because it makes our sequence reflect the best available data on relationships. Although this is based on essentially a single gene tree, at least it is based on something other than historical momentum without published rationale (i.e., our current sequence).

Literature Cited:

Austin, J. J., V. Bretagnolle, AND E. Pasquet. 2004. A global molecular phylogeny of the small *Puffinus* shearwaters and implications for systematics of the Little-Audubon Shearwater complex. *Auk* 121: 847-864.

Oberholser, H. C. 1917. Notes on the genus *Puffinus* Brisson. *Auk* 34: 471-475.

Penhallurick, J, AND M. Wink. 2004. Analysis of the taxonomy and nomenclature of the Procellariiformes based on complete nucleotide sequences of the mitochondrial cytochrome b gene. *Emu* 104, 125-147.

Pyle, P., A. J. Welch, AND R. C. Fleischer. 2011. A new species of shearwater (*Puffinus*) recorded from Midway Atoll, northwestern Hawaiian Islands. *Condor* 113: 518-527.

Submitted by: Van Remsen

Date of Proposal: 8 March 2016

Separate Cathartiformes from Accipitriformes

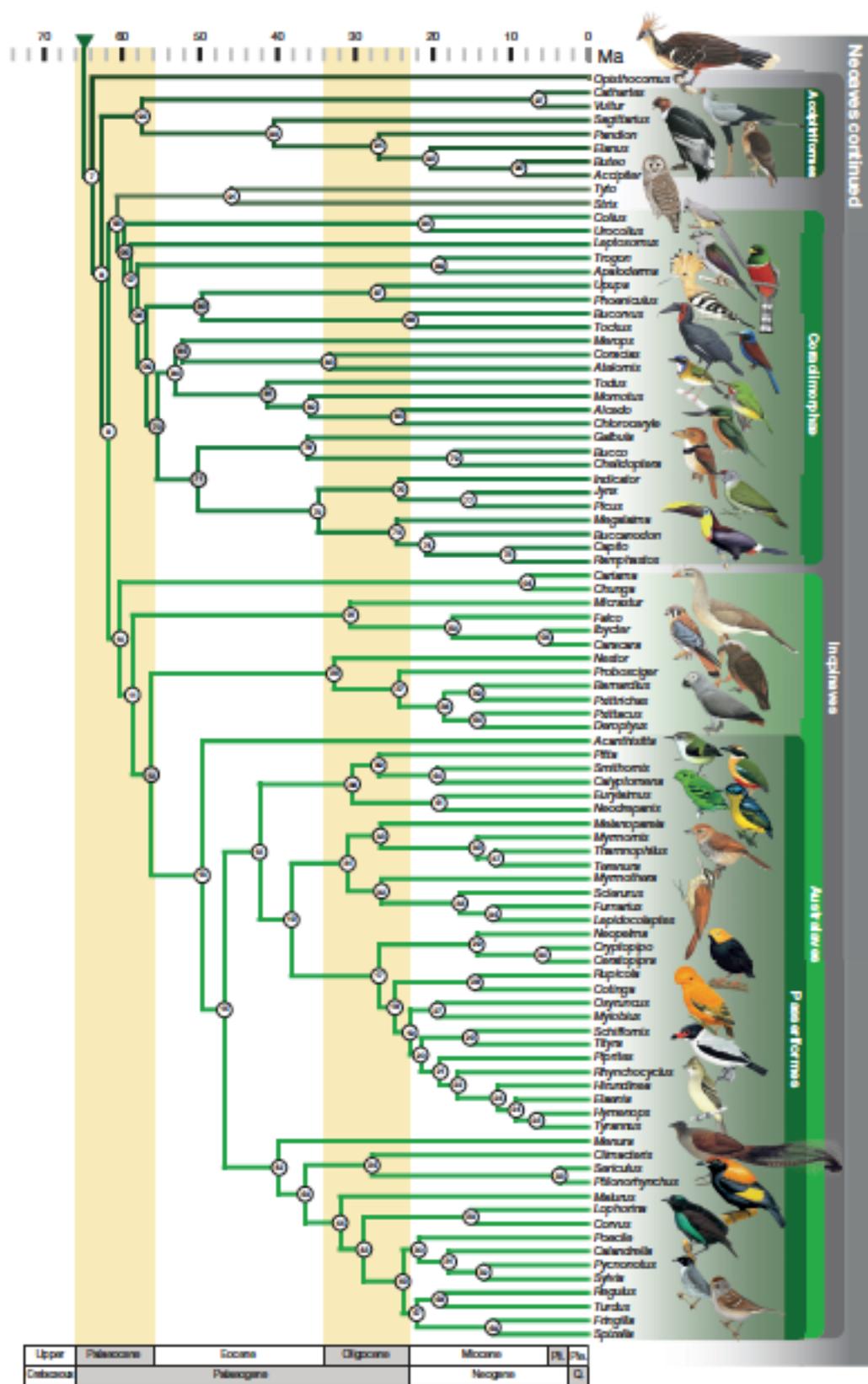
Background:

As most of you know, I've been campaigning for more objective criteria for assigning ranks at higher levels of classification, specifically with respect to roughly comparable lineage ages (and what I really should do is write this up as an *Auk* commentary). Encouraged by the reception to my previous proposal dealing with the caprimulgiform groups, I here take another step towards treating groups that have been evolving separately since the mid-Eocene as orders. This case differs from the caprimulgiform case, however, in that monophyly is not an issue.

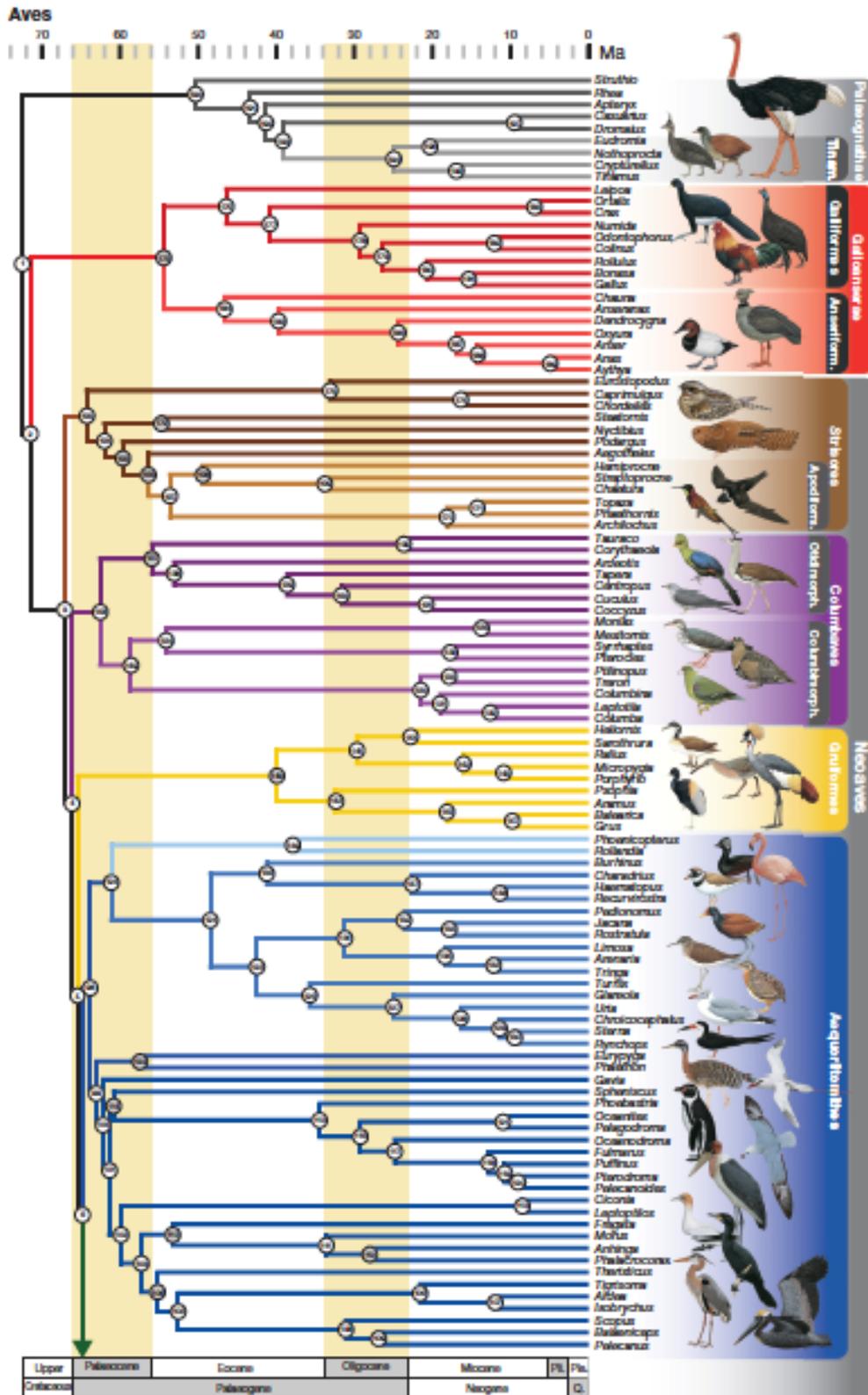
In this particular case, the New World vultures, Prum et al.'s (2015) calibrations (with all appropriate caveats concerning this sort of data) suggest that the cathartids have been evolving as a separate lineage from other accipitriform lineages since the Paleocene, ca. 54 mya. On the next page is the Prum et al. (2015) time-calibrated tree, with geological time periods along the bottom; nodes are calibration points, which are enumerated in the Supplementary Material. The resolution here is lousy; so if anyone needs a pdf, just let me know.

If you look at the Paleocene/Eocene boundary, you can see that all other lineages that are of comparable age to the New World vultures are ranked as orders. From top to bottom, the lineages predicted to be evolving separately by the end of the Paleocene are:

1. Opisthocomiformes
2. Cathartidae
3. Accipitriformes minus Cathartidae
4. Strigiformes
5. Coliiformes
6. Trogoniformes
7. Upupiformes + Bucerotiformes
8. Coraciiformes
9. Piciformes
10. Cariamiformes
11. Falconiformes
12. Psittaciformes
13. Passeriformes



The pattern is even more dramatic in the other half of Prum et al.'s Figure 1 – again, be sure to see the original for better resolution:



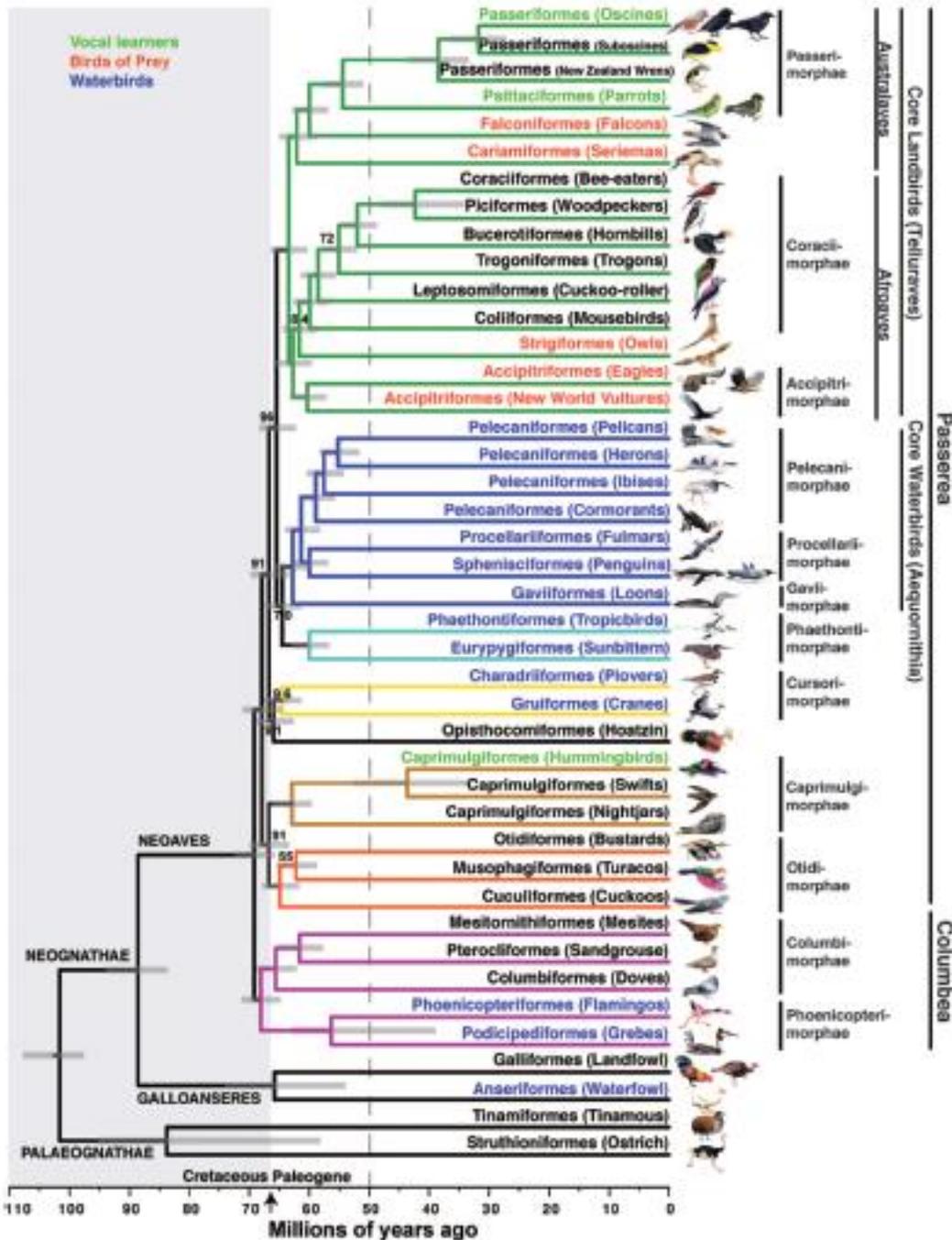
The lineages predicted as separate at the end of the Paleocene are:

14. all ratites plus tinamous
15. Galliformes + Anseriformes
16. Caprimulgiformes
17. Steatornithiformes
18. Nyctibiiformes
19. Aegotheliformes
20. Apodiformes
21. Musophagiformes
22. Cuculiformes + Otidiformes
23. Mesitornithiformes + Pterocliiformes
24. Columbiformes
25. Gruiformes
26. Phoenicopteriformes + Podicipediformes
27. Charadriiformes
28. Eurypygiformes
29. Phaethontiformes
30. Gaviiformes
31. Sphenisciformes
32. Procellariiformes
33. Ciconiiformes
34. Suliformes
35. Pelecaniformes

Thus, the New World vultures are the only lineage as old as the Paleocene not ranked as an order, and several lineages of comparable estimated age consist of two or more orders. As a point of clarification, moving the arbitrary boundary between order and family to a more recent date, the mid-Eocene, produces a classification that maximizes consistency with current higher-level ranks and thus minimizes instability; this proposal addresses only the most extreme case, the New World vultures. Note that the New World vultures have been treated in their own order, Cathartiformes, in much paleontological literature, and SACC has treated them in their own order since 2008 - see [SACC proposal 361](#). Thus, recognizing Cathartiformes is not a radical new idea. Wikipedia has an entry for Cathartiformes, and a Google search on Cathartiformes produces 42,000 hits.

I emphasize that I recognize that the Prum et al. tree represents preliminary analyses of new data, and that modifications are inevitable. Nonetheless, using Prum et al. (2015) at least represents an objective approach to higher classification that differs from the current data-free approach that is maintained by historical momentum.

Jarvis et al. (2014), with more limited taxon-sampling but using a whole-genome approach, found similar estimates of lineage age in their time-calibrated tree (let me know if you need a pdf for better resolution):

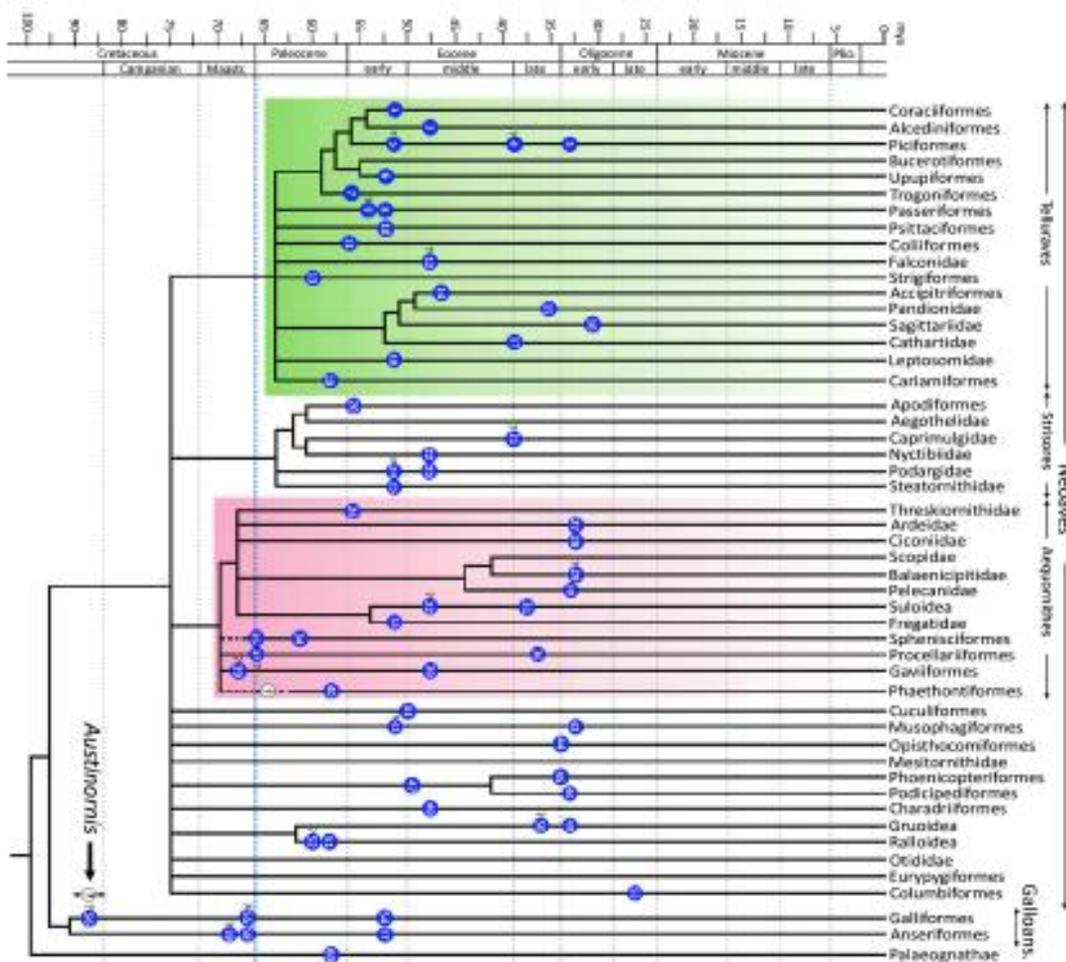


Their estimates for lineage age for the New World vultures is roughly 60 my, older than that of many lineages ranked as orders. The only older lineages not treated as separate orders are the Pelecaniformes and Caprimulgiformes, both of which we've already split into several orders.

Claramunt & Cracraft's very recent (2015) paper used data from Jarvis et al. (2014) but also used RAG-1 data from 200+ taxa to produce broader taxon-sampling. The figures from that paper are too detailed to reproduce well here as screen shots. The Claramunt & Cracraft (2015) results are broadly congruent with those of the above papers in terms of lineage age (as expected in part because none of the data sets and fossil calibrations is completely independent). You can see the figures online at:

<http://advances.sciencemag.org/content/1/11/e1501005>. The bottom line is that the cathartids again come out as sisters to the other accipitrids, and the separation of the lineages, visually extrapolating from the figures, is roughly 58 mya. As in the above analyses, the cathartids are again as old or older than most lineages ranked as orders in our classification.

In terms of oldest known fossils for each lineage, below is the figure from Mayr's (2014) paper that maps the oldest fossils for crown group birds. (I know the resolution isn't good – let me know if you need a pdf):



Synopsis and Recommendation:

The New World vulture lineage is as old or older than many lineages ranked at the level of order, and is the only lineage ranked “only” as a family that is also predicted to have been evolving separately since the end of the Paleocene. It is also morphologically and behaviorally highly distinctive – so distinctive, in fact, that recall that 30 years ago, some morphological data were interpreted as indicating that the cathartids were not particularly close to the other Accipitriformes (then part of Falconiformes) and that they were instead more closely related to Ciconiiformes. Note also that the New World vultures have been treated in their own order in some paleontological literature, and so ranking them as an order is by no means novel. Therefore, I recommend a YES vote on this. The consequence would be that all lineages in the AOU classification predicted to have been evolving separately since the Paleocene would be ranked as orders, thus allowing that classification, at last, to have some justification for taxon-ranking at higher-levels and thus also implementing a classification that has some information content with respect to assignment of one of its higher ranks.

Literature Cited:

- Claramunt, S. AND J. Cracraft. 2015. A new time tree reveals Earth history’s imprint on the evolution of modern birds. *Science Advances* ;1:e150100.
- Jarvis, E. D. et ca. 100 al. 2014. Whole-genome analyses resolve early branches in the tree of life of modern birds. *Science* 346: 1320-1331.
- Mayr, G. 2014. The origins of crown group birds: molecules and fossils. *Palaeontology* 57: 231–242.
- Prum, R. O., J. S. Berv, A. Dornburg, D. J. Field, J. P. Townsend, E. M. Lemmon, and A. R. Lemmon. 2015. A comprehensive phylogeny of birds (Aves) using targeted next-generation DNA sequencing. *Nature* 526: 569-573.

Submitted by: Van Remsen

Date of Proposal: 9 March 2016

Recognize *Colibri cyanotus* as a separate species from *C. thalassinus*

Background:

There are three currently recognized species of *Colibri* violetears that are mostly green: *C. coruscans* (Sparkling Violetear), *C. thalassinus* (Green Violetear), and *C. serrirostris* (White-vented Violetear). The species are very similar in plumage and differ primarily in extent of violet on throat and belly (see photos below).

The problem, as can be seen in the photos, is that *C. thalassinus*, as circumscribed since Peters, consists of two subspecies groups, both of which occur in the NACC area, and one of those, nominate *thalassinus*, looks more like *C. coruscans*, and the other group looks more like *C. serrirostris*.





New Information:

Remsen et al. (2015) proposed that species limits in the *Colibri thalassinus* group be revised. Here is the text:

“*Colibri thalassinus*. As defined for most of the last 75 years (Peters 1945, Schuchmann 1999, Dickinson & Remsen 2013), this species consists of several subspecies found in montane areas from central Mexico to northwestern Argentina. The subspecies fall into two groups (Dickinson & Remsen 2013): (1) nominate *thalassinus* from Mexico to Nicaragua, and (2) the *cyanotus* subspecies group, which consists of the subspecies *cabanidis* of Costa Rica and W Panama, and *cyanotus* and other subspecies of South America. These two subspecies groups differ from each other in plumage nearly as much as the green species of *Colibri* differ from each other. Nominate *thalassinus*, from Mexico to Nicaragua, is more like South American *C. coruscans* in its conspicuous blue coloration in the ventral plumage than it is to the Central and South American subspecies group, in which blue is absent (group of AOU 1998, Dickinson & Remsen 2013). Nominate *thalassinus* has a faint line of blue that connects the blue face patches across the chin, also suggesting the broader blue across the chin of *coruscans*; the Central and South American subspecies group has the chin completely green. The two subspecies groups were formerly treated as separate species (Ridgway 1911, Cory 1918), but Peters (1945) treated them as conspecific without providing any rationale. Our sampling included only *C. t. crissalis* of the *cyanotus* group, and we were thus unable to determine whether broadly defined *C. thalassinus* is monophyletic. Even if monophyletic, field studies of the vocalizations and behavior in this group of taxa would

illuminate whether two or more species should be recognized within *C. thalassinus* under the Biological Species Concept. Because nominate *thalassinus* differs in plumage and size from the *cyanotus* subspecies roughly to the same degree as other taxa ranked as species within *Colibri*, we consider that the burden-of-proof falls on treating them as conspecific and propose that nominate *thalassinus* and the *cyanotus* group should be treated as separate species until data indicate otherwise.”

Analysis and Recommendation:

Our argument was that the species limits prior to Peters should be restored given that (1) Peters did not present any explicit rationale, and (2) nominate *thalassinus* is closer in plumage to *C. coruscans*, which is clearly a separate species (partially sympatric) from South American *thalassinus* populations and therefore nominate *thalassinus* should also be treated as separate from the *cyanotus* group. Also, the *cyanotus* group is actually closer in plumage to *Colibri serrirostris* than to nominate *thalassinus*. This is a weak argument, of course, but the idea is to return to the species limits of Robert Ridgway until better data allow a more modern evaluation (e.g., analysis of voice and display). So, I recommend a YES on this. Reasons to vote NO would include retaining status quo until better data available (e.g., comparative genetic distances and vocal data).

English Names:

If this passes, I recommend a return to the names used by Ridgway, i.e. Mexican Violetear for *thalassinus* and Lesser Violetear for the *cyanotus* group. “Mexican” is not ideal because its range extends to Nicaragua, but *thalassinus* is often referred to as “Mexican Green Violet-ear”. “Lesser” is insipid, but appropriate because it is the smallest species in the genus; this also resurrects a name for the daughter species of the split, thus restricting use of “Green Violetear” to a broadly defined *thalassinus*.

Literature Cited:

Remsen, J. V., Jr., F. G. Stiles, & J. A. McGuire. 2015. Classification of the Polytminae (Aves: Trochilidae). *Zootaxa* 3957: 143-150.

Submitted by: Van Remsen

Date of Proposal: 10 March 2016

Change the English name “Brush-Finch” to “Brushfinch”

Note: This is a modified version of [SACC proposal 653](#), which passed.

This proposal addresses a minor item with respect to consistency in our policy on hyphenation. I'm sure most of you have lost sleep over the fact that recent genetic data show that the species we called “Something Brush-Finch” do not form a monophyletic group, now that *Arremon* and *Atlapetes* are no longer sisters and *Arremon* has expanded to include *Buarremon* and *Lysurus*.

Species that would be affected are in bold below:

Arremon aurantirostris (Orange-billed Sparrow)

Arremon crassirostris (Sooty-faced Finch)

***Arremon brunneinucha* (Chestnut-capped Brush-Finch)**

***Arremon virenticeps* (Green-striped Brush-Finch)**

***Arremon costaricensis* (Costa Rican Brush-Finch)**

***Arremon atricapillus* (Black-headed Brush-Finch)**

Arremonops rufivirgatus (Olive Sparrow)

Arremonops chloronotus (Green-backed Sparrow)

Arremonops conirostris (Black-striped Sparrow)

***Atlapetes albinucha* (White-naped Brush-Finch)**

***Atlapetes pileatus* (Rufous-capped Brush-Finch)**

One solution was to fix this by changing “Brush-Finch” to “Brush Finch”, but this means that these birds would be indexed under “Finch”, and they are not really “finches” sensu Fringillidae (not that this problem isn't found elsewhere, e.g., *A. crassirostris* = Sooty-faced Finch). Removing the hyphen and making the name a single word “Brushfinch” removes this problem, at least in terms of rules for hyphens. It does not solve the problem that “Brushfinch” is also not a monophyletic group, but few English last names are monophyletic nowadays – they simply refer to ecomorphs, e.g. finch, sparrow, grosbeak etc. And the planet will continue to rotate on its axis.

Submitted by: Van Remsen

Date of Proposal: 11 March 2016

Change the English name of *Ramphastos ambiguus*

Note: This is a modified version of [SACC proposal 663](#), which passed unanimously.

When we merged *Ramphastos swainsoni* into *Ramphastos ambiguus* (52nd Supplement, 2011), we retained the name “Black-mandibled Toucan” for the new composite species. When treated as separate species, “Black-mandibled” was appropriate for *R. ambiguus sensu stricto* vs. “Chestnut-mandibled Toucan” for *swainsoni* to highlight the only difference between the two taxa.

Haffer (1974), who proposed the merger based on vocal similarities, named the broadly defined species “Yellow-throated Toucan”, and this has been followed in most subsequent classifications, e.g. Short & Horne (2001), Short & Horne (2002), del Hoyo & Collar (2014), and now SACC. This had the additional advantage of creating a new (and appropriate) name for the parent species to avoid confusion with the daughters. I see no reason not to follow this.

Literature Cited:

- Del Hoyo, J., and N. J. Collar. 2014. HBW and BirdLife International Illustrated Checklist of the Birds of the World. Vol. 1: Non-passerines. Lynx Edicions, Barcelona.
- Haffer, J. 1974. Avian speciation in tropical South America. Publications of the Nuttall Ornithological Club, No. 14.
- Short, L. L., and J. F. M. Horne. 2001. Toucans, Barbets and Honeyguides. Oxford University Press, Oxford.
- Short, L. L., and J. F. M. Horne. 2002. Family Ramphastidae (toucans). Pp. 220-273 in “Handbook of the Birds of the World, Vol. 7. Jacamars to woodpeckers.” (J. del Hoyo et al., eds.). Lynx Edicions, Barcelona.

Submitted by: Van Remsen

Date of Proposal: 11 March 2016

Split Plain Wren *Cantorchilus modestus* into three species

Background:

The Plain Wren *Cantorchilus modestus* (Cabanis, 1860) is distributed across Middle America from southern Mexico to central Panama. Five subspecies have been recognized based on size and plumage coloration: *C. m. modestus* (Cabanis 1860) from Chiapas, Mexico, to the Pacific Slope of Costa Rica; *C. m. roberti* (Phillips 1986) in El Salvador; *C. m. vanrossemi* (Phillips 1986) in Honduras; *C. m. elutus* (Bangs 1902) in southwestern and central Panama; and *C. m. zeledoni* (Ridgway 1878) in the Caribbean Slope of southern Nicaragua south through Costa Rica to northwestern Panama. Various taxonomic treatments have differed in their recognition of these taxa, with *modestus*, *elutus*, and *zeledoni* being the most widely accepted. According to the 7th edition of the A.O.U. Checklist (1998) the Plain Wren comprises two groups: “*modestus*” and “*zeledoni*”. The latter, from the more humid environs of the Caribbean Slope, has often been considered a separate species because of its larger size, darker plumage, and allopatric distribution (Stiles and Skutch 1989, Kroodsma and Brewer 2005). The taxonomy of this group has been questioned, and Stiles and Skutch (1989) quoted: “...a study to determine their status is needed”.

New Information:

We recently published results of a phylogeographic study of this species that used morphometric, plumage color, and mitochondrial DNA data from a comprehensive geographic sampling (Saucier et al. 2015). Our analyses of these data support the existence of 3 distinct and highly divergent clades within *C. modestus*, largely congruent with the three most widely recognized subspecific taxa: *modestus*, *elutus*, and *zeledoni* (corresponding respectively with Clade 1, Clade 2, and Clade 3 in the paper), with the exception of populations in the southern Pacific slope of Costa Rica, long been considered to be part of *modestus*, actually belonging to *elutus*.

Genetic divergence estimates between the clades in our ND2/ND3 dataset were greater than or equivalent to those of recent splits in the family Troglodytidae (e.g., Toews and Irwin 2008, Lara et al. 2012). The mean pairwise divergence between *elutus* and *zeledoni* was 6.7%, and divergences between these two southern taxa and the widespread northern populations (*modestus*) were about 7.6%.

Likewise, the greatest degree of variation in morphometrics of shape existed between *modestus* and the two southernmost clades (*elutus* and *zeledoni*). However, we found significant levels of phenotypic divergence among all three of these clades. *Modestus* was especially distinctive in terms of tail length, with a significance level exceeding all other pairings in our morphological dataset.

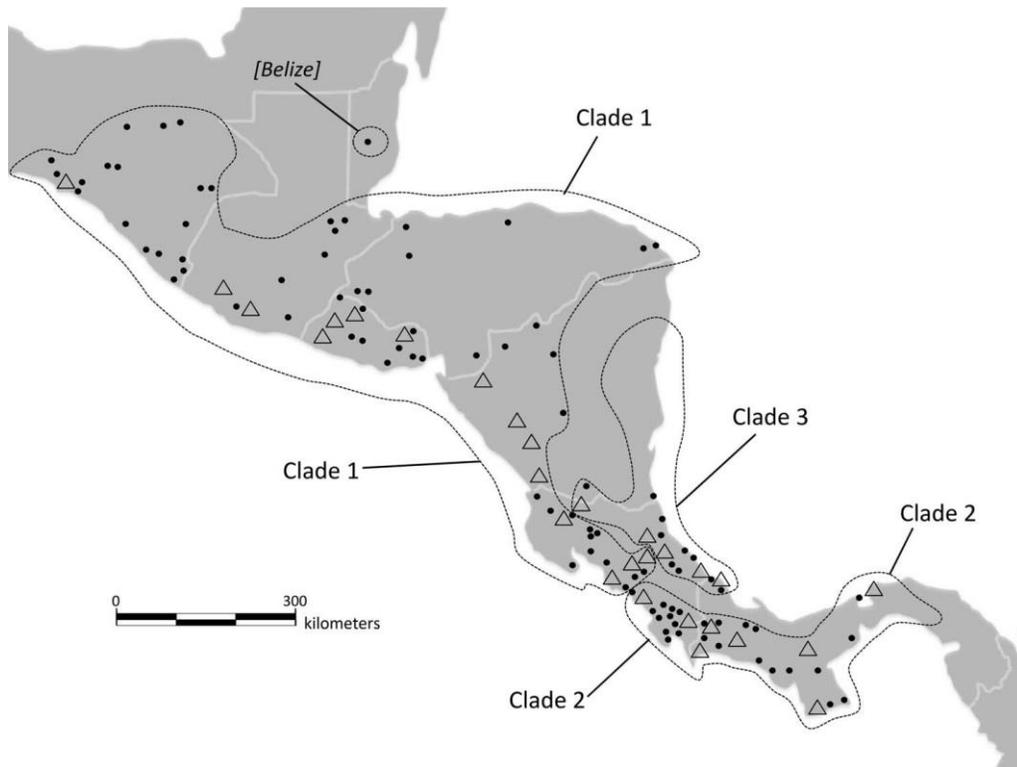


Figure 2 from Saucier et al. (2015). Map depicting the geographic distributions of major clades of *Cantorchilus modestus*, based on our genetic and morphological analyses.

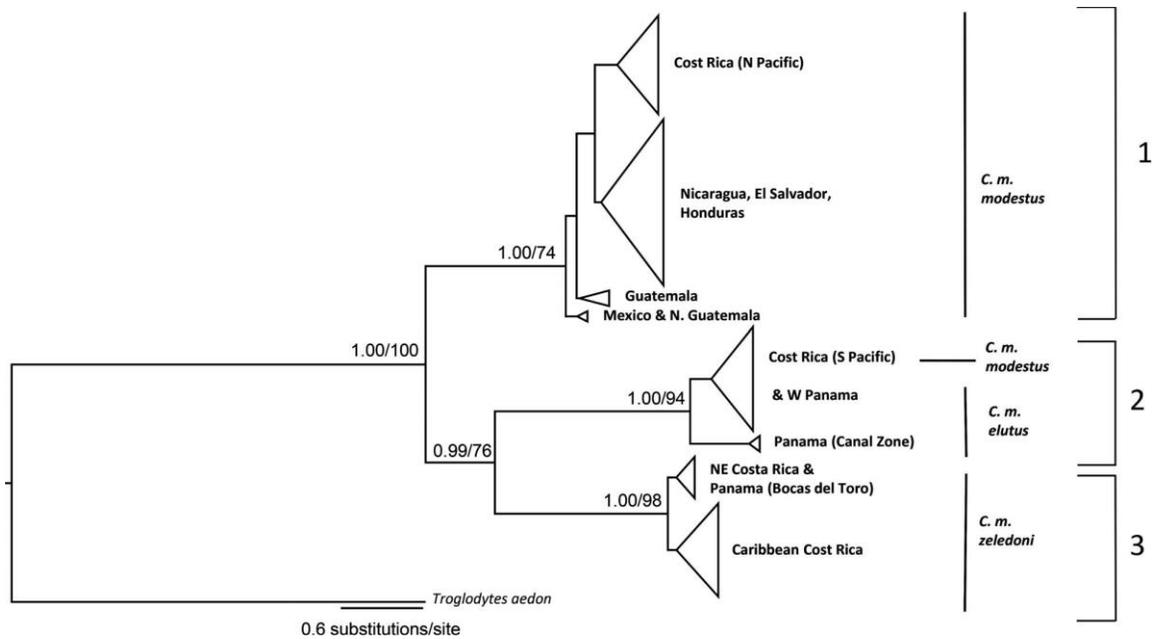


Figure 3 from Saucier et al. (2015). Phylogeny of *Cantorchilus modestus* based on a concatenated ND2/ND3 dataset (1,316 bp) using a Bayesian analysis; the maximum-likelihood analysis produced an identical topology. Nodal support values are given (Bayesian posterior probabilities and likelihood bootstrap values, respectively) for major clades only. Traditional subspecies limits are indicated by name, whereas clade designations (referred to in the text as “Clade 1,” “Clade 2,” and “Clade 3”) are indicated on the far right.

Table 5 from Saucier et al. (2015). Pairwise significance values determined using a MANOVA of morphological measurements controlled for size. *Cantorchilus modestus* populations are grouped according to all historically recognized subspecies (rows 1–5) and by clades identified in our phylogenetic analyses (rows 6–9). El Salvadoran (*C. m. roberti*, “rob”), Honduran (*C. m. vanrossemi*, “van”), and Belizean populations were tested against surrounding populations of *C. m. modestus* (“mod”) (“elu” = *C. m. elutus*; “zel” = *C. m. zeledoni*). Significant values are in bold.

	Morphometrics			Color		
	Pillai's trace	F	P	Pillai's trace	F	P
mod/zel	0.82	58.8	<0.001	1.0	20.6	<0.001
mod/elu	0.61	11.1	<0.001	0.7	6.0	<0.001
zel/elu	0.66	10.5	<0.001	1.0	46.9	<0.001
rob/mod	0.20	1.4	0.2	NA	NA	NA
van/mod	0.12	0.7	0.7	NA	NA	NA
[Belize]/mod	0.49	3.0	0.02	0.8	1.1	0.5
Clade 1/Clade 3	0.82	58.8	<0.001	1.0	20.6	<0.001
Clade 1/Clade 2	0.75	21.7	<0.001	0.7	6.0	<0.001
Clade 2/Clade 3	0.66	10.5	<0.001	1.0	46.9	<0.001

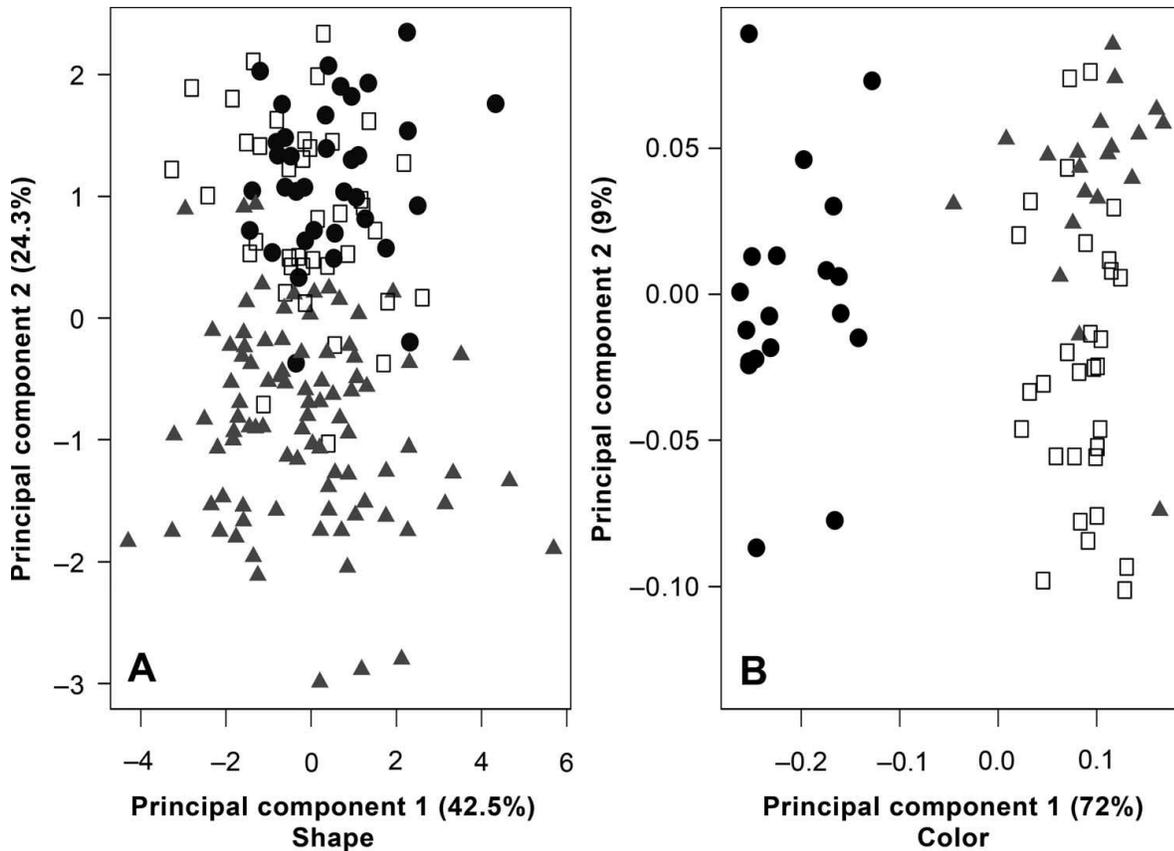


Figure 4 from Saucier et al. (2015). Plot of principal component scores showing the arrangement of subspecies in morphometric (left) and colorimetric space (right). Gray triangles = Clade 1 [*modestus*], black boxes = Clade 2 [*elutus*], and black circles = Clade 3 [*zeledoni*].

Plumage coloration was also differed significantly among the three taxa, although the pattern differed slightly from the one uncovered by genetics and morphometrics. Individuals from *modestus* and *elutus* were shown to have some significant differences in plumage color, despite being virtually inseparable in the field. However, the distinctly darker *zeledoni* accounted for the majority of the variation in plumage color. This pattern may be attributable to *zeledoni*'s isolation in a more mesic environment (on the Caribbean Slope) driving selection toward darker, eumelanin-based pigment types.

To help understand the patterns that we were seeing in genetics and morphometrics, we conducted topology tests, which showed that populations in southern Central America (*elutus* and *zeledoni*) were most likely derived from the widespread northern populations belonging to *modestus*. Ancestral populations may have originated from the north and were subsequently isolated in the south. An event separating northern and southern populations (*modestus* / *elutus* + *zeledoni*) would likely have preceded a separate event that stimulated divergence between the southern populations (*elutus* /

zeledoni). The possible causes of these events, the formation of the Nicaraguan Depression and the uplift of the Cordillera de Talamanca, are addressed in more detail in the paper. However, these events and our mitochondrial divergence estimates coincide roughly with a period of biogeographic upheaval in southern Central America, starting ~3-4 Ma.

The taxon *zeledoni* has long been considered a potentially separate species, following its description by Ridgway in 1878. Thought to be completely allopatric, our results were the first to confirm any contact at all between this taxon and nominate *modestus*. Our results also confirmed limited hybridization between *modestus* and *zeledoni*, although we found this to be restricted to very narrow zones of contact with no sign of further introgression. Significant differences in morphometrics and color also seem to be highly conserved outside of these narrow contact zones. Interbreeding at these zones of contact may be further constrained by differences in breeding phenology between *modestus* and *zeledoni* (Marshall-Ball and Slater 2003). Concerning song, the anatomy of the dueting song of *zeledoni* has been shown to be similar to that of *modestus* (Slud 1964, Cuthbert and Mennill 2007); however, previous authors (Stiles and Skutch 1989, Kroodsma and Brewer 2005) have noted qualitative differences in song (especially the simple song) that are detectable in the field. We feel that these substantial genetic (7.6% from *modestus* and 6.7% from *elutus*), phenotypic, and vocal differences warrant the recognition of *zeledoni* as a distinct species.

The deep genetic divergence (7.6%) between *elutus* and *modestus* was surprising due to their tremendous similarity in phenotype. In fact, the cryptic nature of these taxa was such that their exact zone of contact had previously gone undetected. Previous taxonomic limits placed nominate *modestus* throughout the Pacific Slope of Costa Rica, whereas our results revealed the contact zone to be much farther north, coinciding with an ecotone between two major (wet vs. dry) regions in the central Pacific slope of Costa Rica. The placement of this phylogeographic break was also borne out in the morphometric and colorimetric data, demonstrating significant levels of phenotypic divergence. The absence of any meaningful vicariant barriers between *modestus* and *elutus*, and the lack of shared haplotypes in our genetic analyses, suggest the type of sharp phylogeographic break in parapatry that one would expect from the competitive exclusion of two ecologically similar species (Bull and Possingham 1995).

As noted above, the location of this break coincides with the presence of an ecotone between two major ecoregions: the Central American Dry Forests (CADF) of northwestern Costa Rica (Fund and Hogan 2013) and the Isthmian-Pacific Moist Forest (IPMF) of southwestern Costa Rica and Panama (Olson et al. 2001, Fund and Hogan 2012, Stiles and Skutch 1989). The newly defined range limits of *elutus* seems to

closely track the IPMF ecoregion in the northwestern part of its distribution. This phylogeographic break is shared with other animal taxa (e.g., *Physalemus pustulosus* and *Buteo plagiatus/Buteo nitidus*), and work by C. Sanchez (in prep.) may further underscore the importance of this ecotone for numerous other bird species.

With regard to song, studies of the dueting song of the Plain Wren by Mann (2003) noted differences in pattern between *modestus/zeledoni* and those previously described for *elutus* by Farabaugh (1983). To quote Mann:

“This pattern differs from that described by Farabaugh (1983) for the closely related *T. modestus elutus* in Panama, in which the male produces vocalizations like the introductory phrases described here, but only when singing alone. However, preliminary analysis of our data on a third subspecies of Plain Wren, *T. modestus modestus* in Costa Rica, does indicate the presence of a song pattern like that of *zeledoni* (the subject of the present study). There is no doubt from our study that the I-phrase of the Plain Wren is an integral part of the duet, as it is rare for the female to produce her A-phrase without being stimulated to do so by the male.”

The need for precise coordination of these complex dueting songs may accelerate reproductive isolation by amplifying incompatibilities of synchronization that accumulate between populations during periods of isolation (Hall 2004, Marshall-Ball and Slater 2004).

In light of this new information we propose that the Panamanian subspecies *elutus* be recognized as a distinct species.

For further clarification of these points, we recommend reading through the results and discussion of Saucier et al. (2015), as much of it is relevant to this particular question. <http://www.aoucospubs.org/doi/pdf/10.1642/AUK-15-8.1>

Recommendation:

In light of this new morphometric and molecular phylogeographic evidence, we recommend a vote of YES for splitting of *Cantorchilus zeledoni* from *Cantorchilus modestus*. We also recommend a vote of YES for splitting *Cantorchilus elutus* from *Cantorchilus modestus*.

English Names:

For *zeledoni*, the English common name of “Canebrake Wren” has been widely used colloquially and in previous sources (Stiles and Skutch 1989, Kroodsma and Brewer

2005), and we recommend the official adoption of this name. As far as we know, *elutus* has never had a unique English epithet associated with it. Due to the confusingly cryptic similarities between this taxon and the nominate form, we recommend the geographically descriptive name of “Isthmian Wren”, referring generally to the region surrounding the Isthmus of Panama, and the ecoregions (e.g., the Isthmian-Pacific Moist Forest) to which this taxon is closely tied.

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Submitted by: Jacob R. Saucier, Smithsonian Institution National Museum of Natural History; César Sánchez, Louisiana State University Museum of Natural Science; and Matthew D. Carling, University of Wyoming Department of Zoology and Physiology

Date of proposal: 12 March 2016

Recognize the genus *Cercomacroides* (Thamnophilidae)

Note: This is a proposal modified for NACC based on the [SACC proposal # 638](#) submitted by Pepe Tello and approved unanimously.

Only two species of *Cercomacra* occur in the NACC area:

Cercomacra tyrannina Dusky Antbird

Cercomacra nigricans Jet Antbird

As detailed in the SACC proposal, these species belong to different clades of a paraphyletic *Cercomacra*: *nigricans* is part of the clade that contains the type species *brasiliانا* and would retain the name *Cercomacra*, whereas *tyrannina* is the type species of the newly described *Cercomacroides* Tello et al. 2014. Thus, if we adopt this classification, the NACC species would be as follows (and in same linear sequence):

Cercomacroides tyrannina Dusky Antbird

Cercomacra nigricans Jet Antbird

Submitted by: Van Remsen

Date of Proposal: 12 March 2016

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[SACC Proposal 638:](#)

Effect on SACC: This proposal is for the recognition of a newly described genus for several species currently classified in *Cercomacra*.

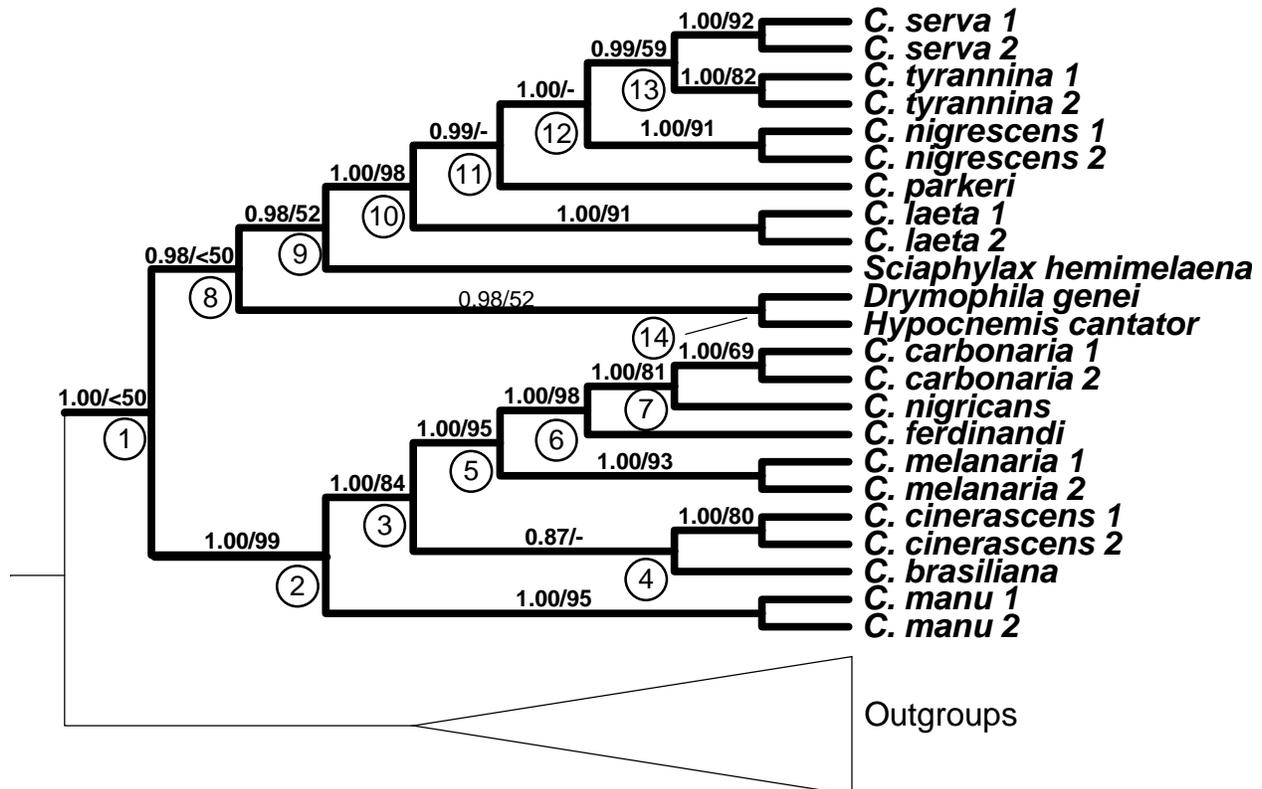
Background: Current SACC footnote 39e summarizes the situation:

“Fitzpatrick & Willard (1990) and Zimmer & Isler (2003) considered *Cercomacra tyrannina*, *C. laeta*, *C. parkeri*, *C. nigrescens*, and *C. serva* form a monophyletic group based on plumage and voice. Tello et al. (2014) confirmed the monophyly of this group and also showed that they are not the sister group to other *Cercomacra*, thus requiring the naming of a new genus, *Cercomacroides*, for them. SACC proposal badly needed.”

Analysis and recommendation: Tello et al. (2014) named a new genus,

Cercomacroides, for the species in the “*tyrannina* group” (whistlers), to include the following taxa:

nigrescens
laeta
parkeri
tyrannina (type)
serva



Their molecular data set included three mitochondrial (*ND2*, *ND3*, *CYTb*) and one nuclear intron (*FIB5*) for a total of 3018 bps. Tello et al.’s ongoing investigation on the systematics of this group has produced ~5k additional nucleotides (including several nuclear introns) that corroborated the monophyly of *Cercomacroides* and helped resolved problematic basal nodes within both *Cercomacroides* and *Cercomacra*.

I recommend a YES vote. Morphological similarities that support the monophyly of *Cercomacra* are vague and maybe plesiomorphic, whereas the recognition of *Cercomacra* and *Cercomacroides* as different genera is consistent with plumage, behavioral, and ecological differences (Zimmer and Isler 2003) and is required to retain

the monophyly of *Cercomacra* (s.s.). Recognizing *Cercomacroides* as a genus is the appropriate taxonomic solution for this particular case.

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Submitted by: Jose G. Tello

Date of Proposal: August 2014

**Split *Oceanodroma cheimomnestes* and *O. socorroensis* from
Leach's Storm-Petrel *O. leucorhoa***

The Leach's Storm-Petrel complex in the northeastern Pacific Ocean presently contains four taxa that we lump within *Oceanodroma leucorhoa*.

O. l. leucorhoa breeds from the Gulf of Alaska south to southern California (Channel Islands). It is the same subspecies as that in the north Atlantic, although it has been considered separate (*O. l. beali*), because of its slightly smaller size. Populations of subspecies *leucorhoa* in the Pacific are larger, however, than the other three Pacific subspecies and have variable white rump patches (actually uppertail coverts, but hereafter "rump patch"), with a cline from almost all with white rumps in the north toward increasing darkness to the south. Size also varies clinally from larger in the north to smaller in the south.

O. l. chapmani breeds on islands of northern Baja California (Coronado Islands south to San Benito Islands). *Chapmani* is smaller than *leucorhoa*, and birds tend to be darker rumped, although white-rumped birds are found within *chapmani* colonies and dark-rumped birds (up to 6% on the Farallon Islands) are found within *leucorhoa* colonies, particularly as you go south.

O. l. socorroensis breeds on islets off the southern end of Guadalupe Island. Colonies are active in the summer. *Socorroensis* is the smallest subspecies in the complex, and tends to have an extensive white rump, though some birds have an almost completely dark rump.

O. l. cheimomnestes also breeds on islets off the southern end of Guadalupe Island, but colonies are active in winter. It is slightly larger than *socorroensis*, somewhat lighter brown in fresh plumage, and most individuals have a somewhat darker rump patch, which is less variable than in *socorroensis*.

Ainley (1980) described *cheimomnestes* and gave an overview of taxonomy, morphometrics, and vocalizations in all of these NE Pacific populations. In morphometrics, as had been noted by Crossin (1974), the Guadalupe populations are distinct from all other populations. In addition, the winter and summer populations on Guadalupe are as different from one another as are the other samples from the Aleutians to San Benito. Ainley (1980) noted that burrow and flight calls were similar between *leucorhoa* and *chapmani*, but differed somewhat among those nesting on Guadalupe. The flight calls especially differed between *cheimomnestes* and

socorroensis and between those two and the others (Figure 4 from Ainley 1980 reproduced below, a= *leucohora*, b-c=*chapmani*, d= *socorroensis*; e= *cheimomnestes*).

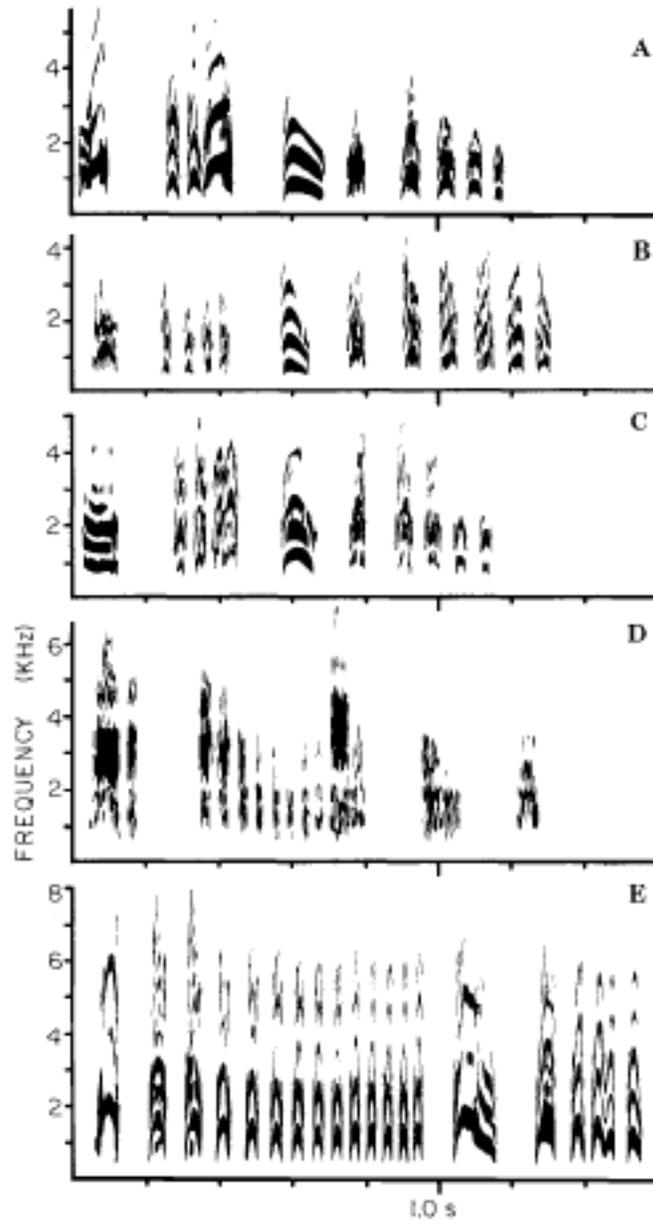


Fig. 4. Sonagrams of Flight Calls in *O. leucohoa* nesting at the Farallon Islands (A); Coronado Islands (B); San Benito Islands (C); and Guadalupe Island, summer (D) and winter (E).

Given the clinal nature of morphometrics, and plumage characters, and similarity of vocalizations, Ainley (1980) synonymized *leucorhoa* and *chapmani*. Ainley (1980) hesitated to treat *heimomnestes* as a species, even though they are clearly syntopic, because:

Three other oceanic birds also exhibit temporally distinct breeding populations: *Pterodroma mollis* in Madeira (Bourne 1957), *Macronectes (giganteus and halli)* on Macquarie Island and other subantarctic islands (Bourne and Warham 1966), and *O. castro* in the Galapagos (Harris 1969). The last shows no morphological or behavioral differences between populations, and thus there is no reason to consider separate taxonomic status. The two populations of *P. mollis* are distinct in several regards, but, as they never meet, Bourne (1957) maintained their subspecific status. The two temporal populations of *Macronectes*, however, nest side by side without interbreeding on Macquarie, their breeding being a few weeks out of synchrony, and they exhibit minor morphological and behavioral differences as well. Bourne and Warham (1966) recommended that they be recognized as distinct but sibling species. On Guadalupe, the two populations of *O. leucorhoa* are morphologically and behaviorally distinct, but, as they do not meet one another, their situation is somewhat similar to that of *P. mollis*. For consistency then, separate subspecific status is appropriate. On the other hand, for the sake of argument, so different are their songs that, if they met, it is questionable that interbreeding would occur. Much more work is needed on vocalizations in *O. leucorhoa*.

However, since those remarks, the north Atlantic forms of *P. mollis* (*P. madeira* from Madeira and *P. feae* from nearby Bugio and also the Cape Verde Islands) have been split from *mollis* and each other, the latter based on differences in timing of breeding and vocal differences (Zino et al. 2008). Sometime prior to the 7th edition, the NACC added *feae* to the Appendix and treated *madeira* as a separate species. Both species have since been added to the main list.

Howell et al. (2009) split *heimomnestes* and *socorroensis* from *leucorhoa*; he included *chapmani* in the latter as a separate subspecies. Howell (2012) later split all four subspecies as species, but did not present a reason for the change in his treatment of *chapmani*. He has been a fervent advocate for this 4-species approach in on-line fora. Howell (2012) mentioned that genetic analyses have been done but not published.

The one-species treatment is followed by del Hoyo and Collar (2014), Clements et al. (2015), and Gill and Donsker (2016). Dickinson and Remsen (2013) also followed the one-species treatment, but cited the Ainley and Howell papers with the statement that more than one species might be involved. Notes under *O. leucorhoa* in the 7th edition

(Banks et al. 1998) make a mess of distributions of *cheimomnestes* and *socorroensis* as described by Ainley (1980), and completely omit his vocal analyses.

It seems clear that two taxa, *cheimomnestes* and *socorroneis*, occur sympatrically but differ in vocalizations, morphometrics, timing of breeding, and somewhat in plumage. Although genetic analyses would be great to capture a bigger picture, I cannot imagine what that data could tell us that we could lead to a different conclusion regarding their status as different species. It also seems clear that *leucorhoa* and *chapmani* are largely different points on a cline. We do not need to make conclusions regarding the subspecies status of *chapmani*, only that *chapmani* is conspecific with *leucorhoa*. Given that *cheimomnestes* and *socorroneis* differ from *leucorhoa/chapmani* in ways that appear to be important for reproductive isolation (namely vocalizations), then it seems wise to consider each of these specifically distinct from *leucorhoa*.

Recommendation:

I recommend that we vote YES to split *cheimomnestes* and *socorroensis* from *O. leucorhoa*.

English Names:

The 7th Edition treats *socorroensis* as a group and calls it Dark-rumped Storm-petrel. This has not been followed elsewhere and seems a bad choice, given that other taxa in this complex (i.e., *chapmani*) are more apt to have even darker rumps. Howell et al. (2009), Howell (2012), and others (Clements et al. 2015, Gill et al. 2016) call *socorroensis* Townsend's Storm-Petrel, and *cheimomnestes* Ainley's Storm-Petrel, after the describers of these taxa. I cannot come up with better names and these seems to have gained some traction. It would be silly to change Leach's Storm-Petrel for the widespread *leucorhoa*.

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Submitted by: Andrew Kratter

Date of Proposal: 13 March 2016