

AOU Classification Committee – North and Middle America

Proposal Set 2017-A

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**Split White-faced Ground-sparrow *Melospiza cabanisi* from  
Prevost's Ground-sparrow *Melospiza biarcuata***

**Background:**

The Prevost's Ground-Sparrow, *Melospiza biarcuata*, is distributed from Southern Mexico to central Costa Rica. Three subspecies have been described based on plumage differences: (1) *M. b. biarcuata* from Southern Mexico above 1000 m to El Salvador and Honduras; (2) *M. b. hartwegi* in Chiapas below 1000 m; and (3) *M. b. cabanisi* at the Central and Turrialba valleys in Costa Rica. Historically, *cabanisi* has been argued to be a separate species from *biarcuata/hartwegi* based on vocal and plumage differences, and allopatric distribution (Sclater & Salvin 1868; Stiles & Skutch 1989; Howell & Webb 1995; AOU 1998; Sánchez et al. 2009). The taxonomic status of *M. b. cabanisi* has been problematic since its description, Sclater and Salvin (1868) declaring: "it is unfortunate that all the naturalists who have met with specimens of [*M. b. cabanisi*] should have identified it wrongly."

**New Information:**

Sandoval et al. (2014) conducted a rigorous phenotypic comparison between the three recognized subspecies. They found that: "...*M. b. cabanisi* can be readily distinguished from the two other subspecies on the basis of morphometrics (*M. b. cabanisi* are smaller), plumage patterns (*M. b. cabanisi* have different facial markings and plumage patches), color differences (*M. b. cabanisi* have plumage patches that differ in color and brightness), and vocalizations (*M. b. cabanisi* have songs and calls that are acoustically distinct from those of *M. b. biarcuata*). By contrast, the two northern subspecies *M. b. biarcuata* and *M. b. hartwegi* were very similar for most traits, supporting previous suggestions that the two northern subspecies should be considered a single subspecies."

Sex-specific differences between subspecies were also observed. Females of *M. b. cabanisi* showed shorter tail length than the other subspecies (Table 1), and males of *M. b. cabanisi* showed shorter tarsus, tail length, and culmen length than other two subspecies (Table 1).

Plumage pattern showed marked differences between *cabanisi* and *biarcuata/hartwegi*: "Around the eye, *M. b. cabanisi* exhibited a thin white eye ring, a small white postocular spot, and a large white preocular spot, whereas *M. b. biarcuata* and *M. b. hartwegi* exhibited a large white facial mask. *M. b. cabanisi* displayed a black moustachial stripe, a white malar stripe, and a black lateral throat stripe; both black stripes were lacking in *M. b. biarcuata* and *M. b. hartwegi*, which instead had a contrasting bicolored auricular

patch (black fading to rust) above an incomplete white nape collar. The breast of *M. b. cabanisi* displayed a large circular black patch below the throat whereas *M. b. biarcuata* and *M. b. hartwegi* had no contrasting markings on a white breast" (Fig. 1). Visual models used to analyze color differences showed that color of cheek and breast were different between *M. b. cabanisi* and *M. b. biarcuata*/*M. b. hartwegi* (Fig. 2).

Vocal evidence showed that male solo song duration was shorter, and had higher maximum frequency and frequency of maximum amplitude in *M. b. cabanisi* than in *M. b. biarcuata* (Table 2, Fig. 3). Calls showed also higher minimum and maximum frequency, and frequency of maximum amplitude (Table 2, Fig. 3).

### Recommendation:

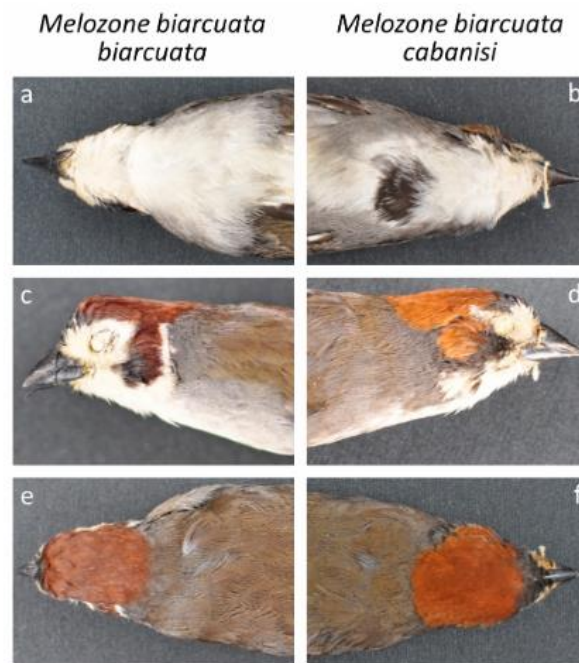
Based on this new evidence, and that *biarcuata/hartwegi* and *cabanisi* showed phenotypic differences of similar degree to those observed in recently recognized species in the *Arremon torquatus* complex (Cadena & Cuervo 2010, Chesser et al. 2012, Remsen et al. 2013), I recommend a vote of YES for splitting *M. cabanisi* from *M. biarcuata* (including *M. b. biarcuata* and *M. b. hartwegi*). The English common name for *M. cabanisi* would be White-faced Ground-Sparrow, and Prevost's Ground-Sparrow for *M. biarcuata*.

**Table 1.** Morphometric difference between subspecies of *M. biarcuata* (Sandoval et al. 2014). Bold text indicates statistically different morphometric measurements, and numbers connected by the same letter per measurement are statistically different.

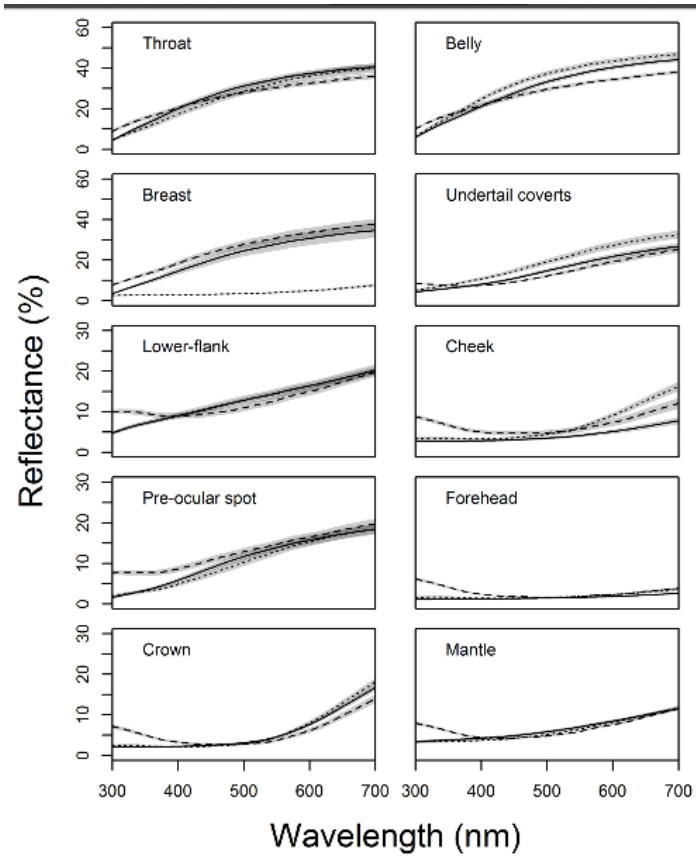
	<i>M. b. biarcuata</i>	<i>M. b. hartwegi</i>	<i>M. b. cabanisi</i>
Females			
Tarsus (mm)	24.6 ± 0.5	24.1 ± 0.2	23.9 ± 0.3
<b>Tail length (mm)</b>	<b>60.2 ± 1.0 (a)</b>	<b>62.3 ± 0.8 (a)</b>	<b>56.7 ± 1.2 (b)</b>
Wing cord length (mm)	65.8 ± 1.8	64.3 ± 0.9	67.2 ± 0.9
Culmen length (mm)	12.6 ± 0.3	13.2 ± 0.2	12.3 ± 0.3
Beak width (mm)	8.1 ± 0.4	8.7 ± 0.2	7.9 ± 0.2
Beak depth (mm)	8.2 ± 0.4	7.7 ± 0.2	8.3 ± 0.2
Males			
<b>Tarsus (mm)</b>	<b>24.9 ± 0.2 (a)</b>	<b>25.1 ± 0.4 (a)</b>	<b>23.9 ± 0.3 (b)</b>
<b>Tail length (mm)</b>	<b>65.9 ± 0.9 (a)</b>	<b>67.3 ± 0.7 (a)</b>	<b>60.0 ± 0.8 (b)</b>
Wing cord length (mm)	69.5 ± 0.6	69.4 ± 0.5	68.4 ± 0.8
<b>Culmen length (mm)</b>	<b>13.0 ± 0.2(a)</b>	<b>13.5 ± 0.1 (b)</b>	<b>12.6 ± 0.1 (c)</b>
Beak width (mm)	7.9 ± 0.2	8.4 ± 0.2	8.3 ± 0.2
<b>Beak depth (mm)</b>	<b>8.3 ± 0.1 (a)</b>	<b>8.9 ± 0.1 (b)</b>	<b>8.3 ± 0.2 (a)</b>

**Table 2.** Vocal differences between subspecies of *M. biarcuata* (Sandoval et al. 2014). Bold text indicates vocal measurement that differ statistically.

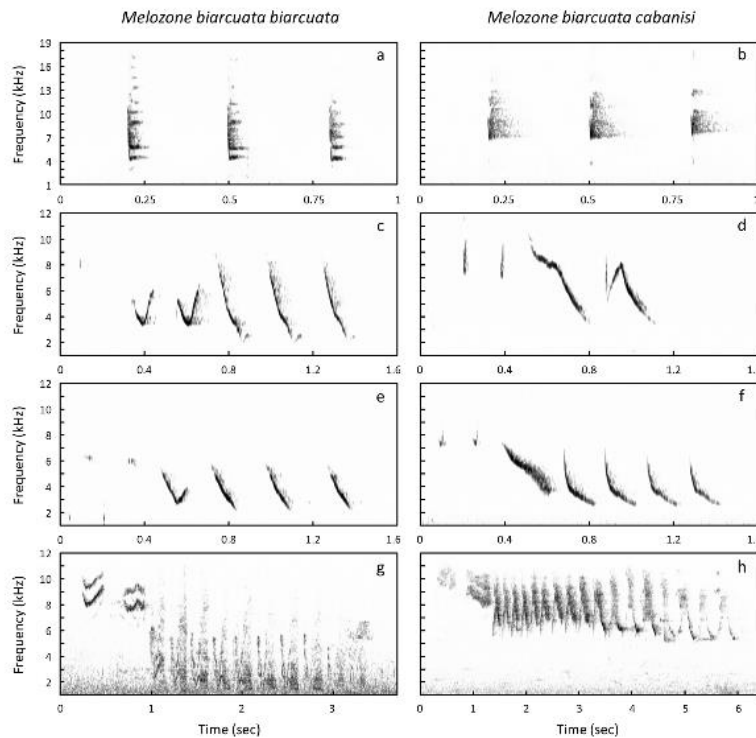
Solo songs	<i>M. b. biarcuata</i>	<i>M. b. cabanisi</i>
Number of elements	6.06 ± 0.38	7.91 ± 0.66
Number of unique element types	3.21 ± 0.22	3.60 ± 0.13
<b>Duration (s)</b>	<b>1.76 ± 0.22</b>	<b>1.46 ± 0.08</b>
Minimum frequency (Hz)	2277 ± 81	2814 ± 225
<b>Maximum frequency (Hz)</b>	<b>8582 ± 360</b>	<b>10460 ± 234</b>
<b>Frequency of maximum amplitude (Hz)</b>	<b>4726 ± 376</b>	<b>5456 ± 188</b>
Calls		
Duration (s)	1.33 ± 0.28	0.81 ± 0.32
<b>Minimum frequency (Hz)</b>	<b>3248 ± 444</b>	<b>5535 ± 570</b>
<b>Maximum frequency (Hz)</b>	<b>9080 ± 433</b>	<b>11719 ± 394</b>
<b>Frequency of maximum amplitude (Hz)</b>	<b>5212 ± 324</b>	<b>6943 ± 456</b>



**Fig. 1.** Plumage pattern differences between *M. biarcuata* subspecies (Sandoval et al. 2014).



**Fig. 2.** Mean reflectance spectra for 10 body regions in *M. biarcuata* subspecies (Sandoval et al. 2014). Solid lines represent *M. b. biarcuata*, dashed lines *M. b. hartwegi*, and dotted lines *M. b. cabanisi*. Gray area around each line is standard error every 1 nm.



**Fig. 3.** Sonograms of calls (a-b), solo songs (c-f), and duets (g-h) of *M. biarcuata* subspecies (Sandoval et al. 2014).

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- Sánchez, J.E., Criado, J., Sánchez, C. & Sandoval, L. (2009) Costa Rica. In: Devenish, C., Díaz Fernández, D.F., Clay, R.P., Davison, I.J. & Yépez Zabala, I. (Eds.), Important bird areas of Americas: priority sites for biodiversity conservation. BirdLife International, Quito, Ecuador, pp. 149–156.
- Sandoval, L., P-P. Bitton, S. M. Doucet & D. J. Mennill. (2014) Analysis of plumage, morphology, and voice reveals species-level differences between two subspecies of Prevost's Ground-Sparrow *Melospiza biarcuata* (Prévost and Des Murs) (Aves: Emberizidae). *Zootaxa* 3895: 103–116
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- Stiles, F.G. & Skutch, A.F. (1989) A guide to the birds of Costa Rica. Cornell University Press, Ithaca, 632 pp.

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

**Proposal date:** 14 April 2016

## Revise the generic classification of the subfamily Anserinae

### Background:

Currently the subfamily Anserinae comprises four genera: *Anser*, *Chen*, *Branta*, and *Cygnus*, as listed below:

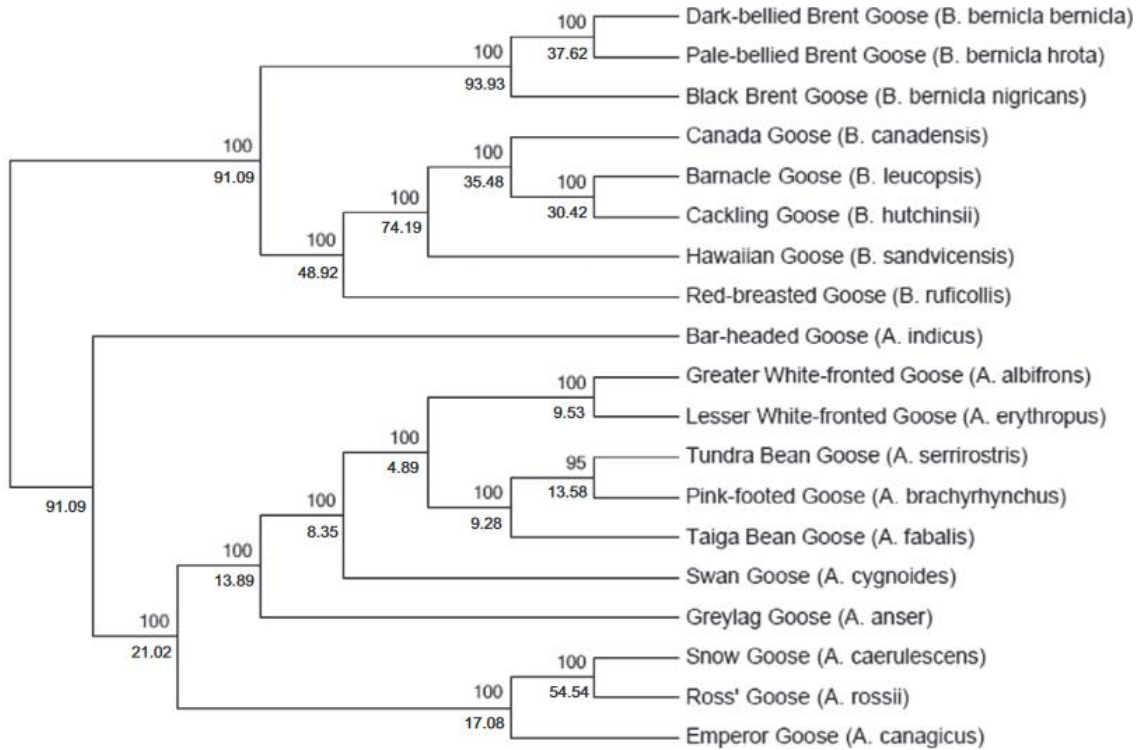
- genus: *Anser*
  - species: *Anser fabalis* (Taiga Bean-Goose, Oie des moissons) A
  - species: *Anser serrirostris* (Tundra Bean-Goose, Oie de la toundra) A
  - species: *Anser brachyrhynchus* (Pink-footed Goose, Oie à bec court) A
  - species: *Anser albifrons* (Greater White-fronted Goose, Oie rieuse)
  - species: *Anser erythropus* (Lesser White-fronted Goose, Oie naine) A
  - species: *Anser anser* (Graylag Goose, Oie cendrée) A
- genus: *Chen*
  - species: *Chen canagica* (Emperor Goose, Oie empereur)
  - species: *Chen caerulescens* (Snow Goose, Oie des neiges)
  - species: *Chen rossii* (Ross's Goose, Oie de Ross)
- genus: *Branta*
  - species: *Branta bernicla* (Brant, Bernache cravant)
  - species: *Branta leucopsis* (Barnacle Goose, Bernache nonnette)
  - species: *Branta hutchinsii* (Cackling Goose, Bernache de Hutchins)
  - species: *Branta canadensis* (Canada Goose, Bernache du Canada)
  - species: *Branta sandvicensis* (Hawaiian Goose, Bernache néné) H
- genus: *Cygnus*
  - species: *Cygnus olor* (Mute Swan, Cygne tuberculé) I
  - species: *Cygnus buccinator* (Trumpeter Swan, Cygne trompette)
  - species: *Cygnus columbianus* (Tundra Swan, Cygne siffleur)
  - species: *Cygnus cygnus* (Whooper Swan, Cygne chanteur)

### New Information:

A recent phylogenetic study of the True Geese (genera *Anser*, *Branta* and *Chen*; see trees below) unravelled the phylogenetic relationships between the different goose species with strong support (Ottenburgs et al., 2016), which previous studies were unable to accomplish (Ruokonen et al., 2000, Lee et al., 2008, Paxinos et al., 2002, Donne-Gousse et al., 2002, Gonzalez et al., 2009). The genus *Branta* consisted of a



clade of White-cheeked Geese: Canada Goose (*Branta canadensis*), Cackling Goose (*Branta hutchinsii*), Barnacle Goose (*Branta leucopsis*) and Hawaiian Goose (*Branta sandvicensis*) – and two basal splits – leading to Brent Goose (*Branta bernicla*) and



**Fig. 2.** Maximum Likelihood Tree for the True Geese based on consensus and concatenation methods. Bootstrap values of the concatenation analysis above branches, concordance factors of the consensus analysis below.

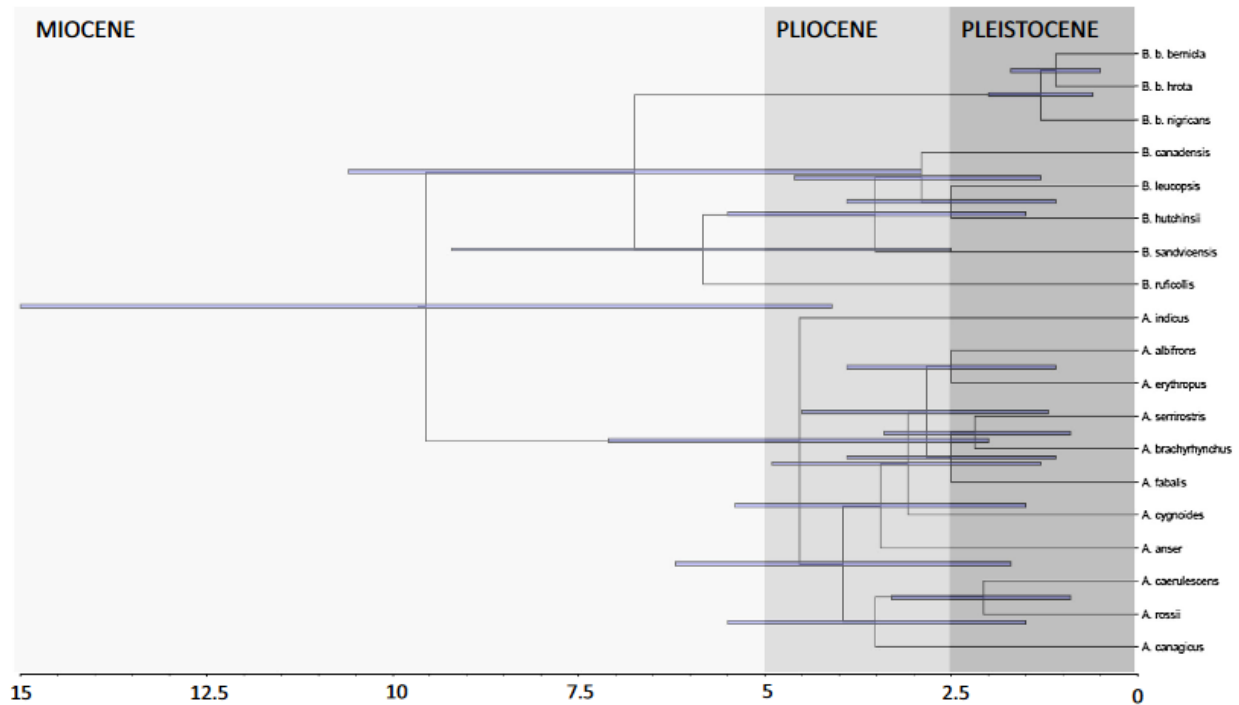


Fig. 3. Timed phylogenetic tree using a global clock approach in MCMCtree. Blue bars indicate 95% confidence intervals.

Red-breasted Goose (*Branta ruficollis*). The most basal split in the genus *Anser* led to the Bar-headed Goose (*Anser indicus*). Next, two main clades can be recognised: the White Geese – Snow Goose (*Chen caerulescens*), Ross’ Goose (*Chen rossii*) and Emperor Goose (*Chen canagica*) – and the Grey Geese – Greylag Goose (*Anser anser*), Swan Goose (*Anser cygnoides*), the White-fronted Geese (*Anser albifrons* and *Anser erythropus*) and the Bean Goose complex (*Anser fabalis*, *Anser serrirostris* and *Anser brachyrhynchus*). The genus *Chen* is thus nested within the genus *Anser*, rendering *Anser* polyphyletic.

### Recommendation:

I recommend including the genus *Chen* in the genus *Anser*, leading to the following classification for *Anser*:

- species: *Anser fabalis* (Taiga Bean-Goose, Oie des moissons) A
- species: *Anser serrirostris* (Tundra Bean-Goose, Oie de la toundra) A
- species: *Anser brachyrhynchus* (Pink-footed Goose, Oie à bec court) A
- species: *Anser albifrons* (Greater White-fronted Goose, Oie rieuse)
- species: *Anser erythropus* (Lesser White-fronted Goose, Oie naine) A
- species: *Anser anser* (Graylag Goose, Oie cendrée) A
- species: *Anser canagicus* (Emperor Goose, Oie empereur)

- species: *Anser caerulescens* (Snow Goose, Oie des neiges)
- species: *Anser rossii* (Ross's Goose, Oie de Ross)

### Literature Cited:

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- Ruokonen, M., Kvist, L. & Lumme, J. 2000. Close relatedness between mitochondrial DNA from seven *Anser* goose species. *Journal of Evolutionary Biology*, **13**: 532-540.

**Submitted by:** Jente Ottenburghs, Resource Ecology Group, Wageningen University

**Proposal date:** 12 July 2016

**Transfer Blue-gray Noddy *Procelsterna cerulea* to the genus *Anous*****Background:**

The noddies are currently considered to belong to two genera: *Anous* Stephens 1826 for the dark-plumaged species *stolidus*, *tenuirostris*, and *minutus*, and *Procelsterna* Lafresnaye 1842 for the lighter-plumaged species *cerulea* and *albivitta* (Dickinson and Remsen 2013), an arrangement that has long been recognized (e.g., Peters 1934). Early editions of the Checklist only included members of the genus *Anous*, but with the expansion of the AOU area to include the Hawaiian Islands (AOU 1983), *cerulea* was added to the Checklist, and the NACC classification has since recognized three species of noddies in two genera:

*Anous stolidus* (Brown Noddy)

*Anous minutus* (Black Noddy)

*Procelsterna cerulea* (Blue-gray Noddy)

**New Information:**

Cibois et al. (2016) produced a molecular phylogeny of noddies using two mitochondrial and one nuclear loci. They sampled each of the five noddy species and included outgroup taxa from *Sterna*, *Thalasseus*, *Gygis*, and *Larus*. Combined multilocus analyses yielded strong support for a species-level topology with the five noddy species forming a clade and *Procelsterna* embedded within *Anous*. A mitochondrial-only analysis produced the same topology as the combined analysis, but the nuclear-only analysis yielded an unresolved topology.

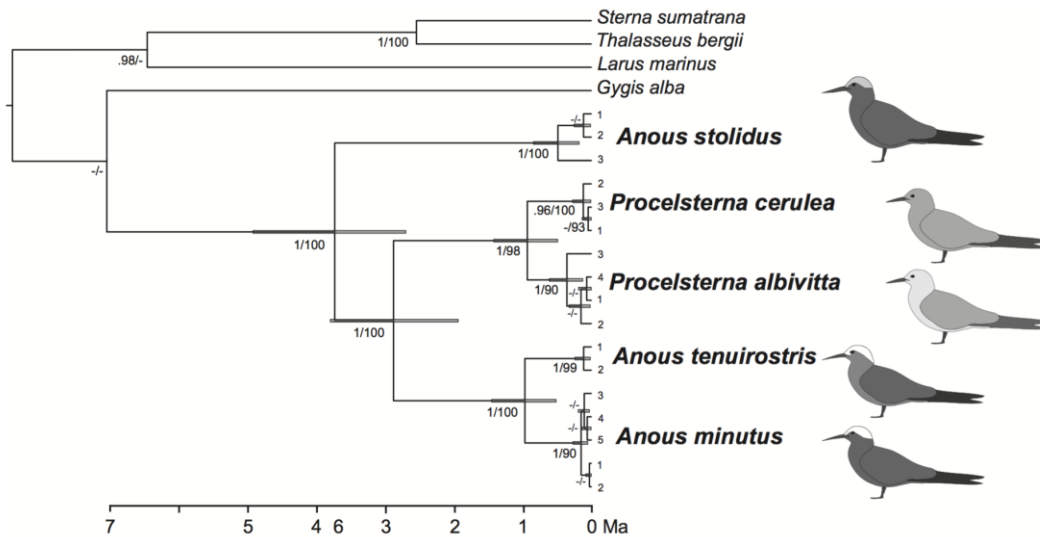


Figure 2 (combined multilocus BEAST analysis) from Cibois et al. (2016)

Cibois et al. (2016) recommended the following: "Based on our molecular phylogeny, we propose here to merge all noddies into the genus *Anous* Stephens 1826, and to consider *Procelsterna* Lafresnaye 1842 as a junior synonym. The alternative would be to retain the genus *Procelsterna* for the Grey and Blue Noddies and the genus *Anous* for the Brown Noddy (the type species), and to resurrect the genus *Megalopterus* Boie, 1826 for the Lesser and Black Noddies (type species *M. tenuirostris* Temminck, 1823). However, the morphological similarities of the five species provide strong support for a single genus that includes all noddies."

### Recommendation:

The tree topology here is driven primarily by the mitochondrial DNA signal. However, that signal is strong and the relevant tree splits are quite deep, which should reduce concerns that the mitochondrial gene tree might not reflect evolutionary history. Given the tree topology above, the taxonomic case for merging *Procelsterna* into *Anous* seems relatively straightforward. The specific epithet *cerulea* would change to *ceruleus* to match the masculine gender of *Anous*.

A YES vote is recommended.

### Literature Cited:

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- Peters, J. L. 1934. Check-list of birds of the world, vol. 2. Harvard University Press, Cambridge, Massachusetts.

**Submitted by:** David L. Slager, Department of Biology & Burke Museum of Natural History and Culture, Seattle, Washington, USA

**Proposal date:** 9 September 2016

**Split North American Red Crossbill *Loxia curvirostra* into two species****Background:**

Previously, a proposal (2009-A-10) was considered and rejected to recognize one “call type” or ecotype of North American Red Crossbill *Loxia curvirostra*, the South Hills crossbill *Loxia sinesciurus*, as a distinct species based on the results summarized in a paper in *The Condor* (Benkman et al. 2009). In short, this call type (Type 9) (1) is larger on average than other call types that occur regularly in the United States, (2) is sedentary and endemic to 70 km<sup>2</sup> of lodgepole pine *Pinus contorta latifolia* forest in the South Hills and Albion Mountains in southern Idaho, (3) differs in contact calls and songs from other, nomadic calls types that occur in the region, (4) shows limited evidence of genetic differentiation based on AFLPs, and (5) shows high levels of premating reproductive isolation (0.999 on a scale from 0 [random mating] to 1 [complete reproductive isolation]) despite sympatry with two other call types (Smith and Benkman 2007, Benkman et al. 2009). The measured frequency of hybridization was substantially lower than that found between Common Crossbills *L. curvirostra*, Scottish Crossbills *L. scotia*, and Parrot crossbills *L. pytyopsittacus* in Scotland (0.7% for South Hills crossbills vs. 3.8–5.4% for the three species in Scotland; Summers et al. 2007). However, criticisms of the proposal included the poor quality of the two type specimens and the need for a larger series (10 or more individuals), the uncertainty of the genetic results, and the absence of a proposal concerning the rest of the Red Crossbill complex.

Since 2009, we have collected and deposited in the Museum of Vertebrates, University of Wyoming, 10 South Hills crossbills with skins with their associated tissues and recordings of their contact calls. Genomic studies of over 18,000 SNPs provide evidence for monophyly and genetic distinctiveness of the South Hills crossbill in comparison to eight other call types in North America (Parchman et al. 2016), consistent with the high levels of premating reproductive isolation measured during six field seasons (Smith and Benkman 2007, Benkman et al. 2009).

**New Information:**

In September 2012, I assisted James Maley, who collected a series of 10 South Hills crossbills that are now in the collection at the Museum of Vertebrates, University of Wyoming (UWYMV 2854 through 2863), along with associated tissue samples and recordings of the contact calls of each individual. Digital recordings of the contact calls

of the two original type specimens of Type 9 have been deposited in the Museum of Vertebrate Zoology at UC Berkeley, where these two specimens were deposited.

The most compelling new evidence in support of recognizing the South Hills crossbill as a species is the genomic analysis of over 18,000 SNPs from 219 individuals of nine of the 10 'call types' in North America (Parchman et al. 2016 available online at the *Molecular Ecology* website: <http://onlinelibrary.wiley.com/doi/10.1111/mec.13825/full>; pdf also available if needed) revealing that the South Hills crossbill is monophyletic (Fig. 1) and the most distinct lineage within the North American Red Crossbill complex (Figs. 2 and 3; see Methods and Results in Parchman et al. [2016] for further details). Even though hybridization occurs infrequently between South Hills crossbills and types 2 and 5 (Smith and Benkman 2007, Benkman et al. 2009), there is little evidence of introgression between them (Figs. 2 & 3). No fixed differences were found between call types. However, the South Hills crossbill had more strongly differentiated loci ( $F_{st} > 0.8$ ) in comparisons to other call types, with the exception of Type 6 (Fig. 4); Type 6 is the Mexican crossbill *L. c. stricklandi* largely allopatric to other call types (Groth 1993). Given that types 2 and 5 occur in and move through the South Hills every year (up to 20% of the crossbills in the South Hills are Type 2 during summer; Smith and Benkman 2007) and some breed (Smith and Benkman 2007, Benkman et al. 2009), our results indicate long-term and strong reproductive isolation between the South Hills crossbill and other call types despite plenty of opportunities for gene flow.

Because evidence for monophyly is weak or absent for all the other call types (Figs. 1), I am hesitant to recommend species recognition for any call type other than the South Hills crossbill. However, a case could be made that the Mexican crossbill Type 6 *L. c. stricklandi* warrants species recognition (Figs. 1–4). Type 6 is distinctly larger than all the other New World call types (Groth 1993; see Fig. 2) including *L. c. mesamericana* from Central America (CWB, unpublished measurements of nearly all Latin American specimens in North American collections). Type 8 or the Newfoundland crossbill *L. c. percna* and *L. c. mesamericana* were not available to include in our analyses; we hope to include them in a subsequent study using DNA from specimen toe pads. One of my graduate students is measuring pre-mating reproductive isolation between types 2 and 5, which commonly breed sympatrically throughout much of the Rocky Mountains. During the last three years he has found that types 2 and 5 hybridize more frequently than do South Hills crossbills (levels of hybridization more similar to those found between crossbill species in Scotland; Summers et al. 2007), consistent with our genetic analyses (Figs. 2 and 3).



**Recommendation:**

I recommend a vote of YES for splitting the South Hills crossbill *Loxia sinesciurus* from the Red Crossbill *Loxia curvirostra* based on the genetic evidence (Parchman et al. 2016) combined with the high levels of premating reproductive isolation (Smith and Benkman 2007, Benkman et al. 2009) despite regular and likely long-term sympatric breeding of multiple call types of Red Crossbill.

**English Name:**

“South Hills Crossbill” has been the only English common name used in the literature beginning in 1999 (Benkman 1999). The South Hills is where over 80% of the population occurs (the rest occurs in the nearby Albion Mountains). An alternative English common name suggested in the review of proposal 2009-A-10 was “Cassia Crossbill” as Cassia County encompasses both the South Hills and Albion Mountains. “Latifolia Crossbill” was also mentioned, but this suffers the opposite problem that the name South Hills Crossbill faces. That is, this crossbill is coevolving with lodgepole pine within but a tiny fraction (<<1%) of the range of *Pinus contorta latifolia*. In addition, Type 5 is also strongly associated with *P. c. latifolia* (Benkman 1993, Groth 1993, Benkman and Miller 1996), but where red squirrels *Tamiasciurus hudsonicus* are present; red squirrels are absent from the South Hills and Albion Mountains, and hence the recommended name *L. sinesciurus*. Tradition is the main reason to prefer the name South Hills Crossbill. However, Cassia Crossbill is more accurate, more succinct, and less confusing (e.g., quite commonly and understandably others refer to the Black Hills instead of the South Hills when discussing this crossbill). If the Committee decides to accept the recommendation for a species split, then perhaps it would be an appropriate time to designate Cassia Crossbill as the English common name.

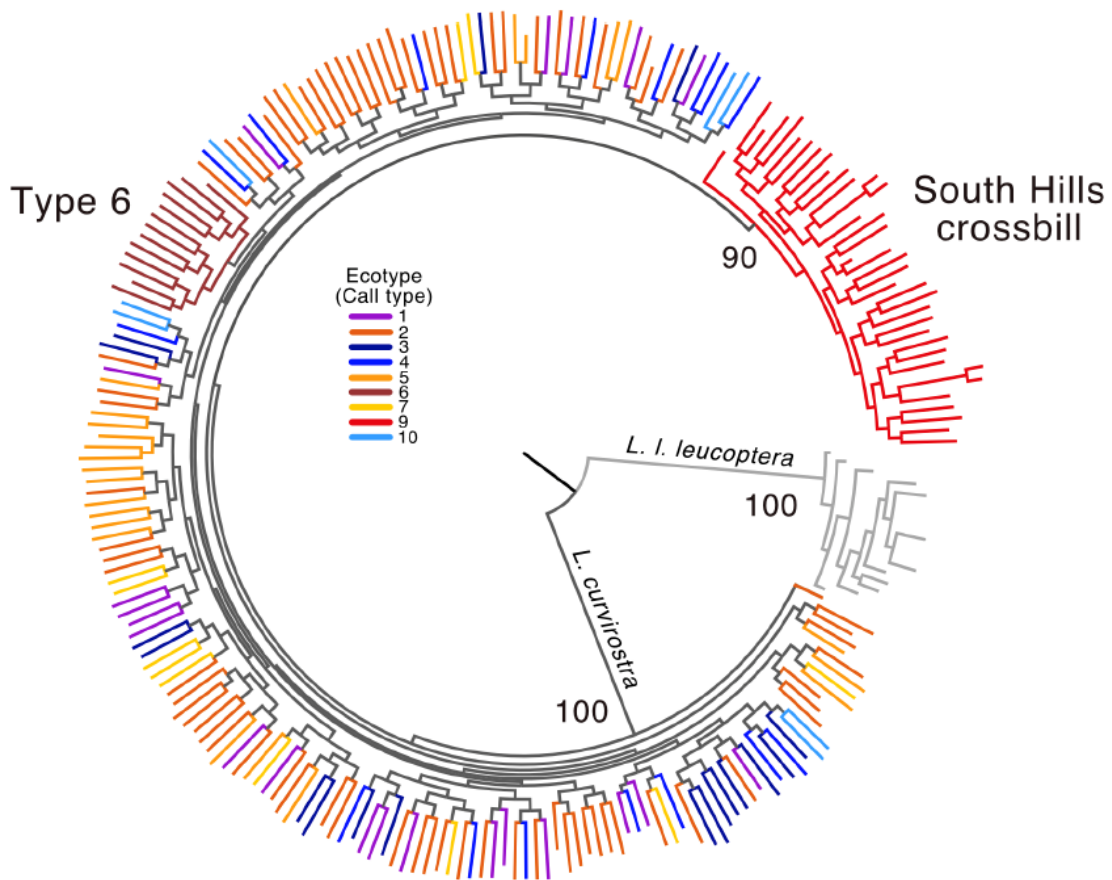


Figure 1. A maximum likelihood tree for the 219 Red Crossbills *Loxia curvirostra* and 12 White-winged Crossbills *L. l. leucoptera* based on 238,615 SNPs; the larger number of SNPs in this analysis than in the other analyses (e.g., Figs. 2 and 3) is the result of including White-winged Crossbills in this analysis but not in the other analyses. Bootstrap support values on the nodes are based on 500 bootstrap replicates, and are only shown for major nodes having >75% support; bootstrap support for monophyly of Type 6 was 10. Figure from Parchman et al. (2016).

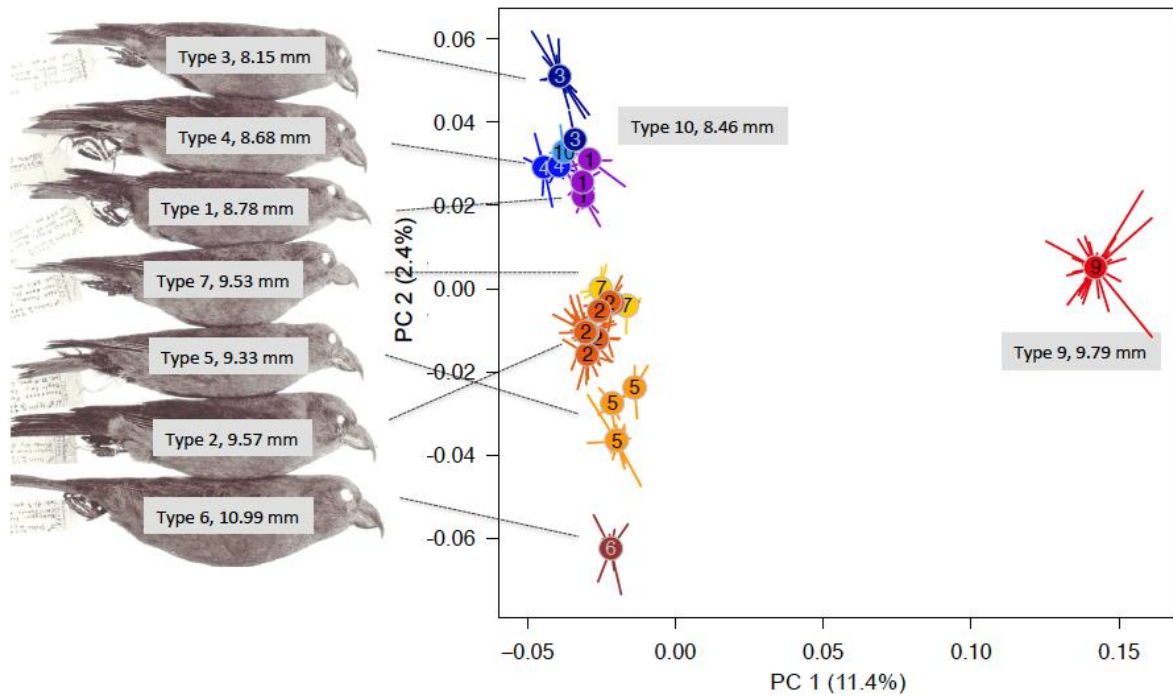


Figure 2. Genotypic variation (based on 18,385 SNPs) among individuals summarized by the first two principal components from a PCA of the matrix of genotype covariances between individuals. Lines connect individual PC values to the mean for each sampled population, with the mean represented by circles. Numbers and colors correspond to ecotypes (call types), and different geographically separated samples from a given ecotype have the same number and color. All geographically separate samples within an ecotype, with the exception of Type 7, overlap in PC1-PC2 space. To the left, are representative study skins and the corresponding mean beak depth of seven of the ecotypes (photograph from Groth 1993). Dotted lines connect the specimen images to their ecotype's mean PC values. Figure from Parchman et al. (2016).

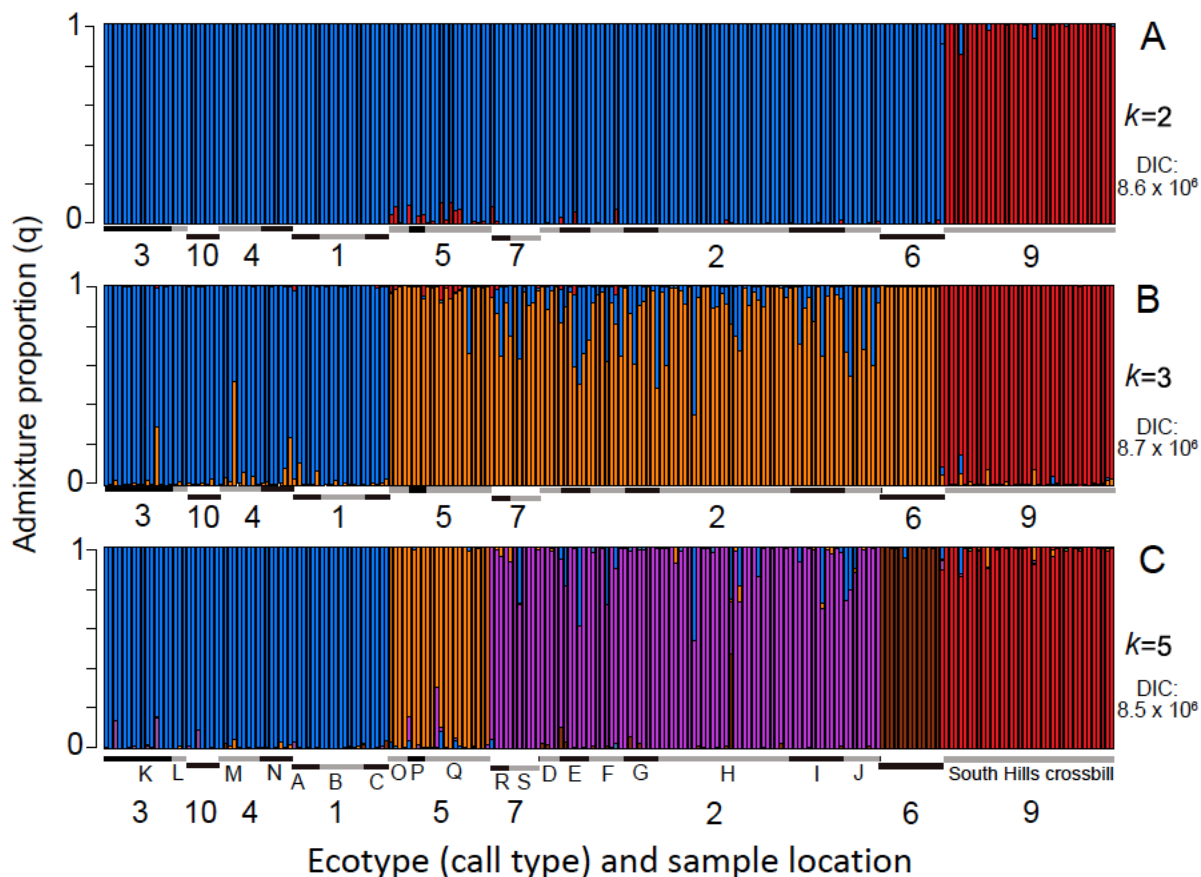


Figure 3. Admixture proportion estimates ( $q$ ) from the hierarchical Bayesian model implemented in entropy (Gompert et al. 2014), which is similar to the correlated allele frequency model of structure. Each vertical bar represents a bird, and bars are colored to reflect the posterior medians of each individual's admixture proportions for each of  $k$  clusters. Results with  $k$  equal to 2, 3, and 5 are shown. Numbers along the abscissa represent ecotype (call type), and letters for geographically separate populations. The gray and black bars indicate boundaries between population samples. Figure from Parchman et al. (2016).

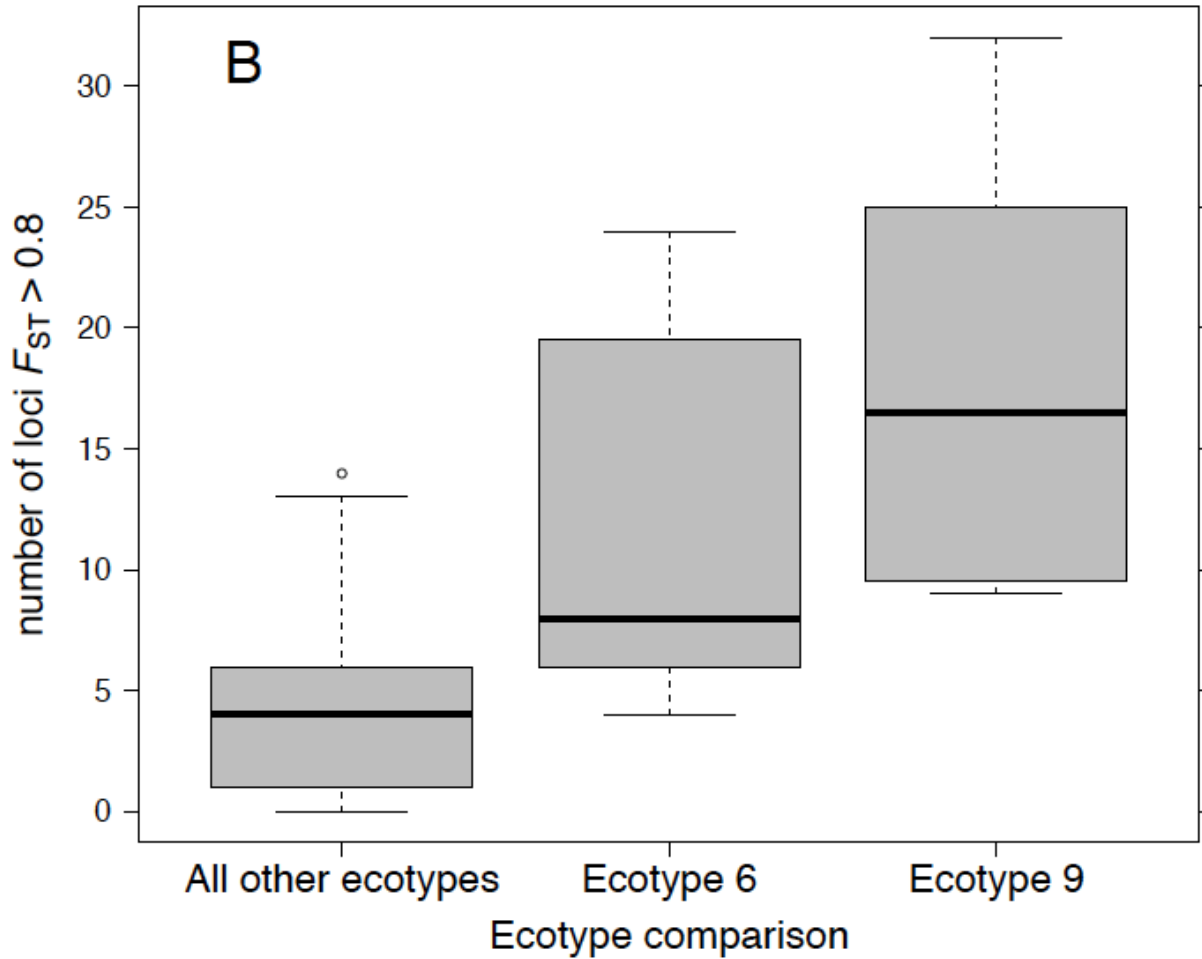


Fig. 4. Ecotypes (call types) 6 and 9 (Mexican and South Hills crossbills, respectively) have more numerous locus-specific  $F_{ST}$  estimates  $> 0.8$  (out of 18,385 loci) in comparison to pairwise estimates between the other ecotypes (ecotype 6 versus all others: Wilcoxon pairwise test,  $Z = 2.48$ ,  $P = 0.013$ ; ecotype 9 versus all others:  $Z = 3.57$ ,  $P = 0.0004$ ; ecotype 6 versus 9:  $Z = 0.16$ ,  $P = 0.16$ ; similar patterns were found for  $F_{ST} > 0.9$ , but are not shown). Figure from Parchman et al. (2016).

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**Submitted by:** Craig W. Benkman, University of Wyoming Department of Zoology and Physiology.

**Proposal date:** 16 September 2016

**Transfer Wilson's Phalarope *Phalaropus tricolor* to a monotypic genus,  
*Steganopus Vieillot 1818***

**Background:**

The AOU (1998) presently treats the three phalarope species in a single genus, *Phalaropus*. Some recent treatments have resurrected the monotypic genus *Steganopus* for Wilson's Phalarope (Livezey 2010, Del Hoyo and Collar 2014). This is a good case for revisiting the question "What is a genus?" It is a very slippery topic: it's like we think we know what a fish is, we can see fish, but it can be very difficult to solidly grab the fish we think we're grabbing in individual cases. Part of this is a discord between the historic concept of genera based on phenotype and phylogenetic trees based on molecular genetic data.

Although genera have historically been based on shared, derived morphological traits considered to be roughly genus-level in nature, the advent of genetic data has provided strong evidence of historical relationships largely independent of the effects of selection on phenotype. Integrating the two at the genus level, which has less definition than, for example, species limits, is difficult. In my view, we have yet to achieve either a convincing integration of the two types of data or an even-handed treatment of genus-level groupings across large groups of birds. Given the scope of the problem, we may not solve these issues soon. In the future, perhaps we'll have an across-Aves homologous molecular dataset that enables us to delineate chrono-clades roughly equivalent to today's phenotypically based genera and applicable across the class Aves. In the meantime, we are probably going to have to hand-wave about what we collectively think constitutes evidence for genus-level splits. The phalaropes represent a good case, involving an interesting history and just about every aspect of genus-level information one might wish.

Vieillot (1818) described *Steganopus* based on external phenotype. The AOU (1886) considered each phalarope species to warrant its own genus: *Crymophilus fulicarius*, *Phalaropus lobatus*, and *Steganopus tricolor*. AOU (1889) revised this, eliminating *Steganopus* by putting *tricolor* into *Phalaropus*. Given external morphology, this treatment is not without merit. The second edition of the *Check-list* (AOU 1895) retained this treatment, while the third (AOU 1910) reverted back to a three-genus stance: *Phalaropus fulicarius*, *Lobipes lobatus*, and *Steganopus tricolor*. Ridgway (1919) also used this treatment, which was retained by the AOU through the fifth edition (AOU 1957). In the sixth edition (AOU 1983), the three species were lumped into *Phalaropus*.

The most comprehensive molecular evidence to date indicates that this clade is monophyletic (Gibson & Baker 2012; Fig. 2 as included here). Based on his examination of skeletons, Livezey (2010), stated that the phalaropes were justifiably recognized as having two genera, with *Steganopus tricolor* being monotypic. Del Hoyo and Collar (2014:446) recognized the genus *Steganopus* and stated that it is “Sometimes subsumed within *Phalaropus*, but genetically distinct, and with several ecological and morphological differences; possibly quite close to *Tringa*.”

Personally, I am not fond of monotypic genera, and I lean toward solid morphological differences to define them rather than genetic distances or ecological characteristics, neither of which have played a prominent role in defining genera. I think we’d be mistaken at this time to start trying to implement a genus-level “chrono-clade,” and note that our present treatment relative to Gibson & Baker’s (2012) tree (Fig. 2 in this proposal) is consistent at the genus level with the phalaropes’ closest relatives. In short, we are treating each of four clades arising from an unresolved polytomy (at the top of the tree in the figure) as a genus: *Tringa*, *Actitis*, *Phalaropus*, and *Xenus*.

Given morphology and history, I’d either go back to a three-genus treatment (which I think suboptimal) or leave them in *Phalaropus*. Here are the options we should vote on (please vote yes on one of them; I recommend voting NO on the titular question and YES on C, maintaining the status quo):

- A) Resurrect *Steganopus* for *Phalaropus tricolor*.
- B) Return to historic recognition of three monotypic phalarope genera, *Phalaropus fulicarius*, *Lobipes lobatus*, and *Steganopus tricolor* (AOU 1910, 1957, Ridgway 1919).
- C) Maintain the status quo of the single genus *Phalaropus* for the three phalarope species.





Figure 1. a & B) Adult female specimens of *Phalaropus tricolor*, *P. lobatus*, and *P. fulicarius* (bottom to top). C) Some skeletal elements of each species, in the same order (left to right).

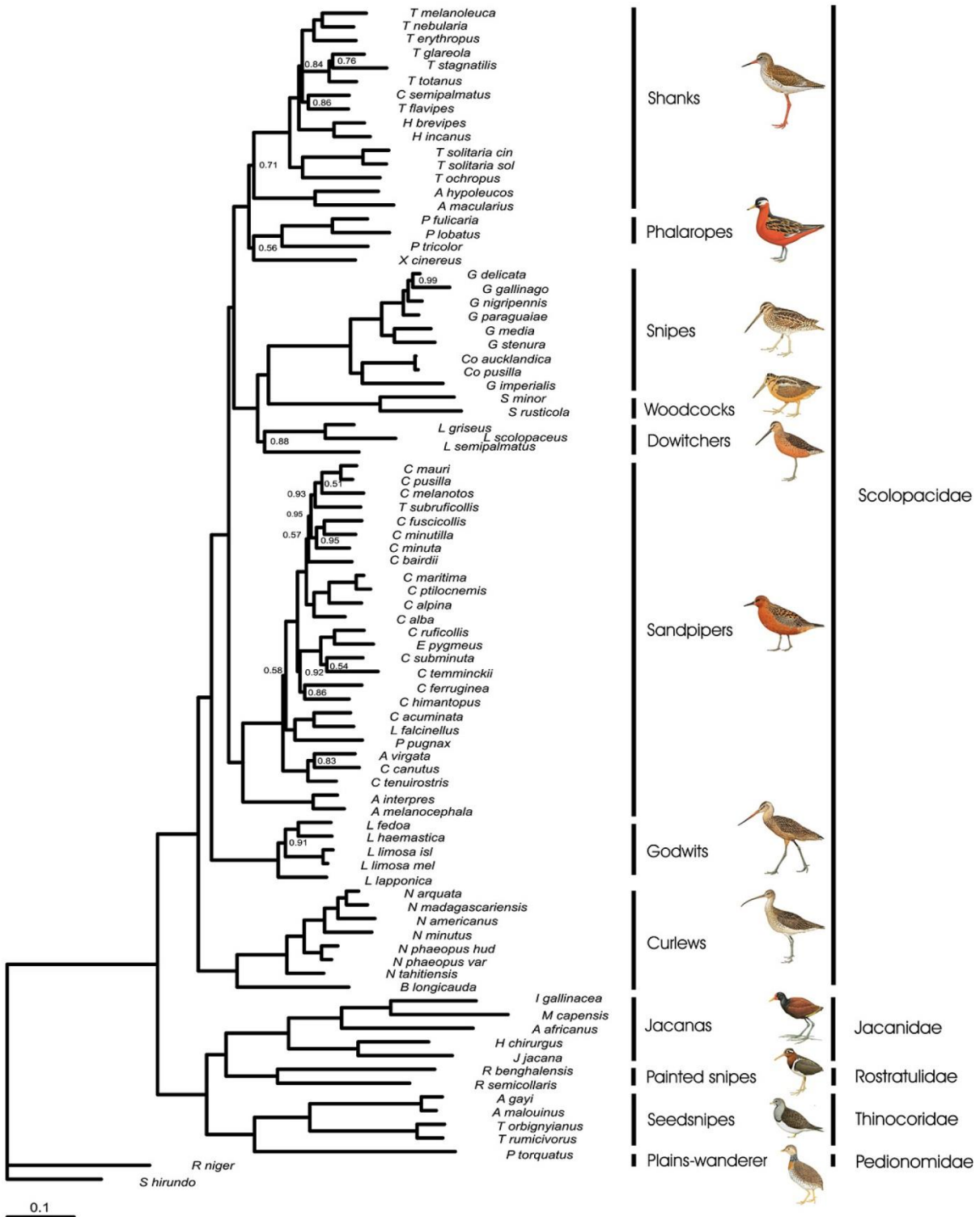


Fig. 1. Phylogeny based on sequences of five genes (RAG1, CYT B, 12S, ND2, and COI) estimated with partitioned Bayesian analysis for 84 species of the Scolopaci. All nodes received a posterior probability of 1.00 unless otherwise labeled.

Figure 2. Phylogenetic tree of the Scolopacidae from Gibson & Baker (2012), based on DNA sequence from five genes (from two loci) and partitioned Bayesian analysis.

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**Submitted by:** Kevin Winker

**Proposal date:** 3 November 2016

**Change the English name of the Ring-necked Duck *Aythya collaris***

I am writing today to bring to the attention of the committee an issue I believe is important for establishing continuity between the name of this species (currently the Ring-necked Duck) and its actual physical appearance and field markings. As a citizen scientist and wildlife educator, it is important for me to represent and present birds and other wildlife in a way that is easily understood and maintains consistency - both in bookwork and out in the field. I find the current name of this species, the Ring-necked Duck to be misleading. It leads observers to contrive a mental picture of a duck with a conspicuous 'ring' - clearly visible as a distinct field marking, such as is the case for the ground bird species known as the 'Ring-necked Pheasant'. On the contrary, this species' 'ring' is very inconspicuous and not often seen, making it very difficult to call it a distinctly noticeable feature useful for identification. As you know, the virtually unnoticeable 'ring' referred to in this instance is a slightly lighter 'brownish collar' on the neck, which occurs in the drake alone.

In an era in which birding is becoming an ever more popular form of recreation, I think it is important to make bird identification simple and accessible for birders of all skill level - beginners, intermediate and experienced alike. For that reason, I propose changing the English common name of the 'Ring-necked Duck' to the 'Ring-billed Duck' - which I feel is a far more accurate description of this species. Both the hen and the drake exhibit very conspicuous white rings on their bills.

My attention was drawn to this issue by an article on the Audubon website by Peter Cashwell, in which he makes a very valid point..."Luckily, there is a clear and obvious field mark on both the drake and the hen: a white band circling the blue-gray bill, one so easily discerned that hunters have already adopted the nickname "Ringbill" for the bird." (<http://www.audubon.org/news/its-time-rename-ring-necked-duck>)

Since sportsmen already call this species by a more appropriate name - shouldn't we as the birding community have the benefit of the same? Peter Cashwell stresses that names in science are used as tools to describe something - and he closes by saying, among other things, "You can give us the tool we need." And I would add, by officially changing the name of the Ring-necked Duck to the Ring-billed Duck, you would be doing a great service the birding community as a whole, now and for future generations of birders to come from us.

In addition to the main article cited in my proposal, here are a few other articles for your consideration, to be used as literature in further discussion about renaming this species:

"Ringbill" is the name hunters have given this diving duck of forested ponds and bogs, because the two white rings on its bill are much more visible than its brownish collar." - Oklahoma Department of Wildlife Conservation

(<http://www.wildlifedepartment.com/wildlifemgmt/species/ringneck.htm> )

"The cinnamon neck ring is usually difficult to observe, which is why the bird is sometimes referred to as a "ringbill"." - Wikipedia article "Ring-necked Duck"

([https://en.wikipedia.org/wiki/Ring-necked\\_duck](https://en.wikipedia.org/wiki/Ring-necked_duck) )

"The "ringneck" name is derived from a faint brownish ring around the base of the neck, which is visible only upon close inspection." - Ducks Unlimited

(<http://www.ducks.org/hunting/waterfowl-id/ring-necked-duck> )

Thank you so much for your consideration of my proposal. I would be honored to be a small part of making a difference in the field of ornithology in this way.

**Submitted by:** Jessi Wasell, Owner of Wasell Gardens ([www.wasellgardens.com](http://www.wasellgardens.com))

**Proposal date:** 7 November 2016

**Transfer (a) Intermediate Egret *Mesophoyx intermedia* and  
(b) Cattle Egret *Bubulcus ibis* to *Ardea***

**Background:**

We currently include five species from the NACC area in the genus *Ardea*: Great Blue Heron *A. herodias*, Cooi Heron *A. cocoi*, Great Egret *A. alba*, and two accidentals, Gray Heron *A. cinerea* and Purple Heron *A. purpurea*. Intermediate Egret *Mesophoyx intermedia*, an accidental species transferred to the main list in Supplement 48 (Banks et al. 2007), and Cattle Egret *Bubulcus ibis* are currently placed in monotypic genera, *Mesophoyx* following *Ardea* in our linear sequence and *Bubulcus* following *Egretta*. Both species have been considered taxonomically problematic: the Intermediate Egret has been considered to share characters with both *Ardea* and *Egretta*, whereas uncertainty in relationships of the Cattle Egret has largely resulted from its morphological adaptations to a terrestrial mode of foraging (Kushlan and Hancock 2005).

**New Information:**

Several molecular phylogenetic trees of the Ardeidae have been published over the past 30 years. The various papers of Sheldon and colleagues (Sheldon 1987a, b; Sheldon et al 1995; Sheldon et al 2000), which were based largely on DNA-DNA hybridization but later included sequences of the mitochondrial gene cytochrome-b, sampled 13-28 species; Sheldon 1987a included both *Bubulcus* and *Mesophoyx*. Other recent studies have also included *Bubulcus* and *Mesophoyx*. These studies have been based either on sequences of single mitochondrial genes, such as Chang et al (2003; phylogeny of 14 species based on 12S sequences) and Huang et al (2015; barcode tree of 32 species based on CO1 sequences), or on complete mitochondrial genomes (Zhou et al 2014; phylogeny of 16 species).

Complete trees or relevant parts of trees are shown below. Note that Great Egret *A. alba* is listed in the trees below as *Casmerodius albus*, *Egretta alba*, or *Ardea modestus* (the “Eastern Great Egret”):

Sheldon 1987a:

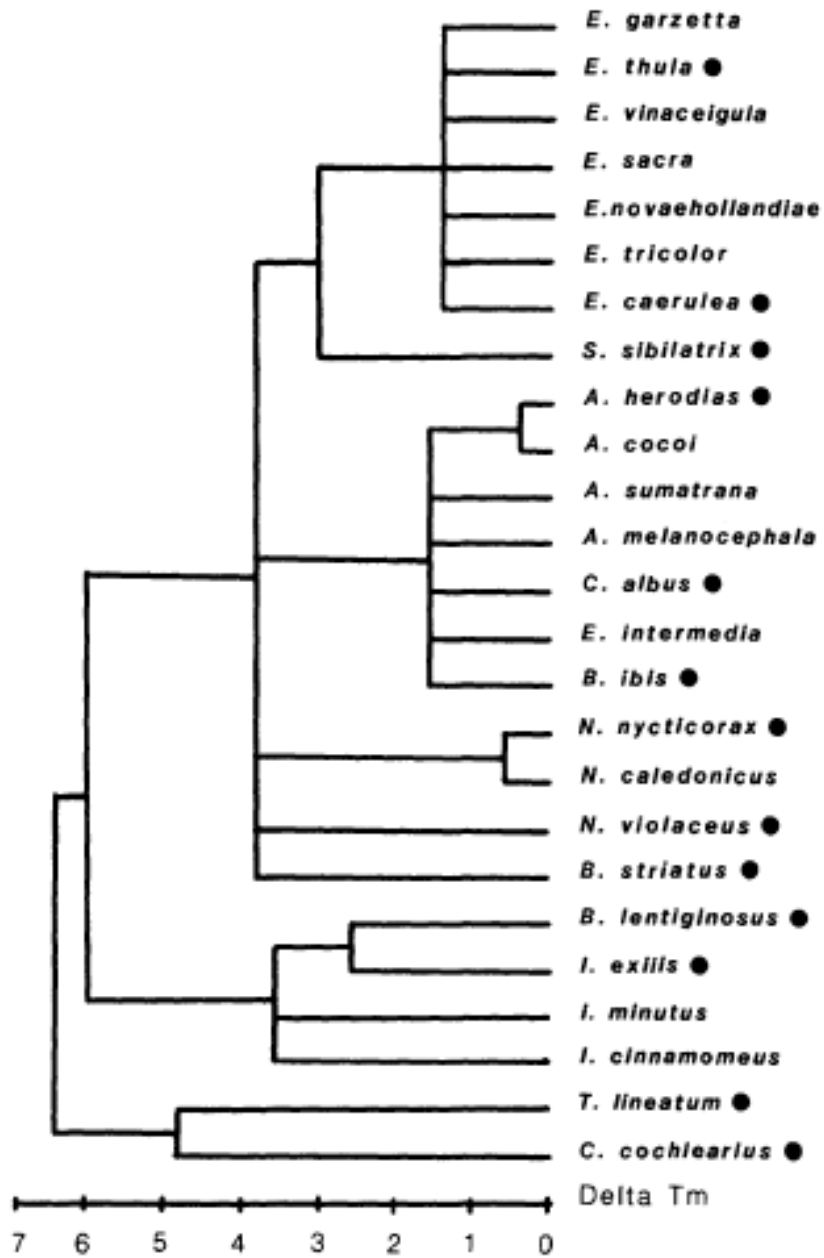
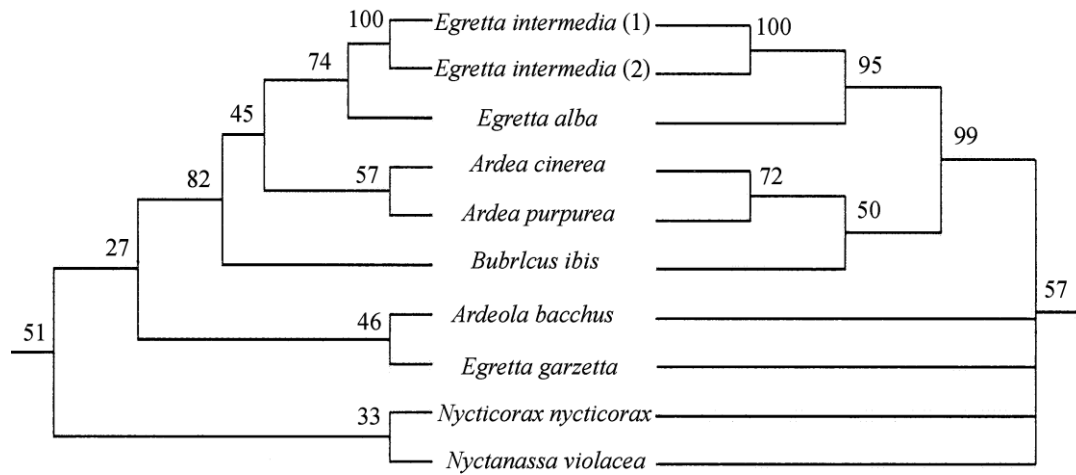


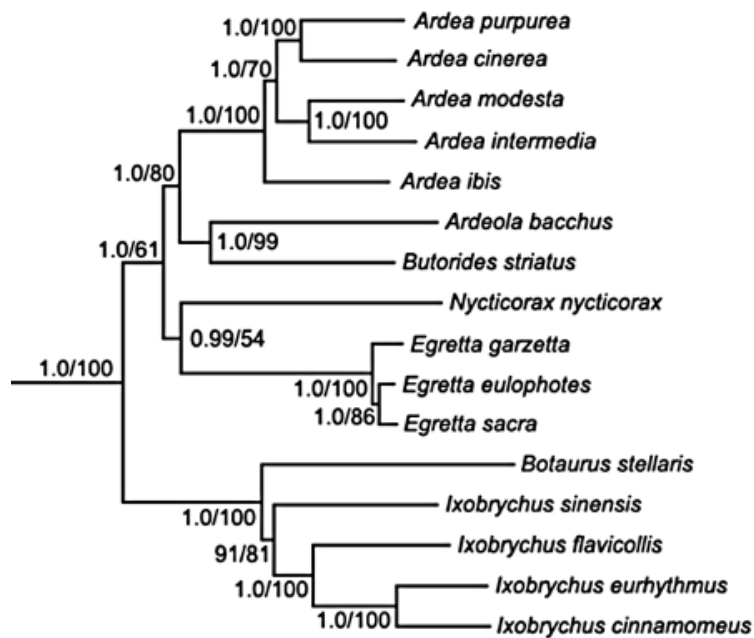
Figure 1. Phylogeny based on DNA-DNA hybridization data.

Chang et al 2003:



**Fig. 2.** The maximum parsimony tree (left) and neighbor-joining tree (right) resulting from analysis of the 12S rRNA gene sequences of Ardeidae.

Zhou et al 2014:



**Figure 3.** Phylogenetic relationships, based on complete mitochondrial genomes, among the sequenced ardeid birds. Numbers at the nodes are Bayesian posterior probabilities (left) and ML bootstrap percentages (right).



Finally, the barcode tree of Huang et al (2015), which includes excellent taxon sampling but poor resolution of interspecific relationships, can be accessed at <http://www.geneticsmr.com/year2016/vol15-3/pdf/8270-su2.pdf>

### **Recommendation:**

Transferring *M. intermedia* to *Ardea* seems like an easy YES. In the two better-resolved mtDNA phylogenies in which it was included (Zhou et al 2014 and Chang et al 2003), it is sister to *Ardea alba/modestus* and embedded within *Ardea*. Thus, a change should be made for reasons of monophyly. Bootstrap support for the sister relationship with *alba/modestus* was 100% in the mt genome study of Zhou et al and 74% in Chang et al. In the barcode study (Huang et al 2015), *M. intermedia* was sister to *Ardea alba + Bubulcus ibis*, and this clade was sister to the rest of *Ardea*, but there was little support for these relationships. The DNA hybridization tree in Sheldon 1987a included *intermedia* in a clade of seven species, all of which are now in *Ardea* except for *M. intermedia* and *B. ibis*. The transfer of *intermedia* to *Ardea* has already been accepted by such references as Kushlan and Hancock (2005), Dickinson and Remsen (2013), and Gill and Donsker (2016).

The proposed transfer of *B. ibis* to *Ardea* is more nuanced, but should also be considered. This species formed a polytomy with six other species (all now in *Ardea* if the transfer of *M. intermedia* is approved) in the DNA hybridization tree of Sheldon (1987a), but a cytochrome-b tree including three of these species (Sheldon et al 2000) resolved *B. ibis* as sister to *A. alba* and *A. herodias*. Likewise, *B. ibis* was sister to the clade of *Ardea* species in both Zhou et al. (2014) and Chang et al (2003). Thus, *ibis* could be retained in *Bubulcus* and this would be in keeping with the topology of the trees. The internode distance between the clade of *Ardea* species and the clade of *Ardea + B. ibis* is short, however, especially in the mt genomes tree (Zhou et al 2014), and in both phylogenies the bootstrap support for *Ardea + B. ibis* is stronger than that for *Ardea* without *B. ibis* (100% vs. 70% in Zhou et al, 82% vs. 45% in Chang et al). Based on their phylogeny, Zhou et al (2014) considered *ibis* to be part of *Ardea*, as had Kushlan and Hancock (2005), based solely on the 12S phylogeny in Chang et al (2003). Dickinson and Remsen (2013) did not make this transfer, but the mt genomes paper (Zhou et al 2014) had not yet been published and was not available for them to consider (although Gill and Donsker 2016 have not made this transfer, either). The complete mt genomes seemingly make a much stronger case than the 12S data (Chang et al 2003) that persuaded Kushlan and Hancock, and would suggest that *B. ibis*, in addition to *M. intermedia*, be transferred to *Ardea*. However, this is a judgment call, and a good case can also be made for keeping *Bubulcus* in view of the distinctive morphological adaptations and behavior of the Cattle Egret, and the fact that the topologies of the

trees do not require this change for reasons of monophyly. A UCE-based phylogeny of the herons and egrets is in the works (F. Sheldon, pers. comm.), so I would suggest voting NO on moving Cattle Egret from *Bubulcus* to *Ardea* until those results are in. If necessary, we can revisit this issue later when more data are in hand.

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**Submitted by:** Terry Chesser

**Proposal date:** 9 November 2016

## Revisit the proposed split of *Circus cyaneus* and *Circus hudsonius*

### Background:

In 2015 the committee considered but narrowly rejected (by seven votes to five) a proposal (2015-C-9) to split *Circus cyaneus* and *C. hudsonius*, the latter currently considered a subspecies of the former. (For convenience the 2015 proposal is appended to this one, followed by committee votes and comments.) The primary basis behind some committee members' rejection of the split was the weak genetic sampling coupled with the relatively low genetic divergence (1.1–1.7). Another objection was the lack of demonstrated vocal differences.

### New Information:

Etherington and Mobley (2016) compared *cyaneus* and *hudsonius* in DNA, plumage, measurements, and ecology, and recommended on these bases that they should be considered separate species. These authors sequenced a few new samples of cyt b (8 frozen tissues of *hudsonius* and 3 toepads of *cyaneus*), and used GenBank samples of COI from bar-coding (4 *hudsonius*, 7 *cyaneus*) and Oatley et al.'s (2015) ND1 sequences for further analyses. They found in each of their analyses that *cyaneus* and *hudsonius* form monophyletic clades. They also found genetic distances ranging from 1.3–1.8% between the two taxa. They noted that in several other cases genetic distance between undisputed species-pairs of raptors is in this range, well below 2%.

The morphological data presented by Etherington and Mobley (2016) confirm that, sex-for-sex, *hudsonius* is larger than *cyaneus*. They review the sexual and age-related differences between the taxa, noting that adult males differ by 13 morphological characters, females by about four, and juveniles by three or more.

In the discussion, Etherington and Mobley (2016) note “numerous differences between *cyaneus* and *hudsonius* when it comes to vocalization, habitat, distribution and movements, mate choice and breeding biology”, and yet their vocal analysis is limited to two paragraphs summarizing characteristics of sonagrams in the Western Palearctic handbook (Cramp and Simmons 1980) and the BNA account (MacWhirter and Bildstein 1996); no mention is made of online resources nor commercial CDs. They conclude based on this tiny sample that the taxa differ vocally in that *cyaneus* gives *kek* calls at a faster rate than does *hudsonius*, both in male and female distress calls.

Etherington and Mobley (2016) then compare life-history information extracted from the literature. They argue that *hudsonius* is a bird of wetlands, prairies, dry grasslands, and agricultural areas, while *cyaneus* breeds in heather moorland, sand dunes, young coniferous forest, sedge-rich northern lakes, and woodland (both open- and closed-canopy). (Note that Old World marsh habitat is typically occupied by the larger marsh harriers.) Although *cyaneus* breeds at least mostly in dry upland habitats, *hudsonius* typically breeds among reedbeds in marshes, even constructing platforms that raise the nest above the water level. Other life-history comparisons given by these authors include that in *cyaneus* females have been recorded as displaying much more than males, while the reverse has been found in *hudsonius*; and that female *hudsonius* have been recorded as being much more capable of successfully raising young successfully after desertion by the male than is *cyaneus*. Despite the statement quoted in the previous paragraph, data are not presented on differences in mate choice, and the differences discussed in distribution and migratory route provide no data relevant to species status.

**Subsequent treatments:** As far as I am aware, AOU-CLC is the only major relevant avian taxonomic entity that has yet to adopt this split.

**Effect on AOU-CLC area:** As stated in the 2015 proposal, if this proposal passes we would need a new species account for *cyaneus* (pending verification of the single Attu wing specimen at UAM), and *C. c. hudsonius* would be considered specifically distinct but would not necessarily require an English name change.

### **Recommendations:**

Etherington and Mobley (2016) provide further evidence that *cyaneus* and *hudsonius* are discrete lineages with differing breeding habitats and possibly with behavioral differences. The vocal differences alluded to therein simply do not hold up, however—I reexamined the recordings from commercial CDs that led to our conclusion in Rasmussen and Anderton (2005) that vocalizations are broadly similar (mainly Roché 1996 and Chappuis 2000) for *cyaneus*, and compared these and the few for *cyaneus* on xeno-canto with the now-extensive sample for *hudsonius* from several sources. This expanded sample shows that there is complete overlap in rate of *kek* calls, and I can hear no intertaxon differences in quality of these or the other main vocalization type, the more prolonged mewing calls. That is not to say that careful study of homologous display sounds would not turn up differences, but these must be subtle at best. Since many diurnal raptors lack obvious vocal differences, especially among those (like harriers) that tend to be fairly quiet, I don't think this is particularly consequential. (Note

the dearth of recordings of *cyaneus* even on xeno-canto, and a total lack thereof on Macaulay Library and IBC sites—surprising for a widely distributed Palearctic species.)

However, these taxa are well-differentiated morphologically, more so than most other Holarctic-distributed species (e.g. races of Golden Eagle, Rough-legged Hawk, Common Raven, Greater Scaup, and Common Goldeneye, for example). I've thought them better treated as separate species for a couple of decades now, ever since preparing materials for our book. In retrospect I think that my quote from Oberholser in the original proposal may have led some to be swayed by his viewpoint, which was probably based on examination of specimens with folded wings, and thus not a full accounting of the prominent differences, especially in adult males.

Please vote on (1), and if your vote is yes, also vote on (2):

(1) I recommend splitting *Circus hudsonius* from *C. cyaneus*.

(2) If split, I recommend continuing to use the name Northern Harrier for *C. hudsonius* (rationale given in original proposal, below).

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**Submitted by:** Pam Rasmussen, Michigan State University

**Proposal date:** 13 November 2016

### **Split *Circus cyaneus* and *Circus hudsonius***

#### **Background:**

The Hen Harrier *Circus cyaneus* was long treated as an exclusively Palearctic species, with the Northern Harrier (formerly Marsh Hawk) *C. c. hudsonius* as a full species in the Nearctic, until Hartert (1914), who did not provide any explicit justification beyond brief comparisons, treated *hudsonius* as a subspecies of *cyaneus*. [There was however a much earlier period during which several ornithological works treated *hudsonius* as conspecific with or a variety of *cyaneus*, e.g. Wilson and Bonaparte (1831) and Coues (1877).] Hartert's (1914) treatment was evaluated by Oberholser (1919), who stated "An examination of a large series of both these birds has been made with the object of determining the desirability of this change, with the following result...All the characters that separate *Circus hudsonius* from *Circus cyaneus* are clearly but average, with the exception of the spots on the posterior under surface, which appear to be nearly, if not quite, always present to a greater or less extent in the former bird. There are, however, occasional specimens of *Circus hudsonius*, which in this respect so closely approach the unspotted condition of *Circus cyaneus*, and some of *Circus cyaneus* so much like *Circus hudsonius*, that a trinomial designation best serves to express the relationship now existing between the two birds. This is apparently one of those cases of a subspecies which is in about the last stages of complete specific segregation, and which in the course of time will be entirely distinct. At present, however, our Marsh Hawk should probably stand as *Circus cyaneus hudsonius* (Linnaeus)." Nevertheless, for another decade the AOU continued to treat *hudsonius* as a separate species in the 4<sup>th</sup> edition (1931), but that same year it was lumped into *cyaneus* by Peters (1931), without elaboration, and this change was then accepted in the AOU's 19<sup>th</sup> supplement (according to Avibase).

Since then, the subspecific status of *hudsonius* has been universally accepted until recently. However, the fact that immatures of both sexes and adult male *hudsonius* is (typically) diagnosably distinct from *cyaneus* in plumage, and that *hudsonius* appears in Britain and Ireland as a rare vagrant (BBRC 2015) has led to considerable discussion of the plumage differences and taxonomy of these taxa (e.g., Grant 1983, Thorpe 1988, Dobson and Clarke 2011). The taxonomic treatment of the Cinereous Harrier *Circus cinereus* as a full species has, by contrast, remained relatively stable and

uncontroversial, although, along with *hudsonius*, it was treated as a variety of *cyaneus* (Coues 1877).

### **New Information:**

Wink et al. (1998) considered that their molecular results indicated that *C. cyaneus* and *hudsonius* (written as *hudsoni* [sic] in the Abstract and text, and *hydsoni* [sic] in Fig. 5b) have reached species level (according to the Abstract), while the text states that *hudsonius* “is already well separated” from *cyaneus* and “might represent a distinct species”. In a follow-up paper, Wink and Sauer-Gürth (2004) found 1.7% sequence divergence between *cyaneus* and *hudsonius*, which were sister species in their phylogeny, whereas *C. cinereus* was distantly related to this pair, but closely related to *C. maurus* of South Africa.

A new paper by Oatley et al. (2015) used sequences of one mitochondrial and three nuclear loci of all species and subspecies of the genus *Circus* (the first such comprehensive molecular phylogeny for the group). They found slightly lower (1.1%) sequence divergence between *cyaneus* and *hudsonius*, but *contra* the Wink and Sauer-Gürth (2004) study, they recovered a sister relationship between *hudsonius* and *cinereus*, with *cyaneus* being sister to this clade. This result, which is better supported than in the Wink papers, implies that *hudsonius* and *cyaneus* should not be considered conspecific unless *cinereus* is included as well. The specific distinctness of *cinereus* has not been controversial, and it is well-differentiated in plumage (primarily in the heavily dark-banded underparts of both sexes as opposed to lightly chestnut-spotted underparts in male *hudsonius* and unspotted white underparts in male *cyaneus*; females of neither *hudsonius* nor *cyaneus* are banded below). Vocally all three taxa appear to be very similar, based on limited study (Rasmussen and Anderton 2005 compared *hudsonius* and *cyaneus*; xeno-canto was consulted for recordings of *cinereus*).

All three taxa are strictly allopatric in the breeding season, although the breeding ranges of *cyaneus* (east to eastern Siberia) and *hudsonius* (west to western Alaska) do approach each other. They are also allopatric in the non-breeding season, and vagrants tend to be first-winter birds.

**Subsequent treatments:** Several recent authors (Simmons 2000; Ferguson-Lees and Christie 2001; Rasmussen and Anderton 2005; Brazil 2009; del Hoyo and Collar 2014; Gill and Donsker 2015) have split or followed others in splitting *hudsonius*. Dickinson and Remsen (2013) maintained *hudsonius* as a subspecies of *C. cyaneus*, stating that *hudsonius* may merit treatment as a separate species.

**Effect on AOU-CLC area:** Acceptance of the proposed split would result in a different specific name being used for one species (*hudsonius*), along with a more limited range statement. It would also result in the necessity of a new species account for *C. cyaneus sensu*. A partial salvaged specimen (distal right wing only; UAM 9062) from Attu, June 1999, was identified on wing chord length as a juvenile male *C. c. cyaneus* (Gibson et al. 2013). If the split of *hudsonius* is accepted, this is the first (only?) specimen evidence for the species *C. cyaneus sensu stricto* from North America. Given the importance of this record, its identity should be verified.

*Circus [cyaneus] hudsonius* has been recorded extraliminally in Britain and Ireland, where all the older records have been considered doubtful but a few new ones accepted (BBRC 2015); it has also been recorded in Japan (mainly Hokkaido; Brazil 2009).

The English name need not be affected, as Northern Harrier has never been widely accepted for the Hen Harrier (but some confusion would certainly ensue anyway if it continues to be used only for *hudsonius* in the event of a split). There is no good, obvious, well-established alternative name—Marsh Hawk doesn't indicate generic relationships, and it courts confusion with the marsh harriers, which are not closely related.

#### **Recommendations:**

- (1) I recommend splitting *Circus hudsonius* from *C. cyaneus*, although the evidence is not unequivocal.
- (2) If split, I recommend continuing to use the name Northern Harrier for *C. hudsonius*.

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**Submitted by:** Pam Rasmussen, Michigan State University

**Proposal date:** 21 March 2015

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**votes on 2015-C-9:**

**Split Northern Harrier *Circus hudsonius* from Hen Harrier *Circus cyaneus***

**YES** - 4 without comment.

**NO.** I would like to be convinced but cannot quite make it.

**NO.** It could be that these are separate species, but the sampling includes only 1 *cinereus*, 2 *cyaneus*, and 4 *hudsonius*. The limited sampling, combined with the minor plumage differences and lack of known vocal differences, suggests to me that we should wait for more data (more samples and more genes) before splitting these taxa.

**NO.** Molecular data that are the basis for this proposal are highly equivocal.

**YES.** In my view, it is acceptable that species-level taxonomy can include non-monophyletic taxa (e.g., Common /Green-winged Teal or New World ravens). So, the result that *hudsonius* is closer to *cinereus* than *cyaneus* does not weigh heavily. The question of import is whether *hudsonius* and *cyaneus* are differentiated enough to be reproductively isolated. The clade with these taxa in question also includes *assimilis*, *maurus*, and *macrourus* ("steppe harriers"). All are allopatric except *macrourus* and *cyaneus* (s.s.). All, except the all dark *maurus*, seem to be similar morphologically and in plumage, with gray males, some with various amounts of rufous markings. Though in different parts of the clade *macrourus* and *cyaneus* (s.s.) look fairly similar, yet are broadly sympatric in eastern Europe and west Asia. I therefore feel that the level of differentiation between *cyaneus* and *hudsonius* is sufficient for reproductive isolation.

**NO.** This is a rather small number of loci for an accurate species tree at this level of divergence, so I put more stock in the phenotypic evidence; it looks like phenotypically the taxa fit the subspecies concept better. Even if the tree is accurate, within-species paraphyly should not be in and of itself a determiner of species limits.

**YES.** Not the strongest case, but the plumage differences in adult males and juveniles between the two taxa are generally pronounced, to the degree where they really do look like what we normally call different species, unless we have good reasons not to. Without larger samples and further study, the vocal resemblances noted between taxa in one call type may not mean much, because harriers have fairly extensive vocal repertoires and I doubt if the other call types have been carefully compared. Although atypical individuals of these taxa do resemble each other in some aspects of plumage, that is a pretty common situation between different species—within-species variation is the norm. And, why recognize paraphyletic species when we have a ready alternative? What is the justification for recognizing *cinereus* as a species but not *hudsonius*? I don't think there is any, other than stability, which is a dubious reason since many sources already recognize *hudsonius* as a species.

Note that Hartert wrote almost nothing to justify his lumping; it was Oberholser who provided the later justification cited in the proposal.

**NO.** Although the authors presented a species tree vs. gene tree analyses, it's not clear to me whether or not the *hudsonius+cinereus* (aka "*cinereus*" on p. 155) is driven entirely by ND1 (Fig. 1). The "species tree" in Fig. 2 shows the same branching pattern, but the branch lengths between *cyaneus* and *cinereus* are microscopic (literally), and no support value is presented for the node "L" that joins them (it may be in text but I can't find it). What I need to know from the experts is whether enough variable loci have been sampled to have confidence in their species tree.

The authors also attempt to argue that genetic distance also favors species rank for *hudsonius*: "The subspecies relationship between *C. c. cyaneus* and *C. c. hudsonius* has been previously questioned (Simmons et al., 1987; Johnsen et al., 2010; Dobson and Clark, 2011), while 1.7% mtDNA sequence divergence has also provided evidence of these taxa being distinct species (Wink and Sauer-Gürth, 2004). The level of mtDNA divergence between these two taxa presented here is slightly lower (1.1%) than in previous work, likely due to the fact that we sequenced a different mitochondrial locus."

However, those who lost souls who try to use genetic distance as a metric for species rank typically use 2% as the cutoff. It is clear that these three *Circus* are weakly differentiated in terms of mtDNA, much less so than many bird taxa treated as subspecies. What stands out in this case is that the breeding range of *hudsonius* comes no closer than roughly 1000 km to that of *cyaneus* or roughly 3000 km to that of *cinereus* despite this low level of genetic differentiation. In fact, I wonder if a plausible case could be made for conspecific treatment of all three? On the other hand, the "marsh harrier" branch of *Circus* shows even lower genetic distances among taxa traditionally ranked as species (*ranivorus* and *aeruginosus*, and *approximans*, *spilonotus*, *maillardi*), so perhaps that is the rationale that the authors were using, although unstated?

Regardless of the branching pattern, I'm fine with "paraphyletic" species in such weakly differentiated taxa in part because the term "monophyly" is problematic with recently diverged populations (as noted by Hennig, for example). Pending responses to queries above, I would prefer to wait for a larger array of genes before declaring broad *C. cyaneus* to be paraphyletic and before making a decision on taxon rank. What Hartert wrote makes sense to me. The minor differences in plumages between *cyaneus* and *hudsonius* are expected in such disjunct populations of a single species – I am not impressed. For example, Red-tailed Hawk populations as much plumage variation, with no hint at interruption of gene flow, than do these harriers. In general, plumage variation in accipitrids would seem to be a risky criterion for species limits given well-known individual, geographic, age, and sex variation in plumage characters. The lack of any vocal differences is also worrisome (unless sympatric harrier spp. also all sound the same). Our *hudsonius* has courtship vocalizations, and so a comparison among *Circus* species would be enlightening.

**YES.** I think the proposal is well-crafted and the question might be better raised is why were these two lumped in the first place? I haven't looked at Hartert's works carefully, but my initial biased thoughts (his lumping of Asian White-winged Scoter in 1914, a separate work from the one cited here on the harrier lumping, seemed to be the death knell for treating that taxon as a separate species) is that he was a lumper.

To my eye, and my field experience is limited to only a few sightings of nominate *cyaneus* (though as recent as February 2015 in Japan), *cyaneus* and *hudsonius* look pretty different, especially adult males and juveniles. They look as different as various other Old World *Circus* do to other sympatric species (think *C. cyaneus cyaneus* from *C. macrourus*). The females and juveniles between these and other species are a quagmire of identification difficulties and long identification articles have been written on this in various European journals. I think we tend to get biased over here in North America where we have just one species of harrier and we look at the Old World relative and say...."looks pretty similar." Well try birding over there at a raptor migration place (e.g. Eilat, Israel) and then figuring out the juveniles and adult female harriers passing by. Adult male Old World Hen Harriers to my eye look pretty ghostly pale gray with more limited black in the wing.

The split of New and Old World birds seems straight-forward to me, EXCEPT for the matter of vocalizations. As noted by others, the calls seem to be pretty similar, and from my brief overview of other Old World species their calls do differ (from one another). This gives one pause.

What tips me back to splitting them is the matter that others have raised about the Cinereous Harrier (*Circus cinereus*). I have no field experience with that species, but can an argument be raised that it is more different from our *hudsonius* Northern Harrier than the Old World *C. c. cyaneus* is to *C. c. hudsonius*? Did Hartert (1914) consider that

issue?? Has anyone lumped Cinereous Harrier with our (and Old World) Northern Harrier?

I think Ferguson-Lees and Christie (2001) summarize the situation well (see p. 486 under geographical variation) in their account for the split Northern Harrier (*C. hudsonius*): "Monotypic. Often treated as race of Palearctic Hen Harrier, but adult is intermediate in various respects between that and Neotropical Cinereous Harrier and juvenile significantly different from juvenile Hen: all three could be considered allopatric and distinct races of one species or, the course followed here, three species forming a superspecies."

I could vote for treating all as one species until vocalizations between the three are clarified, or vote for three. Maintaining just two seems like a less desirable choice other than maintaining stability, however unacceptable that might be.

Literature cited: Ferguson-Lees, J., and D.A. Christie. 2001. *Raptors of the World*. 2001. Houghton Mifflin Company.

### **Split Yellow-rumped Warbler *Setophaga coronata* into three species**

#### **Background:**

Species limits in the Yellow-rumped Warbler complex (*Setophaga coronata* ssp.) have been debated extensively. Under the current NACC taxonomy, four subspecies exist: Myrtle's Warbler (*Setophaga coronata coronata* Linnaeus 1766), Audubon's Warbler (*Setophaga auduboni* Townsend 1837), Black-fronted Warbler (*Setophaga coronata nigrifrons* Brewster 1889), and Goldman's Warbler (*Setophaga coronata goldmani* Nelson 1897). These four subspecies are primarily distinguished by differences in plumage and breed in largely non-overlapping parts of North and Central America (Figure 1). There is also morphological variation that corresponds to variation in migratory behavior: longer-distance *S. c. coronata* migrants have longer and more concave wings compared to sedentary *S. c. goldmani* populations (Mila et al. 2008). Well-documented hybrid zones exist between certain subspecies, however (Hubbard 1969, Brelsford et al. 2011), which has engendered further controversy regarding species delimitation.

A series of genetic studies has furthered our understanding of genetic differentiation within the *Setophaga coronata* complex. Milá et al (2006) used mtDNA sequence data to reveal a deep phylogenetic split dividing the two migratory subspecies (*S. c. coronata* and *S. c. auduboni*) from the two resident subspecies (*S. c. nigrifrons* and *S. c. goldmani*). Furthermore, *S. c. nigrifrons* and *S. c. goldmani* were reciprocally monophyletic (Milá et al. 2006; Figure 2). Subsequently, Brelsford and Irwin (2009) intensively sampled the hybrid zone between *S. c. coronata* and *S. c. auduboni* and examined diagnostic nuclear loci; they found little evidence for assortative mating in the hybrid zone, but did find fixed nuclear differences in strong linkage disequilibrium, evidence of selection against hybrids, and moderate reproductive isolation, presumably via post-mating barriers to gene flow. Further work based on AFLP markers suggested that the subspecies are genetically distinct, with *S. c. goldmani* and *S. c. coronata* the most differentiated, and found extensive mitochondrial and some nuclear introgression from *S. c. coronata* into *S. c. auduboni* (Brelsford et al. 2011). Including additional samples from southwestern United States revealed a cryptic contact zone between ancestral *S. c. auduboni* and *S. c. auduboni* populations that had experienced introgression from *S. c. coronata* (Mila et al. 2011, Toews et al. 2013). Recently, RAD sequencing was used to provide a new genome-wide analysis of genetic differentiation within the Yellow-rumped Warbler species complex (Toews et al. 2016).

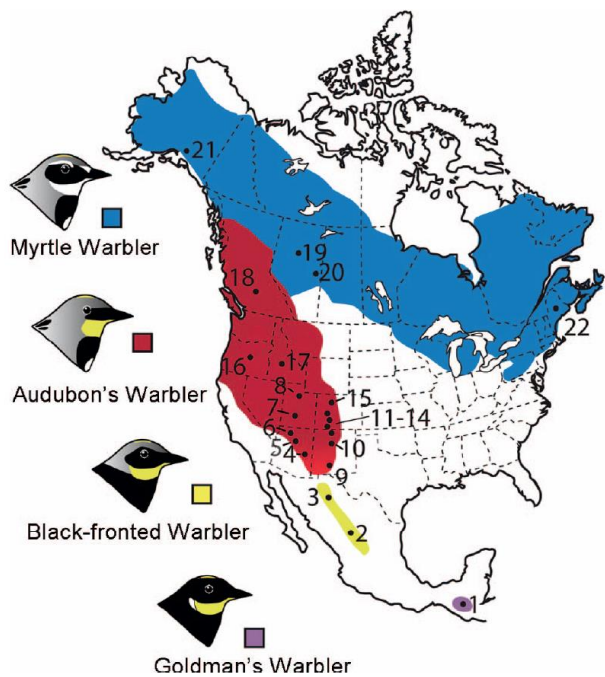


Figure 1: Phenotypic variation and geographic distribution of subspecies within the *Setophaga coronata* species complex. Dots represent sampling localities from Toews et al. (2016).

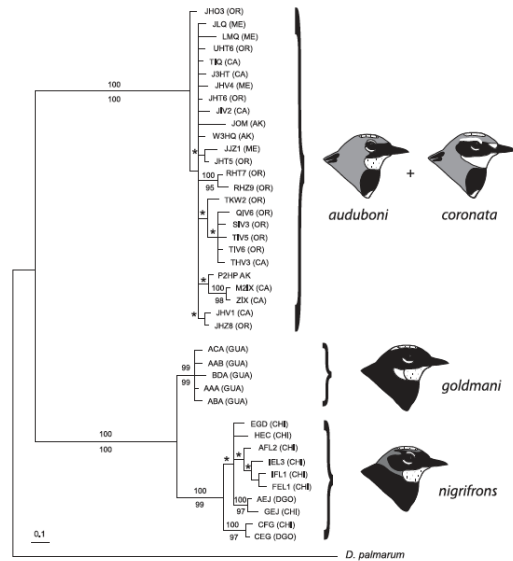


Figure 2: Divergence in mtDNA between subspecies in Yellow-rumped Warbler species complex (*Setophaga coronata* ssp.). Taken from Mila et al. (2006).

### New Information:

A recent study used genotyping-by-sequencing to study genetic differentiation within *Setophaga coronata* (Toews et al. 2016). Based on a panel of loci that was orders of magnitude larger than previous studies, Toews et al. (2016) confirmed that phenotypically divergent subspecies are also genetically differentiated. Toews et al. (2016) included multiple samples from each subspecies, but did not sample birds from the contact zone between *S. c. coronata* and *S. c. auduboni*. A plot of the first two PCA axes based on over 35,000 SNPs three genetic clusters: one cluster included all *S. c. coronata* samples, another included all *S. c. goldmanii* samples, and the last cluster included both *S. c. auduboni* and *S. c. nigrifrons* samples (Figure 3). Furthermore, by performing pair-wise comparisons of allele frequencies (i.e.,  $F_{ST}$ ) among sliding windows across the genome, Toews et al. (2016) identified multiple peaks of divergence, including numerous outlier loci between *S. c. coronata* and *S. c. auduboni* that may be under natural selection. By inspecting patterns of isolation by distance among pairs of individuals within and across subspecies, Toews et al. (2016) found much higher overall levels of  $F_{ST}$  between *S. c. auduboni* and *S. c. coronata* populations (Fig. 4C) relative to comparisons between *S. c. coronata* and *S. c. nigrifrons* (Fig. 4D). This suggests that there is substantially higher divergence between *S. c. auduboni* and *S. c. coronata* with patterns of isolation by distance within *S. c. coronata* and *S. c. nigrifrons*.

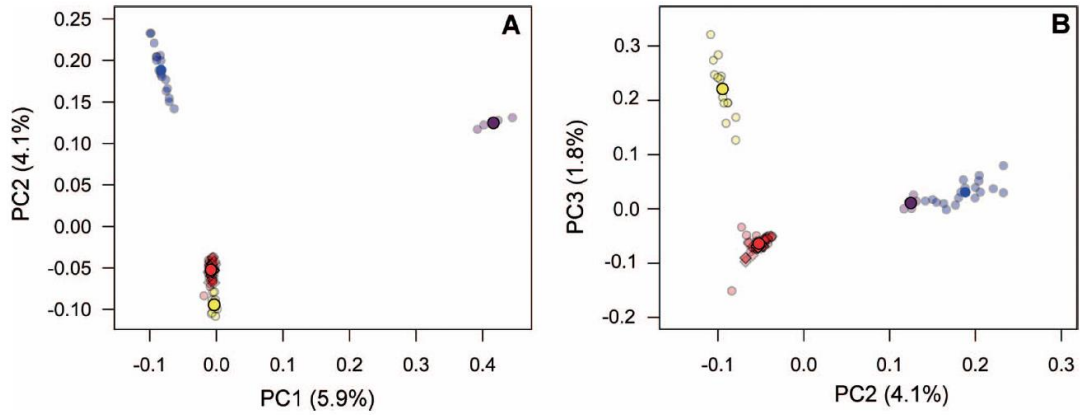


Figure 3: PCA plot based on 37,518 polymorphic SNPs in the Yellow-rumped Warbler complex. Blue corresponds to *S. c. coronata*, purple corresponds to *S. c. goldmani*, red corresponds to *S. c. auduboni*, and yellow corresponds to *S. c. nigrifrons*.

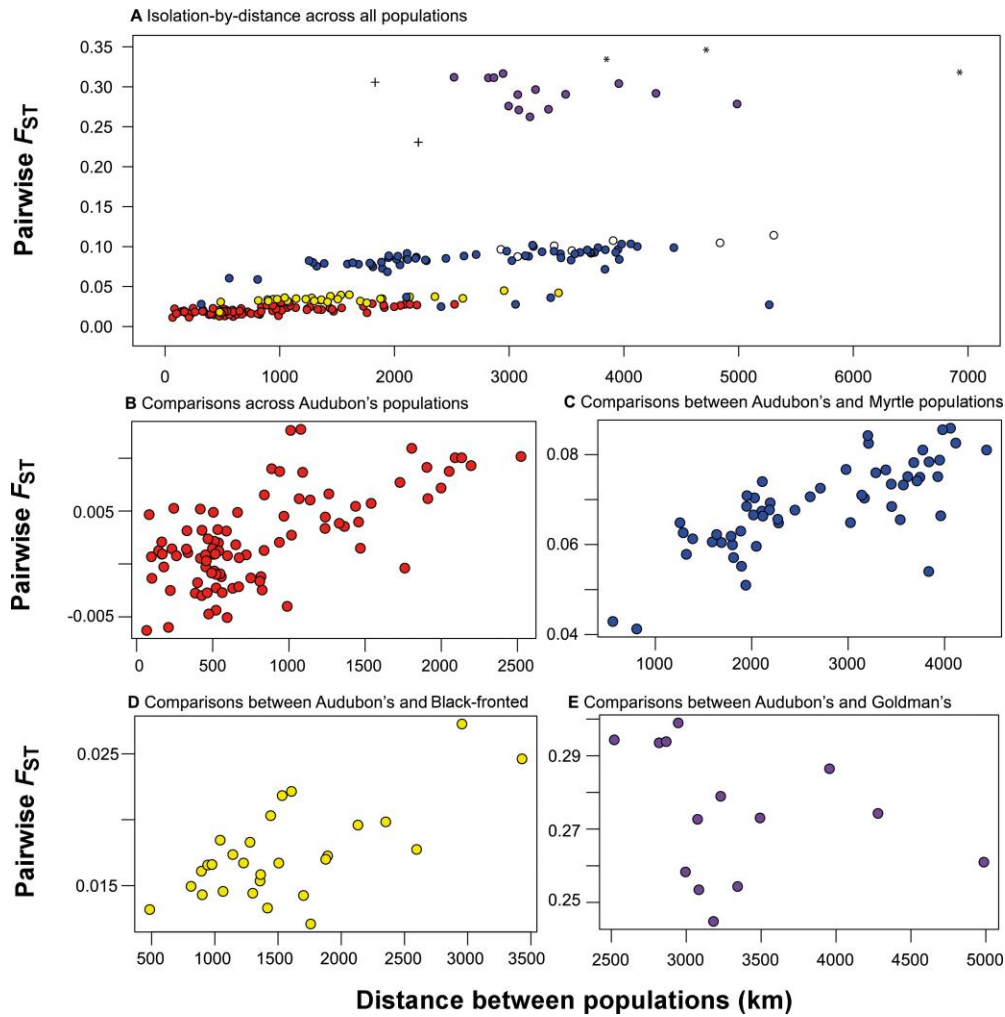


Figure 4: Plots of isolation by distance among different pairings of individuals from subspecies groups within the Yellow-rumped Warbler Complex.



Based on these inferences, the authors suggest that species limits within Yellow-rumped Warbler complex should be revisited. The authors propose elevating *S. c. goldmani* to full-species; this isolated, phenotypically differentiated subspecies (see Mila et al. 2008 for morphological differences; unpublished vocal differences also exist B. Mila, pers. comm.) was consistently the most genetically differentiated in pair-wise comparisons with other subspecies in the complex (Toews et al. 2016). Furthermore, *S. c. coronata* exhibits substantial genetic differentiation from *S. c. auduboni* and other subspecies in the complex across its entire genome. Combined with the presence of numerous outlier loci and indirect evidence for selection against hybrids in the contact zone between *S. c. coronata* and *S. c. auduboni*, Toews et al. (2016) also recommended that *S. c. coronata* and *S. c. auduboni* be considered separate species.

The species status of *S. c. nigrifrons* remains uncertain given the data currently available. Whereas *S. c. nigrifrons* is largely allopatric and phenotypically differentiated from other subspecies within the complex, the overall level of genetic differentiation between *S. c. nigrifrons* and *S. c. auduboni* is low across the genome (global  $F_{ST} = 0.02$ ). Moreover, although the third axis of the PCA clearly distinguishes *S. c. nigrifrons*, there are no genetic markers that exhibit high levels of divergence with *S. c. auduboni*. It is worth noting that migrant *S. c. auduboni* and breeding *S. c. nigrifrons* overlap in early spring without any evidence for interbreeding (B. Mila, pers. comm.). Finally, population comparisons between *S. c. auduboni* and *S. c. nigrifrons* reveal a level of genetic differentiation that is only marginally higher than comparisons between two *S. c. auduboni* populations at a similar geographic distance (Toews et al. 2016). Additional sampling of southern *S. c. auduboni* individuals and northern *S. c. nigrifrons* individuals near the putative contact zones in high-elevation patches of habitat on sky islands will be integral to understanding patterns of gene flow, reproductive isolation; these future data will help determine whether *S. c. auduboni* and *S. c. nigrifrons* should be considered separate species.

### **Priority/dates of subspecies descriptions**

*Setophaga coronata coronata* Linnaeus, 1766

*Setophaga coronata auduboni* Townsend, JK, 1837

*Setophaga coronata nigrifrons* Brewster, 1889

*Setophaga coronata goldmani* Nelson, 1897

### **Recommendation:**

Split Yellow-rumped Warbler (*Setophaga coronata*) into three species: Myrtle Warbler (*Setophaga coronata*), Audubon's Warbler (*Setophaga auduboni auduboni* and

*Setophaga auduboni nigrifrons*), and Goldman's Warbler (*Setophaga goldmani*). This taxonomic treatment is already in use by the IOC.

### **Literature Cited:**

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- Toews, D. P. L., M. Mandic, J. G. Richards, and D. E. Irwin (2013). Migration, mitochondria, and the Yellow-rumped Warbler. *Evolution* 68:241–255.

**Submitted by:** Nicholas A. Mason and David P.L. Toews, Cornell University; Alan Brelsford, UC Riverside.

**Proposal date:** 14 November 2016

### **Split the Willet *Tringa semipalmata* into two species**

If approved, this proposal would split the Willet (*Tringa semipalmata*) into Eastern Willet (*Tringa semipalmata*) and Western Willet (*Tringa inornata*).

#### **Background:**

The Willet (*Tringa semipalmata*) includes two broadly allopatric subspecies that exhibit morphological, ecological, vocal, and genetic differentiation. The eastern subspecies (*T. s. semipalmata* Gmelin 1789) breeds almost exclusively in saltmarshes and brackish coastline habitat along the Atlantic Coast, the Gulf of Mexico, and certain localities in the Caribbean (Lowther 2001; O'Brien et al. 2006). In contrast, the western subspecies (*T. s. inornata*) breeds in brackish and freshwater wetlands in the Great Basin as well as prairies in the northwestern United States and southern Canada (Lowther 2001; O'Brien et al. 2006). The western subspecies winters along rocky habitat on the Pacific coast from the northwestern United States south to Chile. While the two species may co-occur during migration and on certain wintering grounds, pair bonding occurs on breeding grounds (Howe 1982), which are allopatric between the two subspecies.

Differences in plumage and morphology exist between the two subspecies: the western *T. s. inornata* is larger overall with a longer wing and tarsus. Bill measurements exhibit some overlap, but *T. s. inornata* typically has a longer and broader bill. *Tringa semipalmata inornata* is lighter overall with less patterning in prealternate plumage, while other plumage stages are similar between the two subspecies. The two subspecies also exhibit vocal differences, in which the western *T. s. inornata* produces vocal displays that are lower in frequency and shorter than the eastern *T. s. semipalmata* (Douglas 1996, 1998). *Tringa semipalmata semipalmata* preferentially responds to playback of *T. s. semipalmata* rather than *T. s. inornata* vocalizations, which might suggest some level of premating reproductive isolation (Douglas 1998).

Recently, Oswald et al. (2016) examined morphological and genetic differentiation using a large panel of nuclear and mitochondrial loci. Combined with previous evidence for ecological, morphological, and genetic differentiation, these new findings suggest that species limits within *Tringa semipalmata* should be revisited.

## New Information:

Oswald et al. (2016) investigated genetic and morphological differentiation within *T. semipalmata*. Oswald et al. (2016) sampled 19 *T. s. inornata* and 11 *T. s. semipalmata* individuals. For their *T. s. inornata* samples, the authors included six samples from a single breeding locality in Wyoming; the remaining *T. s. inornata* samples were from various wintering populations on the Pacific Coast. The *T. s. semipalmata* samples included representatives of breeding populations from the Atlantic and Gulf Coast, but did not include Caribbean individuals.

Oswald et al. (2016) sequenced a panel of ultraconserved elements (UCEs) from all thirty individuals; the authors used a bioinformatics pipeline to extract SNPs from each UCE locus as well as full alignments for use in multiple downstream programs to examine population structure and the demographic history of the complex. The authors also sequenced the ND2 mitochondrial gene region for 8 *T. s. inornata* and 10 *T. s. semipalmata* samples.

Oswald et al. (2016) recovered 4352 variable UCE loci, which included 19,322 SNPs; the authors identified 42 loci containing 43 SNPs that were fixed for alternative alleles between *T. s. semipalmata* and *T. s. inornata*. Discriminant analyses of principal components (DAPC) recovered two distinct genetic clusters that correspond to *T. s. semipalmata* and *T. s. inornata* (Figure 1). This finding was further corroborated by Structure, which also inferred two distinct genetic clusters with no evidence of admixture between them (Figure 1).

Additional analyses based on species trees built from SNPs revealed strong support for a coalescent-based species delimitation scenario with *T. s. semipalmata* and *T. s. inornata* split into two species (Bayes Factor = 978 with Bayes factors > 10 usually considered 'decisive'; Figure 2A). Furthermore, Oswald et al. (2016) found evidence for reciprocal monophyly in mitochondrial DNA with 0.85% mean sequence divergence, five base pairs separating the most similar haplotypes from the two subspecies, and an estimated divergence time of ~700,000 ya (Figure 2B). The morphological dataset from Oswald et al. (2016) corroborates previous evidence that *T. s. inornata* is larger overall, but that there is overlap in morphospace between the two subspecies.

Taken together, Oswald et al. (2016) find strong evidence of genomic differentiation across thousands of loci and little to no gene flow between *T. s. semipalmata* and *T. s.*

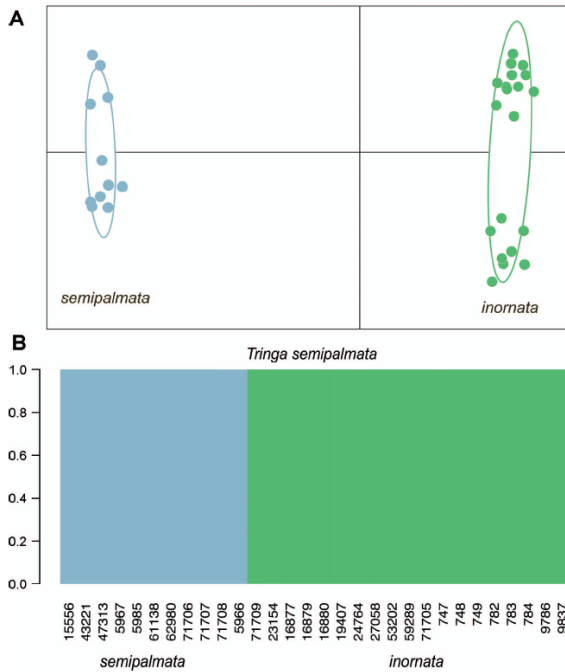


Figure 1: Panel A shows discriminant analyses of principal components with two distinct clusters corresponding to subspecies within the Willet. Panel B shows the output of Structure, which also supports the existence of two distinct population clusters within *T. semipalmata*.

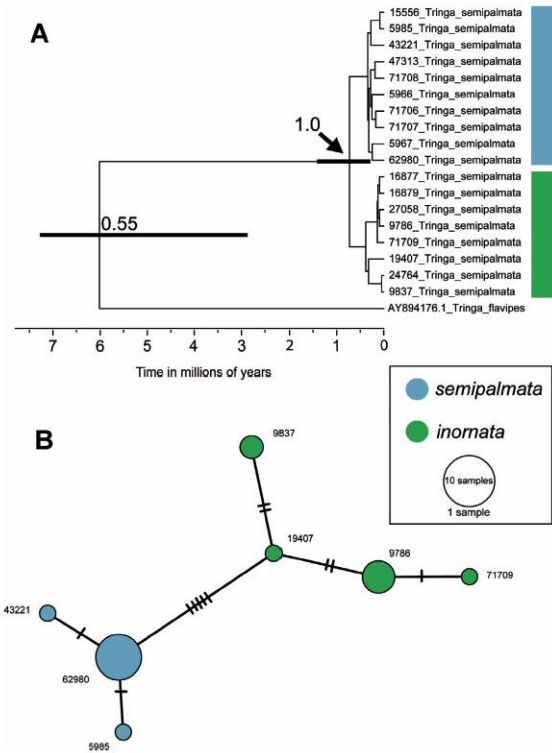


Figure 2: Panel A shows a phylogeny based on SNPs acquired from the ultraconserved element loci. Panel B shows a haplotype network based on ND2 sequences of mitochondrial DNA.

*inornata*. Although the amount of mitochondrial differentiation is somewhat low (0.85%), these findings suggest that *T. s. semipalmata* and *T. s. inornata* are independent evolutionary lineages that are not interbreeding and are on separate evolutionary trajectories. Combined with existing evidence that these two subspecies differ in ecology, vocalizations, and morphology, these data warrant treating *T. s. semipalmata* and *T. s. inornata* as separate species.

### Recommendation:

Split Willet (*Tringa semipalmata*) into Eastern Willet (*Tringa semipalmata*) and Western Willet (*Tringa inornata*).

### Literature Cited:

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**Submitted by:** Nicholas A. Mason, Cornell University

**Proposal date:** 14 November 2016

**Modify our treatment of juncos: (a) recognize *bairdi* as a species, (b) recognize *alticola* as a species, and (c) lump *phaeonotus* and *hyemalis***

**Background:**

We recognized three species of junco in the seventh edition of the checklist (AOU 1998): *Junco vulcani* (Volcano Junco) of Costa Rica, *J. hyemalis* (Dark-eyed Junco) principally of the US and Canada, and *J. phaeonotus* (Yellow-eyed Junco) principally of Mexico and the southwestern US. We recently recognized an additional species of junco, *J. insularis* (Guadalupe Junco) of Guadalupe Island, on the basis of differences in song, morphology, and DNA sequence data (Chesser et al. 2014).

**New Information:**

Milá *et al.* (2016) sequenced the mitochondrial gene COI (690 bp) for an impressive 273 individuals of junco. Although the amount of DNA sequenced per individual was modest and included no nuclear sequence, their taxonomic and geographic coverage was excellent, including samples of all species and a good mix of the various taxa of “dark-eyed” and “yellow-eyed” juncos. The resulting trees consisted of five distinct clades: (1) *vulcani* (VOJU in the tree below), (2) *bairdi* of southern Baja California (BAJU), (3) *insularis* (GUJU), (4) *alticola* of Guatemala and also southeastern Chiapas (GTJU), and (5) all other forms:

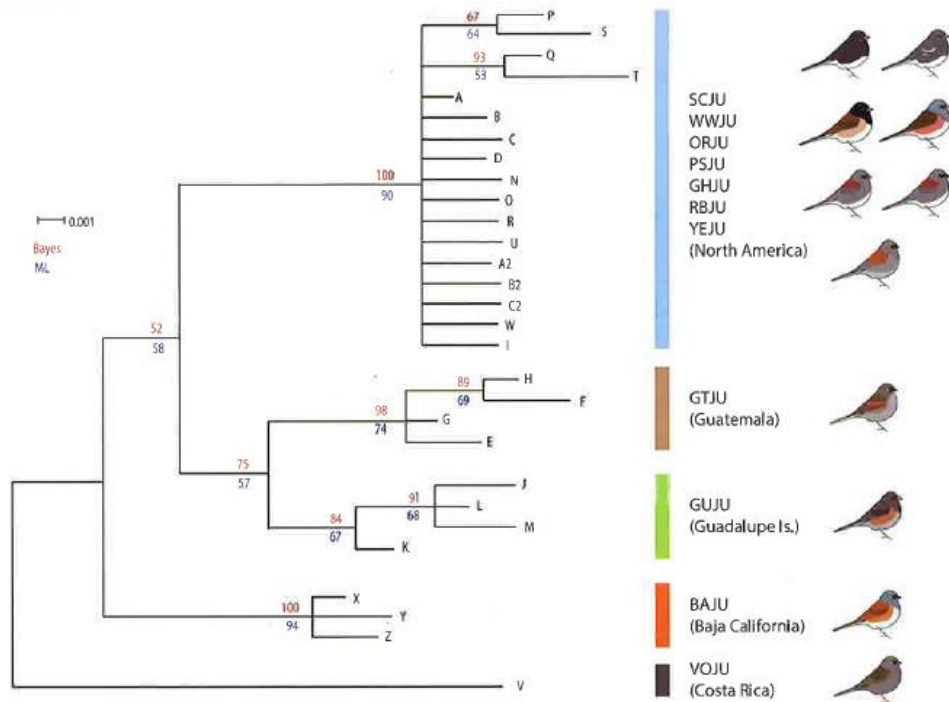


PLATE 3. Evolutionary relationships among the main forms within the genus *Junco* are illustrated in this preliminary phylogenetic tree, based on an analysis of mitochondrial DNA sequence data (cytochrome *c* oxidase I [COI], 690 base pairs). Branch support values correspond to a Bayesian analysis (above branches) and a maximum likelihood analysis (below branches). For details see chapter 8, this volume.

We currently recognize two of these clades (*vulcani* and *insularis*) as species, whereas *bairdi* and *alticola* are currently included in Yellow-eyed Junco *J. phaeonotus*. The fifth clade consisted of all forms of Dark-eyed Junco *J. hyemalis* plus two groups of Yellow-eyed Junco: *phaeonotus*, which is widespread in Mexico and the southwestern US, and *fulvescens* from the interior of Chiapas. Although these results are tempered by the limited quantity of sequence and the fact that only mtDNA was sequenced, we should consider whether *bairdi* and *alticola* should be recognized as species and whether *phaeonotus* and *hyemalis* should be lumped.

A previous study based on sequencing of eight nuclear genes (McCormack et al 2011) had also demonstrated the distinctiveness of *bairdi* and the close relationship of various forms of *phaeonotus* and *hyemalis*:



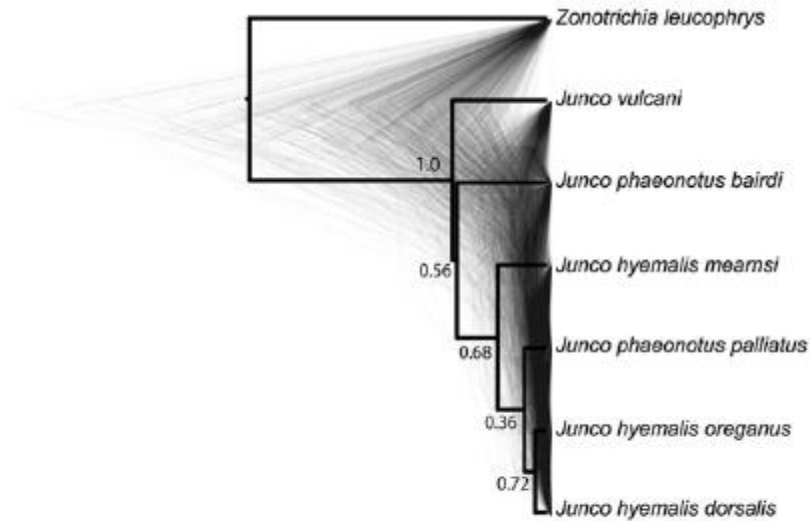


Fig. 5. Species tree of sparrows and juncos based on eight genes that included representatives of all terminal taxa.

Unfortunately, samples of *alticola* and several other forms of *phaeonotus* and *hyemalis* (as well as *insularis*) were not included in this study.

Songs of *bairdi* differ quantitatively from those of nominate *phaeonotus* and *phaeonotus palliatus* (of southeastern Arizona), showing significant differences from *phaeonotus* in six characters and from *palliatus* in 11 characters (Pieplow and Francis 2011), measures of many of which appear not to overlap. Howell and Webb (1995) had previously noted the vocal distinctiveness of *bairdi* (“song ... strikingly different from mainland Yellow-eyed Juncos”) and recognized it as a species separate from *phaeonotus*. Howell and Webb (1995) described the song of *alticola* as “much like *phaeonotus*” although their descriptions of their respective calls differ somewhat.

Both Ridgway (1901) and Miller (1941) considered *bairdi* and *alticola* to be species, but they recognized a lot of species of junco (14 total species for Ridgway and 10 for Miller). In contrast, Hellmayr (1938) recognized only five species of junco, and considered *bairdi* a subspecies of *oreganus* and *alticola* a subspecies of *phaeonotus*. According to Miller, who examined more than 11,000 specimens (!) for his monograph on juncos, the affinities of *bairdi* are with *phaeonotus* but it differs from all forms of *phaeonotus* by its extensive cinnamon sides lacking eumelanin, lighter duller back, and shorter wing, tail, and tarsus. In contrast, *alticola* is most closely related to *phaeonotus fulvescens* but differs in several non-overlapping characters, including the color of the sides (buffy brown vs. Sayal brown) and darker breast, underparts, and pileum (Miller 1941). Both *bairdi* and *alticola* are geographically isolated from other juncos, *bairdi* in the Sierra

Victoria on the southern tip of Baja California, and *alticola* in highlands in western Guatemala and extreme southeastern Chiapas.

With regard to *phaeonotus* and *hyemalis*, our current division of and allocation of subspecies to these species largely dates from the sixth edition of the checklist (AOU 1983). The fifth edition (AOU 1957) recognized seven species of junco from the restricted AOU area of North America and Baja California (i.e., not including *vulcani* or *alticola*). Most of the changes were made in the 32nd supplement (AOU 1973): *aikeni*, *oreganus*, and *insularis* were merged into *hyemalis* (although *caniceps*, then under study, was temporarily maintained as a species), and *bairdi* was merged into *phaeonotus*. In a review of Miller (1941), Mayr (1942), referencing Miller's apparent basing of species status on degree of morphological difference, stated, "Would not it be much simpler and biologically more nearly correct to include all the juncos in a single superspecies, with three species: (1) *vulcani*, (2) the yellow-eyed group, and (3) the brown-eyed group?" This arrangement was adopted by Phillips et al (1964), who stated that "the various races of Brown-eyed Junco intergrade with each other and accordingly constitute one species" distinguished from the Yellow-eyed Junco by eye color, song, and gait. Furthermore, Yellow-eyed Juncos "do not join their dark-eyed cousins, but stay to themselves, in groups not exceeding family size. All of these traits, as well as the total lack of interbreeding and complete geographic separation in the breeding season, proclaim this as a species distinct from *Junco hyemalis*..." (Phillips et al. 1964). The same classification was subsequently followed by Paynter (1970) and the AOU (1983, 1998), although we used the English name Dark-eyed Junco rather than Brown-eyed Junco.

Apart from the substantial intraspecific variation in plumage, this taxonomic arrangement masks some uncertainties in the classification of particular subspecies, especially the "Gray-headed" Dark-eyed Junco subspecies *J. h. dorsalis* of Arizona, New Mexico, and west Texas. Phillips et al (1964) noted that *dorsalis* is distinguished from all other subspecies of *hyemalis* by its large black bill (the rest have pinkish bills), and Hellmayr (1938) actually classified *dorsalis* as a subspecies of *phaeonotus*. Indeed, *dorsalis*, despite its dark eyes, is similar in song, calls, and appearance to the *phaeonotus* group of the Yellow-eyed Junco (Sullivan 1999).

### **Recommendations:**

**(a) recognize *bairdi* as a species.** We have vocal, morphological, and molecular (nuclear and mitochondrial) evidence in favor of this split, and we recommend that we recognize *bairdi* as a species. The evidence is similar to that used previously for splitting *insularis*.

**(b) recognize *alticola* as a species.** The data here are weaker than for *bairdi*. Songs are similar (note that Howell and Webb did not split *alticola* from *phaeonotus*) and molecular differentiation is based solely on a short piece of mtDNA (*alticola* was not sampled by McCormack et al 2011). We recommend voting against recognizing *alticola* as a species.

**(c) lump *phaeonotus* and *hyemalis*.** Molecular data (nuclear and mitochondrial) indicate that these species are very closely related and probably not resolvable into monophyletic groups, and the yellow-eyed/dark-eyed dichotomy may break down in the case of *dorsalis*, but this is a complex situation that deserves more concentrated study. At this time we recommend maintaining these taxa as separate species.

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**Submitted by:** Terry Chesser and Jim Rising

**Proposal date:** 17 November 2016

**Addendum to Proposal 2017-A-11:** In December 2016, following submission of this proposal, a new paper on junco phylogenetics was published (Friis et al. 2016). In addition to Sanger sequencing several mitochondrial genes and one nuclear intron for >100 juncos from throughout their range, the authors used genomic techniques to sample 95 juncos for thousands of SNP (single nucleotide polymorphism) loci. Their combined Sanger tree (see Fig. A1 below) matched the mitochondrial tree from Milá et al. (2016) above, except that resolution within the *phaeonotus-hyemalis* group was improved, including the resolution of *fulvescens* of Chiapas as sister to all other taxa within this group.

An unrooted analysis of the SNP data (see Fig. A2 below) resolved a large central cluster consisting of most of *phaeonotus-hyemalis* group; *bairdi* and *insularis* were on extremely long branches off of this group, and *alticola* and *fulvescens*, in contrast to the mt tree of Milá et al. (2016) and the Sanger-based tree of Friis et al., were sisters and formed moderately long branches off of the central cluster (*vulcani* was apparently not included in this analysis). Apart from *alticola* and *fulvescens*, all of *phaeonotus-hyemalis* formed a monophyletic group, and all individual taxa formed monophyletic groups. The northern dark-eyed *hyemalis* group was monophyletic, but the yellow-eyed *phaeonotus* group was not monophyletic (see Fig. A3 below, in which *fulvescens* was designated the outgroup and *bairdi*, *insularis*, and *alticola* excluded from the analyses). Instead, *phaeonotus* and *palliatu*s were successive sisters to a monophyletic dark-eyed group. Interestingly, the next successive sister (in other words, sister to the rest of the dark-eyed *hyemalis* group) was *dorsalis*, the dark-eyed taxon that shares several other phenotypic characters with the yellow-eyed group.

These results strengthen our recommendations above by (1) reinforcing the genetic distinctiveness of *bairdi*; (2) demonstrating that *alticola* is not particularly distinct genetically from the *phaeonotus-hyemalis* group, and indeed was sister to *fulvescens* of the yellow-eyed group in the SNP network; and (3) emphasizing the complexity of and need for more research on the *phaeonotus* and *hyemalis* groups. Thus, our recommendations are unchanged.

(B)

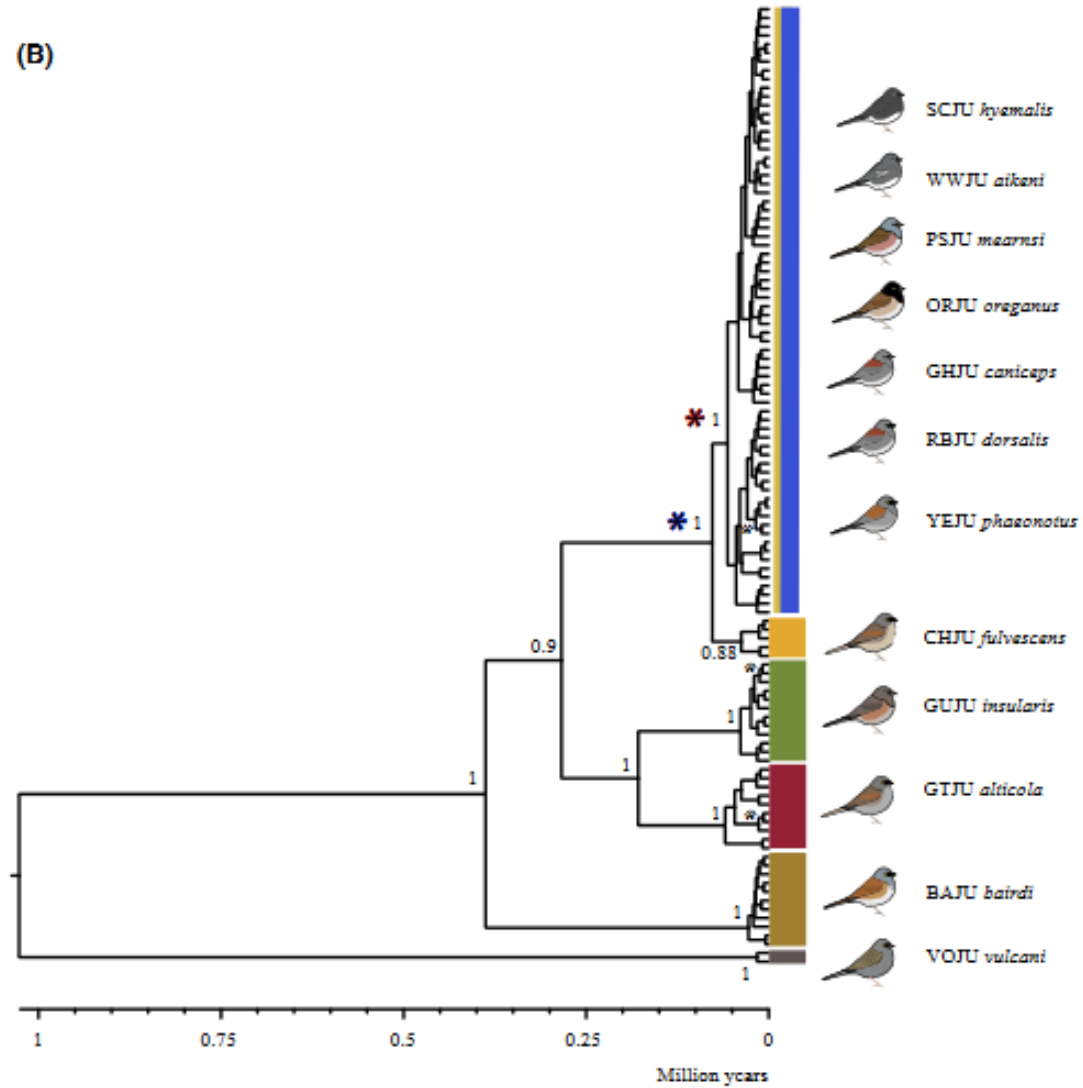


Figure A1 (from Friis et al. 2016). Bayesian phylogeny based on data from four mitochondrial genes and the nuclear intron FGB-I5. Numbers at nodes are posterior probability values.

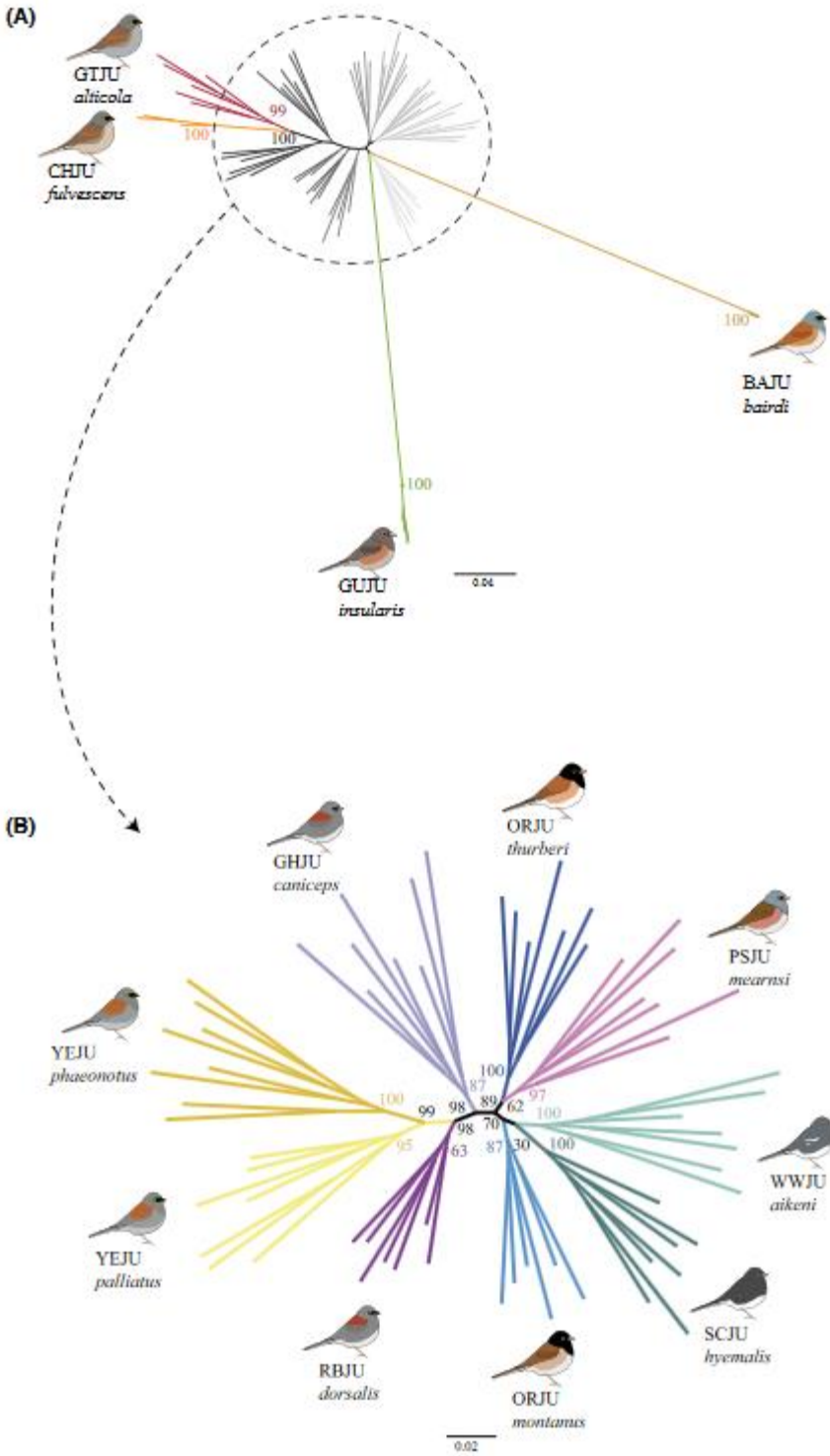


Figure A2 (from Friis et al. 2016). Unrooted maximum-likelihood phylogenies based on genomewide SNP data from (A) all junco taxa (except *vulcani*, apparently), and (B) recently diverged northern junco taxa only. Numbers at nodes indicate bootstrap values.

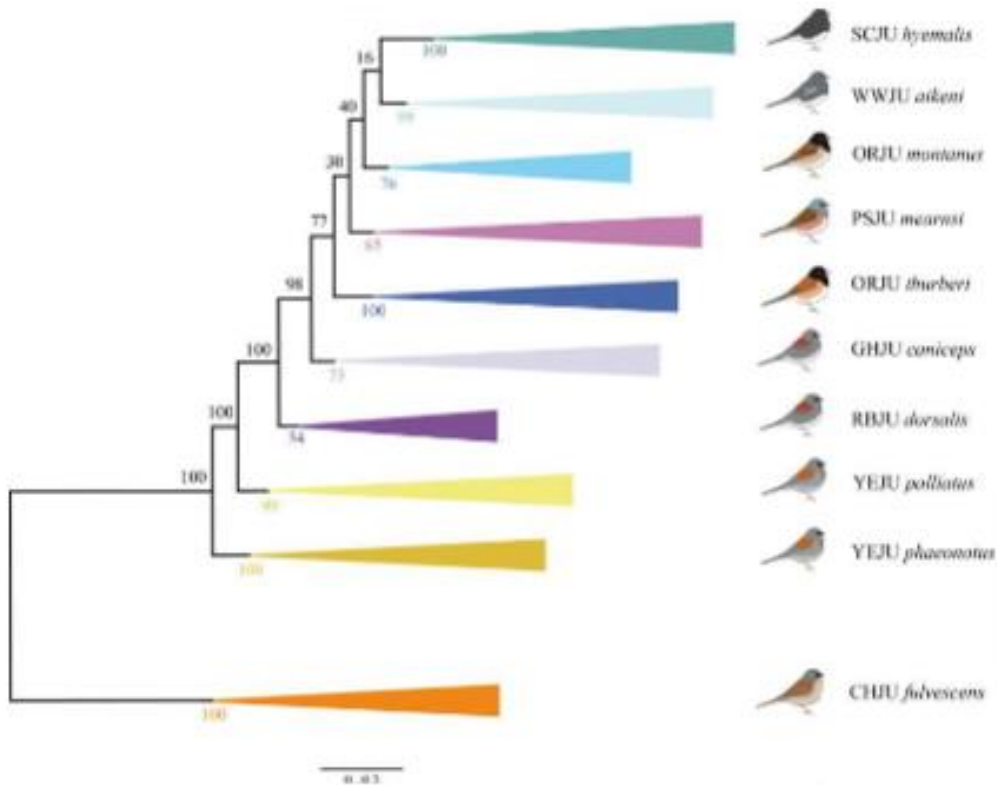


Figure A3 (from Friis et al. 2016). Maximum-likelihood phylogeny of northern juncos based on the 25% of SNP loci with the highest global  $F_{ST}$ , rooted using *fulvescens*. Numbers at nodes presumably indicate bootstrap values.

#### Additional Literature Cited:

Friis, G., P. Alexandre, R. Rodríguez-Estrella, A. G. Navarro-Sigüenza, and B. Mila. 2016. Rapid postglacial diversification and long-term stasis within the songbird genus *Junco*: phylogeographic and phylogenomic evidence. *Molecular Ecology* 25: 6175-6195.

Addendum submitted by: Terry Chesser

Date of addendum: 22 March 2017

### Change the linear sequence of species in Scolopacidae

This is a cleanup proposal to change our current linear sequence of species (and a couple of genera) in the Scolopacidae to match the relationships determined by Gibson and Baker (2012). In the proposed sequence, the source is Gibson and Baker (2012; tree copied below) for all the taxa that it includes. Placement of *Numenius borealis*, Eskimo Curlew, is unclear but is retained as we have done in the past as sister to *N. minutus* (Mayr and Short 1970). Similarly, placement of *N. tenuirostris* follows traditional placement as sister to *N. arquata*. Placement of *Lymnocyptes* relative to *Scolopax* and *Gallinago* is based on Baker et al. (2007). Placement of *Gallinago solitaria* follows Dickinson and Remsen (2013) but might be considered incertae sedis for all I can find.

The current sequence can be seen here: <http://checklist.aou.org/taxa/>. Our new sequence would be as follows (scientific names of taxa that have been moved are shown in red rather than blue):

family: [Scolopacidae](#)

- subfamily: Numeniinae
  - genus: [Bartramia](#)
    - species: [Bartramia longicauda](#) (Upland Sandpiper, Maubèche des champs)
  - genus: [Numenius](#)
    - species: [Numenius tahitiensis](#) (Bristle-thighed Curlew, Courlis d'Alaska)
    - species: [Numenius phaeopus](#) (Whimbrel, Courlis corlieu)
    - species: [Numenius minutus](#) (Little Curlew, Courlis nain) A
    - species: [Numenius borealis](#) (Eskimo Curlew, Courlis esquimau)
    - species: [Numenius americanus](#) (Long-billed Curlew, Courlis à long bec)
    - species: [Numenius madagascariensis](#) (Far Eastern Curlew, Courlis de Sibérie) N
    - species: [Numenius tenuirostris](#) (Slender-billed Curlew, Courlis à bec grêle) A
    - species: [Numenius arquata](#) (Eurasian Curlew, Courlis cendré) A
- subfamily Limosinae
  - genus: [Limosa](#)
    - species: [Limosa lapponica](#) (Bar-tailed Godwit, Barge rousse)
    - species: [Limosa limosa](#) (Black-tailed Godwit, Barge à queue noire) N
    - species: [Limosa haemastica](#) (Hudsonian Godwit, Barge hudsonienne)
    - species: [Limosa fedoa](#) (Marbled Godwit, Barge marbrée)
- subfamily Arenariinae
  - genus: [Arenaria](#)
    - species: [Arenaria interpres](#) (Ruddy Turnstone, Tournepierre à collier)
    - species: [Arenaria melanocephala](#) (Black Turnstone, Tournepierre noir)
  - genus: [Calidris](#)
    - species: [Calidris tenuirostris](#) (Great Knot, Bécasseau de l'Anadyr) A
    - species: [Calidris canutus](#) (Red Knot, Bécasseau maubèche)
    - species: [Calidris virgata](#) (Surfbird, Bécasseau du ressac)



- species: [Calidris pugnax](#) (Ruff, Combattant varié)
  - species: [Calidris falcinellus](#) (Broad-billed Sandpiper, Bécasseau falcinelle) A
  - species: [Calidris acuminata](#) (Sharp-tailed Sandpiper, Bécasseau à queue pointue) N
  - species: [Calidris himantopus](#) (Stilt Sandpiper, Bécasseau à échasses)
  - species: [Calidris ferruginea](#) (Curlew Sandpiper, Bécasseau cocorli)
  - species: [Calidris temminckii](#) (Temminck's Stint, Bécasseau de Temminck) A
  - species: [Calidris subminuta](#) (Long-toed Stint, Bécasseau à longs doigts) N
  - species: [Calidris pygmaea](#) (Spoon-billed Sandpiper, Bécasseau spatule) A
  - species: [Calidris ruficollis](#) (Red-necked Stint, Bécasseau à col roux)
  - species: [Calidris alba](#) (Sanderling, Bécasseau sanderling)
  - species: [Calidris alpina](#) (Dunlin, Bécasseau variable)
  - species: [Calidris ptilocnemis](#) (Rock Sandpiper, Bécasseau des Aléoutiennes)
  - species: [Calidris maritima](#) (Purple Sandpiper, Bécasseau violet)
  - species: [Calidris bairdii](#) (Baird's Sandpiper, Bécasseau de Baird)
  - species: [Calidris minuta](#) (Little Stint, Bécasseau minute) N
  - species: [Calidris minutilla](#) (Least Sandpiper, Bécasseau minuscule)
  - species: [Calidris fuscicollis](#) (White-rumped Sandpiper, Bécasseau à croupion blanc)
  - species: [Calidris subruficollis](#) (Buff-breasted Sandpiper, Bécasseau roussâtre)
  - species: [Calidris melanotos](#) (Pectoral Sandpiper, Bécasseau à poitrine cendrée)
  - species: [Calidris pusilla](#) (Semipalmated Sandpiper, Bécasseau semipalmé)
  - species: [Calidris mauri](#) (Western Sandpiper, Bécasseau d'Alaska)
- subfamily: Scolopacinae
  - genus: [Limnodromus](#)
    - species: [Limnodromus griseus](#) (Short-billed Dowitcher, Bécassin roux)
    - species: [Limnodromus scolopaceus](#) (Long-billed Dowitcher, Bécassin à long bec)
  - genus: [Lymnocyptes](#)
    - species: [Lymnocyptes minimus](#) (Jack Snipe, Bécassine sourde) A
  - genus: [Scolopax](#)
    - species: [Scolopax rusticola](#) (Eurasian Woodcock, Bécasse des bois) A
    - species: [Scolopax minor](#) (American Woodcock, Bécasse d'Amérique)
  - genus: [Gallinago](#)
    - species: [Gallinago solitaria](#) (Solitary Snipe, Bécassine solitaire) A
    - species: [Gallinago stenura](#) (Pin-tailed Snipe, Bécassine à queue pointue) A
    - species: [Gallinago gallinago](#) (Common Snipe, Bécassine des marais)
    - species: [Gallinago delicata](#) (Wilson's Snipe, Bécassine de Wilson)
- subfamily: Tringinae
  - genus: [Xenus](#)
    - species: [Xenus cinereus](#) (Terek Sandpiper, Chevalier bargette) N
  - genus: [Phalaropus](#)
    - species: [Phalaropus tricolor](#) (Wilson's Phalarope, Phalarope de Wilson)
    - species: [Phalaropus lobatus](#) (Red-necked Phalarope, Phalarope à bec étroit)
    - species: [Phalaropus fulicarius](#) (Red Phalarope, Phalarope à bec large)
  - genus: [Actitis](#)
    - species: [Actitis hypoleucos](#) (Common Sandpiper, Chevalier guignette) N
    - species: [Actitis macularius](#) (Spotted Sandpiper, Chevalier grivelé)

- genus: [Tringa](#)
  - species: [Tringa ochropus](#) (Green Sandpiper, Chevalier cul-blanc) A
  - species: [Tringa solitaria](#) (Solitary Sandpiper, Chevalier solitaire)
  - species: [Tringa brevipes](#) (Gray-tailed Tattler, Chevalier de Sibérie) N
  - species: [Tringa incana](#) (Wandering Tattler, Chevalier errant)
  - species: [Tringa flavipes](#) (Lesser Yellowlegs, Petit Chevalier)
  - species: [Tringa semipalmata](#) (Willet, Chevalier semipalmé)
  - species: [Tringa erythropus](#) (Spotted Redshank, Chevalier arlequin) N
  - species: [Tringa nebularia](#) (Common Greenshank, Chevalier aboyeur) N
  - species: [Tringa melanoleuca](#) (Greater Yellowlegs, Grand Chevalier)
  - species: [Tringa totanus](#) (Common Redshank, Chevalier gambette) A
  - species: [Tringa glareola](#) (Wood Sandpiper, Chevalier sylvain)
  - species: [Tringa stagnatilis](#) (Marsh Sandpiper, Chevalier stagnatile) A

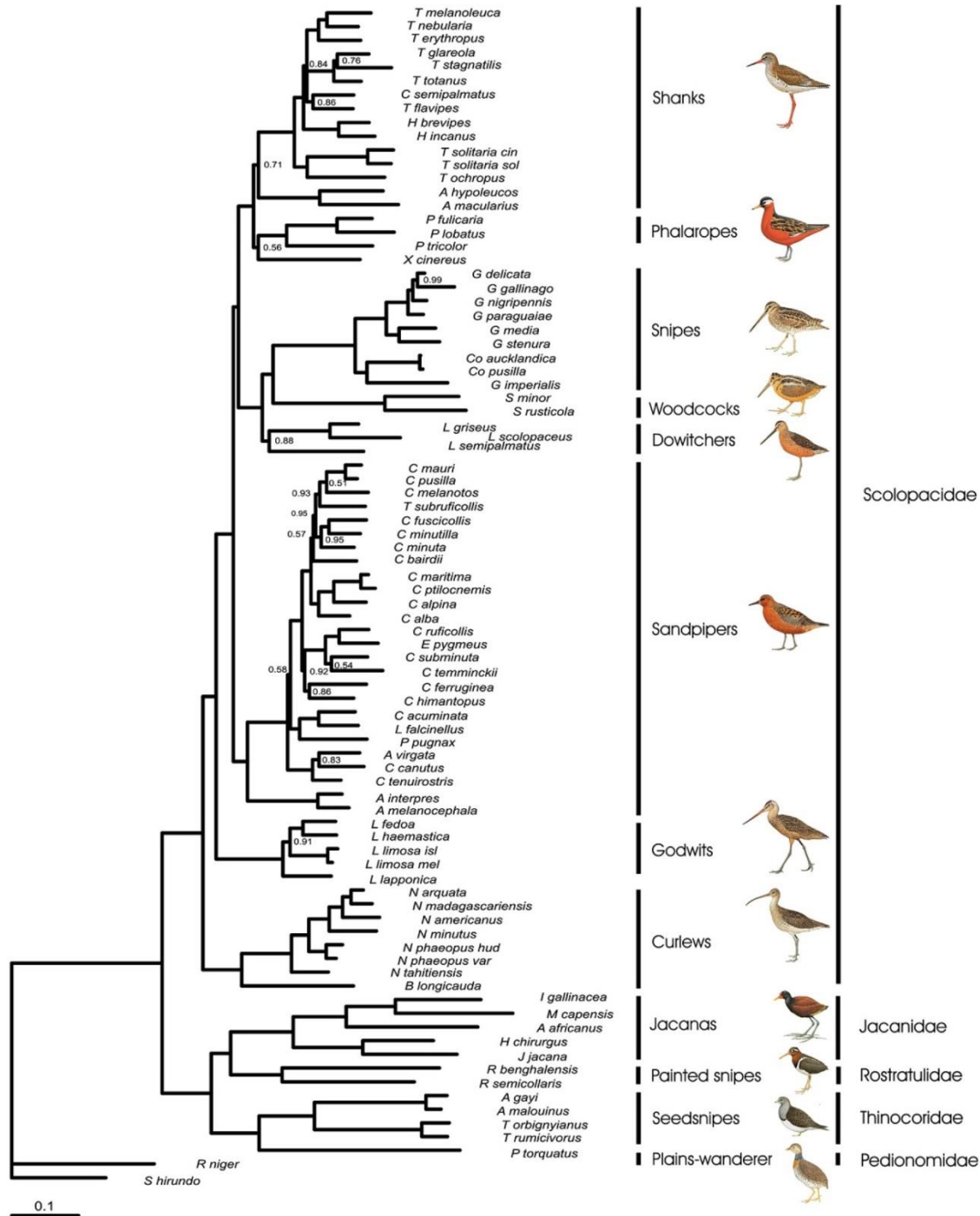


Fig. 1. Phylogeny based on sequences of five genes (RAG1, CYT B, 12S, ND2, and COI) estimated with partitioned Bayesian analysis for 84 species of the Scolopaci. All nodes received a posterior probability of 1.00 unless otherwise labeled.

**Recommendation:**

I recommend a YES vote on this because it brings our sequence into line with the best information available on relationships in this group.

Many thanks to Terry and Van for looking over an earlier draft!

**Literature Cited:**

- Baker, A. J., S. L. Pereira, and T. A. Paton. 2007. Phylogenetic relationships and divergence times of Charadriiformes genera: multigene evidence for the Cretaceous origin of at least 14 clades of shorebirds. *Biology Letters* 3:205-209.
- Dickinson, E. C., and J. V. Remsen, Jr. (Eds.) 2013. *The Howard and Moore Complete Checklist of the Birds of the World, 4<sup>th</sup> ed., Volume 1 Non-Passerines*. Eastbourne, U. K., Aves Press.
- Gibson, R., and A. Baker. 2012. Multiple gene sequences resolve phylogenetic relationships in the shorebird suborder Scolopaci (Aves: Charadriiformes). *Molecular Phylogenetics and Evolution* 64:66-72.
- Mayr, E., and L. L. Short. 1970. *Species taxa of North American birds*. Nuttall Ornithological Club, Cambridge, Mass.

**Submitted by:** Kevin Winker

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