AOS Classification Committee – North and Middle America

Proposal Set 2023-B

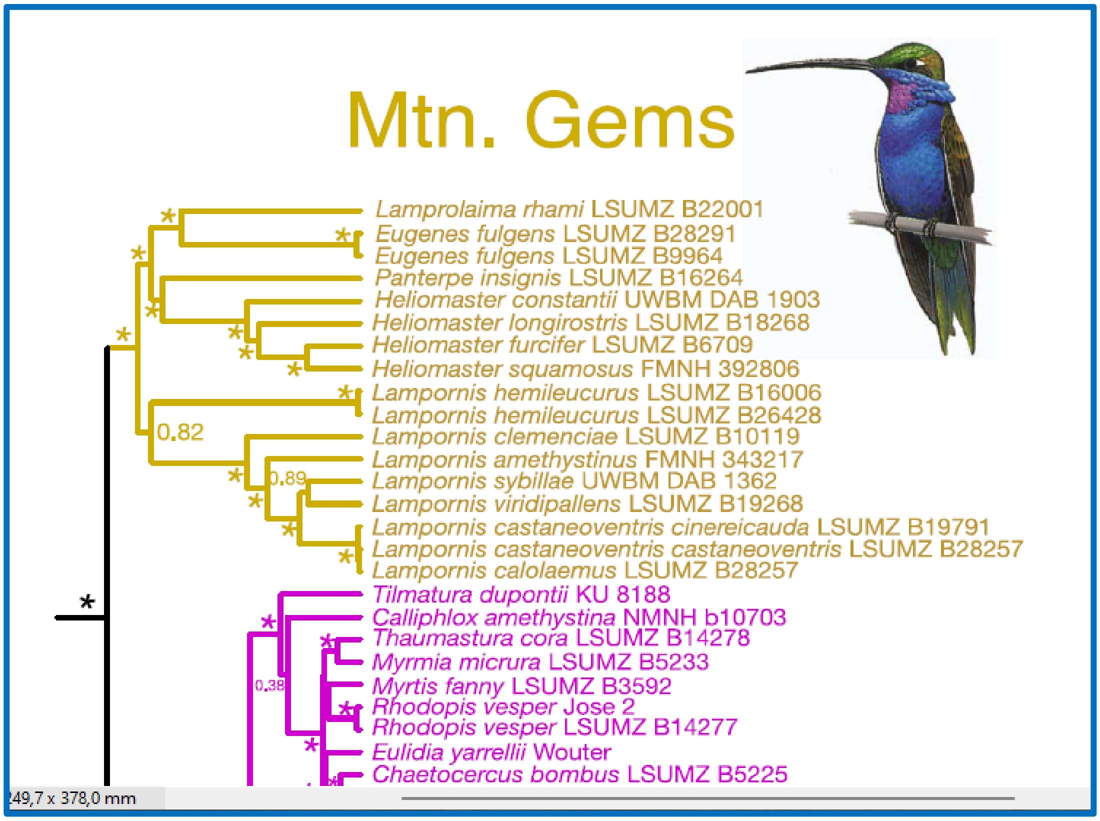
23 December 2022, revised 9 March 2023

Transfer White-bellied Mountain-gem *Lampornis hemileucus* to the monotypic genus *Prodosia*

Background and New Information:

The taxonomy of the Mountain-gem clade is relatively straightforward but does require this adjustment to bring it into line with the phylogenetic tree derived by McGuire et al. (2014).

Genetically, *Lampornis hemileucus* is a clear outlier, only distantly related to the remaining species of *Lampornis*. Although similar morphologically, it is the only species to combine a purple, somewhat indistinctly bordered gorget in the males and white underparts spotted with green only along the sides; its tail is somewhat less forked than other *Lampornis.* It occurs at lower elevations than the other *Lampornis* taxa of Costa Rica and Panama. The degree or timing of the separation of *hemileucus* from the rest of *Lampornis* is quite on a par with those of most other Mountain-gem genera; in fact, it is more entitled to genetic rank than is *Heliomaster*, which seems well-characterized morphologically and behaviorally by the long bills and long-distance traplining of flowers in the canopy by the included species.



The generic name available for *hemileucus*, described for this species, is *Prodosia* Simon, 1919. It is worth noting that in his synopsis and catalogue of the Trochilidae, Simon (1921) gave this name as *Prodoria* (including when citing his own earlier description!) but this name should be considered an incorrect subsequent spelling (ISS). Simon had the curious habit of explicitly or implicitly "correcting" names that he had already published.

Recommendation:

I recommend that *Lampornis hemileucus* be transferred to *Prodosia*.

References:

McGuire, J. A., C. C. Witt, J. V. Remsen, Jr., A. Corl, D. L. Rabosky, D. L. Altshuler & R. Dudley. 2014. Molecular phylogenetics and the diversification of hummingbirds. Current Biology http://dx.doi.org.1016/j. cub.2014.03.16.
Simon, E. 1919. Notes critiques sur les Trochilidés. Revue Francais d'Ornithologie 6:52-54.
Simon, E. 1921. Histoire naturelle des Trochilidae: Synopsis et Catalogue. Encyclopedia Roret L. Mulo, Paris: 420 pp.

Submitted by: F. Gary Stiles

Date of Proposal: 5 February 2022

Transfer subspecies *minor* (and extralimital subspecies *cinerascens*) from *Myiodynastes chrysocephalus* to *M. hemichrysus*, thereby removing *M. chrysocephalus* from the Checklist

The Checklist currently lists four species of flycatchers in the genus *Myiodynastes*, including two species, *M. hemichrysus* and *M. chrysocephalus*, identified as constituting a superspecies. These species are sometimes considered to be conspecific (e.g., Cory and Hellmayr 1927), but when they are separated, *M. hemichrysus* of Costa Rica and western Panama is generally treated as monotypic, whereas *M. chrysocephalus* includes, in addition to nominate *chrysocephalus* of the Andes of Peru, Bolivia, and northwestern Argentina, subspecies *cinerascens* of northern Colombia and Venezuela and subspecies *minor* of extreme eastern Panama south to extreme northern Peru. Although the subspecies included in each species are not specified in the accounts in AOU (1998), it is clear from the distributional statements that this is the subspecies arrangement.

Plumage is somewhat variable within the complex. According to Cory and Hellmayr, *hemichrysus*

> differs immediately from the southern race by the much deeper yellow, wholly unstreaked under parts, leaving only the chin white, and by lacking the conspicuous rufous edges to the rectrices. In wing-markings it more nearly resembles *M. c. chrysocephalus.*

The typical allocation of subspecies thus follows the most conspicuous plumage features, and this allocation is followed by most global sources (e.g., Dickinson and Christidis 2014, Clements et al. 2021, Gill et al. 2021). Birdlife, however, has recently partitioned the subspecies in a different way, transferring *minor* and *cinerascens* to *M. hemichrysus*. The rationale for this change was as follows:

> Races *minor* and *cinerascens* here transferred from *M. chrysocephalus* because their dawn songs (repeated “kweee!-tee-tu”) and daytime songs (strident “skeeeuw!”) are identical to those of present species [i.e., *M. hemichrysus*] and very different (scores of 3 for each) from those of *chrysocephalus* (respectively “kwee!-tlu-tee” and “ku-weet!.. weet!”, the “weet!” sharply rising and much higher-pitched than first note)…

They further note that *M. chrysocephalus* also differs from *M. hemichrysus* by its longer wing and tail and much buffier and more restricted rufous edges to the tail.

The vocal descriptions above are condensed versions of the conclusions of Boesman (2016), who compared vocalizations of all four taxa in this complex. The similarity of the dawn and day songs of *hemichrysus*, *minor*, and *cinerascens* are apparent from his figure and measurements comparing the vocalizations (see following pages), as are the differences with *chrysocephalus*. Boesman’s summary of the differences is as follows:

Voice of *Myiodynastes hemichrysus* is about identical to *M. c. minor* and *M. c. cinerascens.* We would need a large number of samples to prove any consistent difference, but in any case it would be very small. (Possibly the note shape is slightly different, with *M. hemichrysus* having a little notch at the right side of the day-time song). Difference score for these taxa is thus 0 (or possibly 1).

Difference with *chrysocephalus* at the other hand is quite noticeable: Day-time song has 2 (or 3) distinct notes (score 3) with very different note shape (score 1) and slightly longer overall length (score 1). Dawn song ends with a fairly emphasized rising note (unlike all other races which end in subdued notes) (score 2) and note shape of first note different (score 1). The fact that both dawn song and day-time song are clearly different makes this case even more convincing.

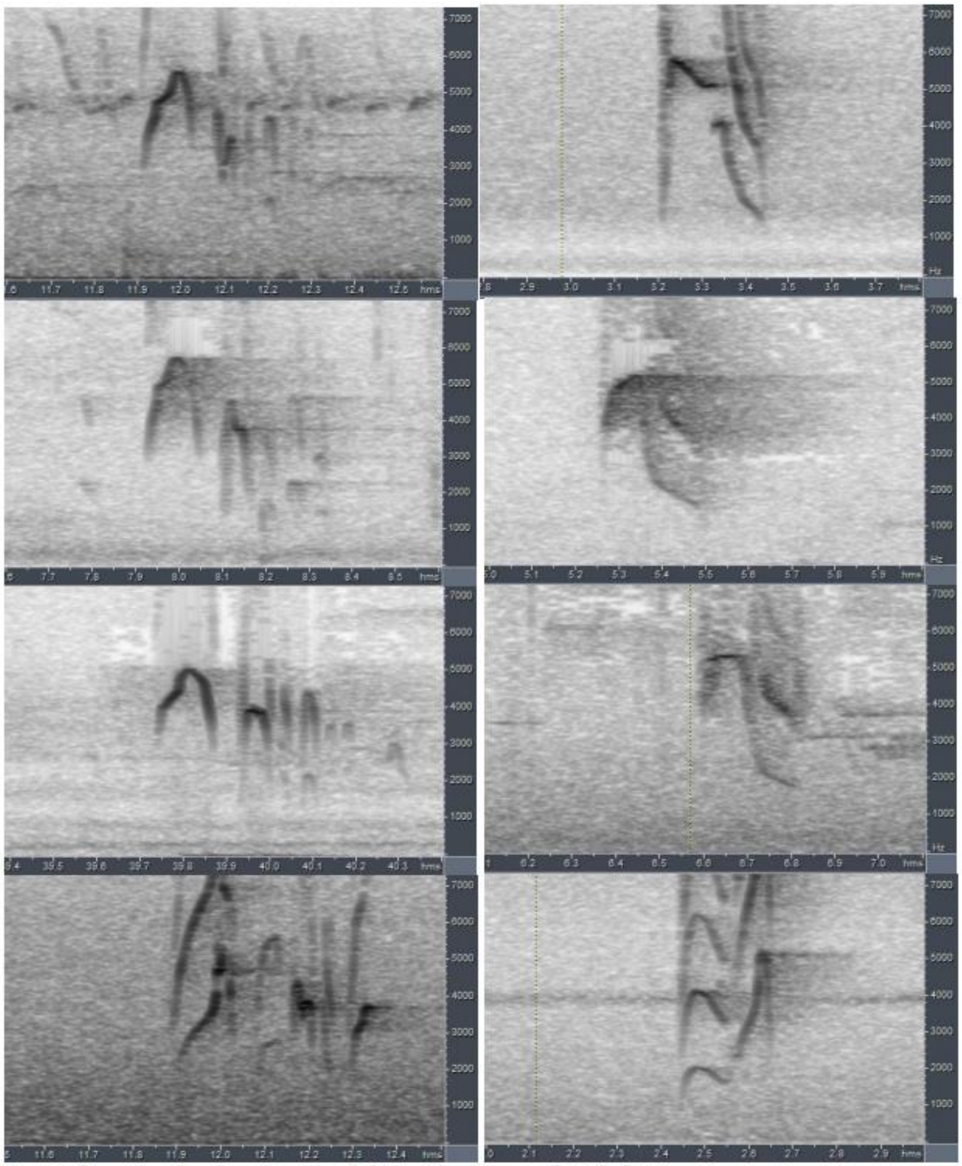


Figure 1: from top to bottom: dawn song (left) and day-time song (right) of *M. hemichrysus, M.c.minor, M.c.cinerascens* and *M. c. chrysocephalus*

Myiodynastes hemichrysus
dawn-song: a repeated "kwee!-tee-t-tu" (n=1)
min. freq. 2140Hz
max. freq. 5600Hz
total length 0.39s
length 1st note 0.13s

day-time song: a repeated loud strident "skeeew!" (n=6)
min. freq. 1200-1550Hz
max. freq. 5350-5830Hz
total length 0.18-0.25s

M. c. minor
dawn-song: a repeated "kwee!-tee-tu" or "kwee!-tee-tu-ti-lu" (n=3)
min. freq. 1380-1590Hz
max. freq. 5290-5740Hz
total length 0.32-0.43s
length 1st note 0.12-0.14s

day-time song: a loud strident "skeeeuw!" (n=6)
min. freq. 1030-1450Hz
max. freq. 5000-5550Hz
total length 0.15-0.29s

M. c. cinerascens
dawn-song: a repeated "kwee!-tee-tu" (n=2)
min. freq. 1300-1320Hz
max. freq. 5030-5120Hz
total length 0.37-0.39s
length 1st note 0.15-0.16s

day-time song: a loud strident "skeeew!" or "skeeeuuw!" (n=6)
min. freq. 1060-1400Hz
max. freq. 4540-6340Hz
total length 0.17-0.28s

M. c. chrysocephalus
dawn-song: a repeated "kwee!-tlu-tee" (n=2)
min. freq. 1950-2050Hz
max. freq. 5220-5300Hz
total length 0.42-0.46Hz
length 1st note 0.12-0.13s

day-time song: a loud strident "ku-weet!" or "ku-weet!.. weet!" (weet! sharply rising and much higher-pitched than first note) (n=8)
min. freq. 1150-1380Hz
max. freq. 4000-5300Hz
total length 0.22-0.66s
# of notes 2-3

Sample sizes for these comparisons aren't huge, especially for dawn songs, but recordings available on the xeno-canto and Macaulay Library websites confirm the differences between the two species and clearly place *minor* and *cinerascens* with *M. hemichrysus* rather than *M. chrysocephalus*.

These differences were also recognized in the field guide to the birds of Peru (Schulenberg et al. 2007), in which a clear distinction was made between the vocalizations of *minor* of northern Peru and those of the more widespread *chrysocephalus*, although without comparing the vocalizations of *minor* with those of Central American *hemichrysus.*

Recommendation:

I recommend that we transfer subspecies *minor* (and extralimital subspecies *cinerascens*) from *M. chrysocephalus* to *M. hemichrysus*. Although plumage favors the traditional placement of *minor* and *cinerascens* in *chrysocephalus*, this is contradicted by the vocal data, which indicate that these two subspecies belong in *M. hemichrysus*. Vocalizations are innate and primary indicators of species limits and affinities in suboscine birds, and in this case they demonstrate that the traditional allocation of subspecies in the complex was in error. If adopted, this change would remove *M. chrysocephalus* from the Checklist.

References:

Boesman, P. 2016. Notes on the vocalizations of Golden-crowned Flycatcher (*Myiodynastes chrysocephalus*) and Golden-bellied Flycatcher (*Myiodynastes hemichrysus*). HBW Alive Ornithological Note 141. In: Handbook of the Birds of the World Alive. Lynx Edicions, Barcelona. (retrieved from http://www.hbw.com/node/932065 on 10 August 2016).

Schulenberg, T. S., D. F. Stotz, D. F. Lane, L. B. McQueen, J. P. O'Neill, and N. John Schmitt. 2007. Birds of Peru. Princeton University Press, Princeton.

Submitted by: Terry Chesser

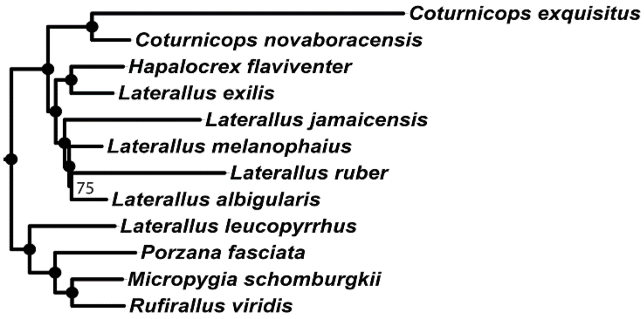
Date of Proposal: 12 October 2022

Modify the classification of the Rallidae: (a) transfer *Micropygia schomburgkii* to *Rufirallus*, (b) transfer *Neocrex erythrops* and *N. colombianus* to *Mustelirallus*, (c) transfer *Cyanolimnas cerverai* to *Mustelirallus* or *Neocrex*, and (d) slightly alter the linear sequence

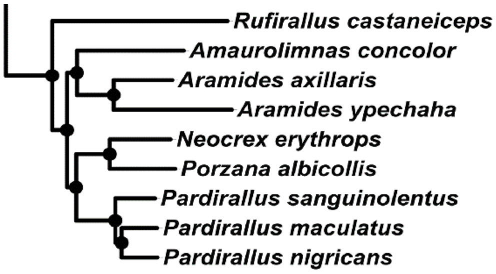
Recent research on the Rallidae includes two phylogenetic studies of the family (Garcia-R et al. 2014, 2021); these papers were the basis for our recent revision of the linear sequence of the Rallidae (Chesser et al. 2020). Now two additional studies have been published, one focused on phylogenetics of the entire family (Kirchman et al. 2021), sampling 82 of the ca. 130 species in the family, and the other focused on phylogenetic relationships of the Zapata Rail *Cyanolimnas cerverai* (Brown et al. 2022), a species not successfully sequenced in the Kirchman study.

Two results in Kirchman et al. (2021) are of relevance to our classification:

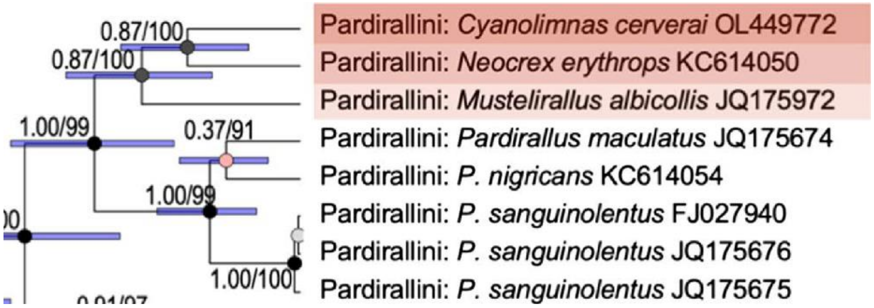
(1) Their results show that *Micropygia schomburgkii* is part of a four-species clade: *M. schomburgkii* is sister to *Rufirallus viridis*, and *Porzana fasciata* and *Laterallus leucopyrrhus* are successive sisters to *Micropygia* + *Rufirallus*. *Micropygia* and *Rufirallus* are monotypic genera, but *P. fasciata* and *L. leucopyrrhus* are representatives, but not the type species, of polyphyletic genera. Therefore, either new or resurrected monotypic genera are required for *P. fasciata* and *L. leucopyrrhus*, or all four species in the clade should be placed in *Rufirallus* (or three species could be placed in *Rufirallus* and *L. leucopyrrhus* placed in a monotypic genus). Kirchman et al. (2021) opted to place the four species in *Rufirallus*, which seems better than creating additional monotypic genera.



(2) Their results, like those of Garcia-R (2014), demonstrate that *Neocrex erythrops* is sister to *Mustelirallus albicollis* (shown in the tree as *Porzana albicollis*). SACC already transferred both species of *Neocrex* (including the unsampled *N. colombianus*) to *Mustelirallus* based on Garcia-R et al. (2014) (see https://www.museum.lsu.edu/~Remsen/SACCprop650.htm). Both species are also found in our area.



Although Kirchman et al. (2021) sampled a toepad of *Cyanolimnas cerverai* for their UCE study, no sequence was recovered. However, Brown et al. (2022) were successful in sequencing fragments of the mitochondrial gene CO1 for this species. Obviously this is not data on the same scale, but it does provide the first genetic information concerning the relationships of this species. Their results place it more-or-less as expected from the morphology, as sister to *Neocrex* within the Pardirallini:



Because *C. cerverai* is sister to the species of *Neocrex* sampled for the Brown et al. (2022) study, it appears to form part of the clade that includes both *Neocrex* and *Mustelirallus*. As noted in the SACC proposal referenced above, a sister relationship between *Cyanolimnas* and *Neocrex* is also supported by phenotypic characters: *C. cerverai* shares red legs and a red bill base with species of *Neocrex*. If the proposal to merge *Neocrex* into *Mustelirallus* is adopted, then *C. cerverai* should also be transferred to *Mustelirallus*. If the proposal to merge *Neocrex* into *Mustelirallus* is rejected, then we should vote on transferring *C. cerverai* to *Neocrex*.

The result in Brown et al. (2022) will also require a slight adjustment to our linear sequence because the addition of *C. cerverai* to the *Mustelirallus*-*Neocrex* clade means that it now contains more species (4, including *N. colombianus*) than does the *Pardirallus* clade (3), so *Pardirallus* will have to be moved to precede *Cyanolimnas* and *Mustelirallus*-*Neocrex*. Fortunately, no other adjustments to our linear sequence are necessitated by this paper or the Kirchman et al. (2021) phylogeny.

Recommendation:

I recommend that we (a) transfer *Micropygia schomburgkii* to *Rufirallus*, (b) transfer *Neocrex erythrops* and *N. colombianus* to *Mustelirallus*, (c) transfer *Cyanolimnas cerverai* to *Mustelirallus*, and (d) make the suggested adjustment to the linear sequence.

References:

Brown, A. F., Y. Lawrie, T. J. Shannon, J. M. Collinson, G. M. Kirwan, A. Kirkconnell, and M. Stervander. 2022. First genetic data for the critically endangered Cuban endemic Zapata Rail *Cyanolimnas cerverai*, and the taxonomic implications. Journal of Ornithology 163:945-952.

Chesser, R. T., S. M. Billerman, K. J. Burns, C. Cicero, J. L. Dunn, A. W. Kratter, I. J. Lovette, N. A. Mason, P. C. Rasmussen, J. V. Remsen, Jr., D. F. Stotz, and K. Winker. 2020. Sixty-first supplement to the American Ornithological Society's *Check-list of North American Birds*. *Auk: Ornithological Advances* 137 (3): ukaa030, pp. 1-24. http://doi.org/10.1093/auk/ukaa030

Garcia-R, J. C., G. C. Gibb, and S. A. Trewick. 2014. Deep global evolutionary radiation in birds: diversification and trait evolution in the cosmopolitan bird family Rallidae. Molecular Phylogenetics and Evolution 81:96-108. https://doi.org/10.1016/j.ympev.2014.09.008

Garcia-R, J. C., and N. J. Matzke. 2021. Trait-dependent dispersal in rails (Aves: Rallidae): historical biogeography of a cosmopolitan bird clade. Molecular Phylogenetics and Evolution 159:107106. https://doi.org/10.1016/j.ympev.2021.107106

Kirchman J. J., N. R. McInerney, T. C. Giarla, S. L. Olson, E. Slikas, and R. C. Fleischer 2021. Phylogeny based on ultra-conserved elements clarifies the evolution of rails and allies (Ralloidea) and is the basis for a revised classification. Ornithology 138:ukab042. https://doi.org/10.1093/ornithology/ukab042

Submitted by: Terry Chesser

Date of Proposal: 12 October 2022, revised 9 March 2023

Treat *Poliocrania maculifer* as a separate species from Chestnut-backed Antbird *P. exsul*

Description of the problem:

Poliocrania exsul is an understory antbird found in tropical lowland forests of Central America and the Chocó, from Honduras to Ecuador (Woltmann et al. 2020). In its current treatment, it consists of five subspecies that can be broadly split into two groups based on the presence or absence of white spots on the wing coverts (Woltmann et al. 2020). The northern *exsul* ("Sclater, PL", 1859) group lacks wing spots and is found in Central America, barely reaching northern Colombia on the Caribbean slope (near Acandí; Hilty and Brown 1986), and consists of the subspecies *exsul* (Caribbean slope from Costa Rica to western Panama), *niglarus* (Wetmore, 1962; central Panama to northern Colombia), and *occidentalis* (Cherrie, 1891; Pacific slope from Honduras to western Panama). The wing-spotted *maculifer* (Hellmayr, 1906) group is found in the Chocó and reaches into the Magdalena Valley of northern Colombia and into eastern Panama in the lowlands of Darién Province on the Pacific slope (Woltmann et al. 2020). This group consists of the southern subspecies *maculifer* and the northern subspecies *cassini* (Ridgway, 1908). Females of the *maculifer* group are also distinguished by brighter chestnut underparts.

Hellmayr (1906) described *maculifer* as a subspecies of *exsul* (also considering *occidentalis* as a subspecies), with the primary differences being the “fulvous-white apical spots on all the wing coverts” in both sexes, and a shorter tail (40-44 mm in male *maculifer* vs. 47-52 mm in males of *occidentalis* and *exsul*). Ridgway (1908), describing *cassini* just two years later, considered both *maculifer* and *cassini* to be valid species, each as distinct from *exsul*, with the only rationale being a footnote under *cassini* that says, “This form is evidently quite distinct specifically from *Myrmeciza exsul* Sclater”. In Ridgway’s description of *cassini*, he stated that:

> This form agrees with *M. maculifer* in its relatively very short tail (as compared with *M. exsul* and *M. exsul occidentalis*), and also in having *all* the wing-coverts marked with a terminal white spot, and may be only subspecifically distinct; but the coloration is so conspicuously different that at present, or until actual intermediates are found, I prefer to designate it by a binomial.

However, Chapman (1917), with a larger series of specimens, noted that intermediates between *maculifer* and *cassini* occurred over a broad region, including some localities containing specimens resembling both taxa, and gave the approximate boundary between the two taxa as the upper Atrato River (southwest of Medellín, Colombia) with *cassini* found north into the Magdalena Valley. Chapman (1917) also noted that specimens of *cassini* from eastern Panama showed no signs of intergradation with *exsul* from the Canal Zone and westward and considered *maculifer* (with *cassini* as a subspecies) to be a separate species from *exsul*. Cory and Hellmayr (1924) considered all taxa to be part of *exsul* (without comment), a treatment followed by Peters (1951), Eisenmann (1955), and most later authors. It is surprising that Cory and Hellmayr (1924) gave no reasoning for lumping *maculifer/cassini* with the northern *exsul* group, as these authors were careful to cite the broad intergradation between *maculifer* and *cassini* described by Chapman (1917) and were typically very thorough in their taxonomic treatments.

However, it appears that individuals with white spots in the wings extend far beyond the contact zone in the central Darién Province of Panama. Wetmore (1962), in describing *niglarus* (of the northern *exsul* group) from Chimán in far eastern Panamá Province (near the Darién border, geographically about halfway between the specimens available to Chapman) noted that some individuals of this subspecies showed intermediate amounts of wing spotting: “The wing coverts are plain in most individuals of this race, with the white spotting typical of *M. e. cassini* and *M. e. maculifer* found only casually in a few. Specimens from the middle Chucunaque Valley, near the mouth of the Rio Tuquesa, are intermediate between the new form and *cassini*, which ranges through the rest of the lowlands of the Tuira basin”. These latter localities are in the central Darién province of Panama. AOU (1983) followed this treatment, noting that “Populations from eastern Panama (eastern Darién) south to western Colombia have sometimes been regarded as a distinct species, *M*. *maculifer* (Hellmayr, 1906) [WING-SPOTTED ANTBIRD], but intergradation occurs in western Darién.” Ridgely and Gwynne (1989) noted that some birds with wing spots can be found as far west as Cerro Jefe on the Caribbean slope of the Canal Zone.

BirdLife International split the *maculifer* group from the *exsul* group based on the following rationale: *P. maculifer* "[h]itherto considered conspecific with *P. exsul*, but (although voices appear identical) differs in its white spots on wing-coverts (3); brighter underparts in female (1); paler grey underparts in male (1); olive-chestnut vs dark chestnut upperparts in both sexes (ns1); shorter tail (effect size -4.9, score 2); narrow zone of hybridization (2)."

Woltmann et al. (2020) described the song as “Two or three full, mellow whistles. […] The first note is more emphatic, with a deliberate, but short (1 s) pause before the next note, which may or may not be of lower pitch. In the 3-note song it is the first syllable that is repeated (the second note sometimes at a higher pitch) and never the last syllable.” They noted that *maculifer* may give the three-note song more frequently than the two-note song.

New information:

Very little. Other than an excellent summary of geographic variation in the *Poliocrania exsul* complex in Woltmann et al. (2020), I can find no recent publications with taxonomic relevance on this group.

The Harvey et al. (2020) suboscine phylogeny included two samples of *P. exsul*, but both were of the subspecies *occidentalis*, one from Limón on the Caribbean coast of Costa Rica, and the other from Coclé, Panama, the latter of which is near the contact zone with *niglarus*. However, no samples were from the southern *maculifer* group.

Below are a series of photos of specimens at the Louisiana State University Museum of Natural Science (LSUMNS), courtesy of Anna Hiller and Nicholas Mason (Figs. 1-3).

Figure 1. Seven specimens from the *maculifer* group. The upper five are of *maculifer* and the lower two are of *cassini*. Note that one of the males of *maculifer* has the wing coverts obscured by flank and scapular feathers, such that any wing spots (if present) are not visible.

Figure 2. A series of specimens of *exsul* (upper 6) and *occidentalis* (lower 3) showing the lack of wing spotting and overall darker coloration of both sexes in comparison with the Chocó taxa.

Figure 3. Females of (L to R) *exsul*, *cassini*, and two *maculifer,* showing especially the brighter underparts of the southern taxa.

Although most photos available online (Macaulay) from Darién Province seem to agree with the LSUMNS specimens (e.g. https://macaulaylibrary.org/asset/48605081), two from central Darién seem to show limited white spotting (https://macaulaylibrary.org/asset/494631221 and https://macaulaylibrary.org/asset/343711101) and although the photo is not clear, one may lack spotting (https://macaulaylibrary.org/asset/223776311). However, topotypical *niglarus* is found only a short distance (about 80 km) to the west of most of these individuals (https://macaulaylibrary.org/asset/202364931), so the contact zone seems to be quite limited in extent. A female from the Canal Zone in Panama shows the darker underparts of the *exsul* group but has small white spots on the wing coverts: https://macaulaylibrary.org/asset/35110341. I found photos of two adult males in Costa Rica

(out of ~1,000 photos available in the Macaulay Library) with very limited white spots on the median coverts:
https://macaulaylibrary.org/asset/178037841 and https://macaulaylibrary.org/asset/54813581.
All individuals in Macaulay from Ecuador and Colombia had clearly spotted wing coverts.

There appear to be no published analyses of vocal differences between taxa, aside from the assertion in Woltmann et al. (2020) that *maculifer* gives 3-note songs more frequently than the *exsul* group. In listening to recordings, I was able to find multiple recordings of 3-note songs in *maculifer* and *cassini*, and although I found only a few examples of 3-note songs in the *exsul* group, they do exist.

maculifer, 3 note*:* https://macaulaylibrary.org/asset/28482
exsul, 3-note: https://macaulaylibrary.org/asset/55245961

However, 2-note songs were also common in *maculifer*, e.g.:
https://macaulaylibrary.org/asset/499635721

And most from *occidentalis* and *exsul* were 2-note: https://macaulaylibrary.org/asset/338492511

Although some recordings from Costa Rica sound a bit higher-pitched, I am unable to detect consistent vocal differences between the northern *exsul* and southern *maculifer* groups. However, a formal analysis is desirable.

Effect on AOS-CLC area:

Splitting *maculifer* from *exsul* would result in one additional species for the AOS area.

Recommendation:

I recommend a **NO** on splitting *maculifer* from *exsul* based on apparent intermediates in the Darién, a lack of published studies on this contact zone, and apparently minimal vocal differences. Based on the data in Wetmore (1962), it appears that there is a (perhaps narrow) hybrid zone in the central/western Darién, although the exact width and evolutionary dynamics of this hybrid zone have not been investigated. Other than the brief mention by Ridgely and Gwynne (1989), there appear to be no data on whether there are intermediate phenotypes on the Caribbean slope of eastern Panama and northern Colombia. Given the utility of vocal divergence as a metric for species-level differences between antbird species (Isler et al. 1998), the minimal vocal differences (in just a scan of recordings available online, formal analysis needed) between the *maculifer* and *exsul* groups also indicate that these are best treated as subspecies for now.

If *maculifer* is split from *exsul*, then an English name proposal should be drafted to address the new names, preferably in coordination with the SACC. Clements/eBird uses the common names of Chestnut-backed Antbird for *exsul* and Short-tailed Antbird for *maculifer*. I prefer Wing-spotted Antbird for *maculifer*, as suggested by AOU (1983), as this is the more obvious morphological character separating this group. Chestnut-backed Antbird has been used for both the *exsul* group and for the entire complex, with no other name published for the *exsul* group.

Literature Cited:

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Submitted by: Oscar Johnson, The University of Texas at El Paso

Date of proposal: 15 November 2022

Treat *Xiphorhynchus aequatorialis* as a separate species from Spotted Woodcreeper X. *erythropygius*

Description of the problem:

Xiphorhynchus erythropygius is an uncommon species of upper tropical and lower montane zones from central Mexico (San Luis Potosí) south through Central America and the Chocoan forests as far south as southern Ecuador (Marantz et al. 2020). Although its distribution is largely contiguous, there are multiple breaks in lowland zones. One of these is in Nicaragua and divides the species into a northern (*erythropygius*) group and southern (*aequatorialis*) group, with the species absent from most of the southern half of Nicaragua (Vallely and Dyer 2018, Marantz et al. 2020). The northern group is composed of *erythropygius* ("Sclater, PL", 1860) from north of the Isthmus of Tehuantepec and *parvus* Griscom, 1937 to the south of the isthmus. The southern group is composed of *punctigula* (Ridgway, 1889) from Nicaragua to central Panama, *insolitus* Ridgway, 1909, from central Panama to central Colombia (including the Magdalena Valley), and *aequatorialis* (von Berlepsch & Taczanowski, 1884) from central Colombia to southwestern Ecuador. Olive-backed Woodcreeper (*Xiphorhynchus triangularis*) of the Andes is part of this complex, and some authors have considered all taxa to be part of *triangularis* (see below). Hilty and Brown (1986) noted that *triangularis* is an upper elevation (above 1,500 meters) replacement of *aequatorialis* on the west slope of the Andes in Colombia.

Taxonomic history:

Ridgway (1911) considered *erythropygius* monotypic but noted that Berlepsch and Stolzmann (1896) considered *erythropygius* to be a subspecies of *triangularis.* Ridgway (1911) split *punctigula* (with *insolitus* as a subspecies) as Spotted-throated Woodhewer, with the following comment: “Somewhat like *X. erythropygius*, but color of pileum, back, and under parts greenish or ocherous olive instead of olive-brown, back without streaks or with very narrow ones on anterior portion only, and throat spotted rather than barred with dusky.” He gave the range of *punctigula*/*insolitus* as Nicaragua (San Rafael del Norte) to northwestern Colombia (Río Truando). Berlepsch & Taczanowski (1884) described *aequatorialis* as a subspecies of *erythropygius*, but *aequatorialis* was overlooked by Ridgway (1911) who considered *punctigula* as the name for the southern group, although *aequatorialis* has priority.

Cory and Hellmayr (1925), perhaps following Berlepsch and Stolzmann (1896), considered all taxa in the complex to be part of *X. triangularis*, with the following English names for the relevant taxa: Pacific Wood-Hewer for *aequatorialis*, Truando Wood-Hewer for *insolitus* (presumably based on the Río Truando in northern Colombia), Spotted-throated Wood-Hewer for *punctigula*, and Spotted Wood-Hewer for *erythropygius*. Cory and Hellmayr’s comments on the reasoning for lumping all these taxa are worth reproducing here in full, as they constitute (as far as we can tell) the most comprehensive comments on plumage variation in the complex, with taxa arranged from south-to-north:

> *Xiphorhynchus triangularis aequatorialis* (Berlepsch and Taczanowski): Differs from *X. t. triangularis* in more brownish (less olivaceous) upper parts; plain (unspotted)

> crown, with only a few narrow buff streaks on forehead; the much deeper chestnut rufous of wings and tail spreading also over the lower back; much deeper buff throat, with the olive markings restricted to small, rounded apical spots; larger spots on breast and abdomen; uniform horn brown maxilla, etc.
>
> *Xiphorhynchus triangularis insolitus* appears to have been based on intergrades between *aequatorialis* and *punctigula*. The specimen listed above, obtained by A. Schott on Lt. N. Michler's Expedition to the lower Atrato [northwestern Colombia], has the back decidedly browner than the majority in the series of the two forms, though it is very nearly matched by a female from Bulun, Prov. Esmeraldas, Ecuador, and an unsexed individual from Chiriqui [Panama]. Markings of throat and spotting on underparts are exactly as in *punctigula*. On the other hand, two skins from Calovevora, Veragua [Panama] hence not far from the type locality of *insolitus* and in the same general region I am quite unable to distinguish from Costa Rican specimens of *punctigula*, which, moreover, is sometimes hard to separate from *aequatorialis*. Individual variation in these birds is much greater than generally admitted.
>
> [Regarding a specimen from San Rafael del Norte in northern Nicaragua] In the amount of spotting above, this bird is exactly intermediate between *punctigula* and *erythropygia*, but resembles the former in olivaceous coloration and restricted rufous uropygial area.
>
> *Xiphorhynchus triangularis punctigula.* Birds from Veragua (Calovevora) and Chiriqui [Panama] are identical with those from Costa Rica. *X. t. punctigula* is exceedingly close to *X. t. aequatorialis*, but generally distinguishable by brighter olivaceous under parts with smaller buff spots, more heavily spotted throat, somewhat lighter rufous rump and wings, etc. Single specimens are, however, not always separable. Through individual variation, it also intergrades with *X. t. erythropygius*, of Guatemala. There is notably a specimen from Chiriqui (at Tring), which combines the greenish olive coloration of *punctigula* with the heavy spotting, both above and below, of *erythropygia*. Similar examples are no doubt responsible for Panama records of the last named race.

In a departure from his typical pattern of lumping taxa without comment, Peters (1951) split the Choco/Middle American taxa from *X. triangularis* (although again without comment), a treatment maintained by Eisenmann (1955), Wetmore (1972), AOU (1983), and most current authors.

Multiple authors (e.g., Eisenmann 1955, AOU 1983) noted that the *aequatorialis* group is sometimes recognized as a separate species from *erythropygius*, a treatment formalized by HBW-BirdLife: "[*aequatorialis*] Hitherto considered conspecific with *X. erythropygius*, but differs in its much less obvious, less teardrop-shaped (and often minimal) pale streaking on mantle and back (2); darker chestnut tail (1); slightly less dense pale spotting on underparts (1); higher maximum frequency of whistles in song after first whistle (2), and overslurred vs downslurred whistles in song after first whistle (2) (Boesman 2016)."

AOU (1983) account: populations from eastern Nicaragua southward, occurring commonly in lowland habitats, are sometimes recognized as a species, *X. aequatorialis* (Berlepsch and Taczanowski, 1884) [SPOT-THROATED WOODCREEPER], distinct from *X. erythropygius*. The widespread South American species, *X. triangularis* (Lafresnaye, 1842), and *X. erythropygius* are regarded as conspecific by some authors; they constitute a superspecies.

New information:

Although many studies have sampled *Xiphorhynchus erythropygius* for phylogenetic work, most included only a single sample, so are not of use here. The sole study we have been able to find that included multiple taxa is Weir (2009), who sampled three individuals and sequenced the mitochondrial locus cytochrome-b. Samples from El Copé, Panama, and Darién, Panama (both *insolitus* under current taxonomy), were sisters, whereas one from the western slope of the Andes (=*aequatorialis*) was sister to those two. However, no genetic distances were reported, and the northern *erythropygius* group was not sampled. Two samples in Harvey et al. (2020) were both of *erythropygius* (*sensu stricto*), whereas two samples in Aleixo (2002) were both of *aequatorialis*. Multiple studies found *erythropygius/aequatorialis* as sister to *X. triangularis*.

Below are photos of most taxa in the group, from the collections at the Louisiana State University Museum of Natural Science (LSUMNS). The two samples of *insolitus* are from Darién, Panama, so east of the canal zone.

The specimens at LSUMNS show a confusing patchwork of plumage variation that do not readily align with current species limits. The one taxon in the complex not represented in the LSUMNS collections is the Venezuelan *X. t. hylodromus* (see photo in Macaulay Library: https://macaulaylibrary.org/asset/205397931).

The plumage character that most readily distinguishes *X. triangularis* from *X. erythropygius* (as currently defined) is the scalloped vs spotted throat. However, nominate *triangularis* (with *hylodromus* based on the Macaulay photo above) shares the extensive and broad streaking on the belly shown by all taxa in *X. erythropygius*, and is quite distinct in this regard from the two southern taxa in *X. triangularis* (*intermedius* and *bangsi*), which show sparse streaks on the belly. Within *X. erythropygius*, the two northern taxa (Spotted group) show extensive dorsal streaking not shown by other taxa, whereas the three southern taxa (Berlepsch's group) show less crown spotting than either the Spotted group or *X. triangularis*, although one specimen of *aequatorialis* seems to show some crown spotting (Figure 1, right hand specimen).

Vocal variation

To our knowledge the only quantitative analysis of vocal variation within the *X. erythropygius* / *X. triangularis* complex comes from Boesman (2016), who described vocal variation within *X. erythropygius*. There is considerable variation among recognized subspecies across the two currently recognized species. We are not aware of any rigorous playback studies on this group.

Between the currently recognized subspecies within *X. erythropygius*, there are some slight differences across the putative split in question, but they are overall quite similar. Both groups

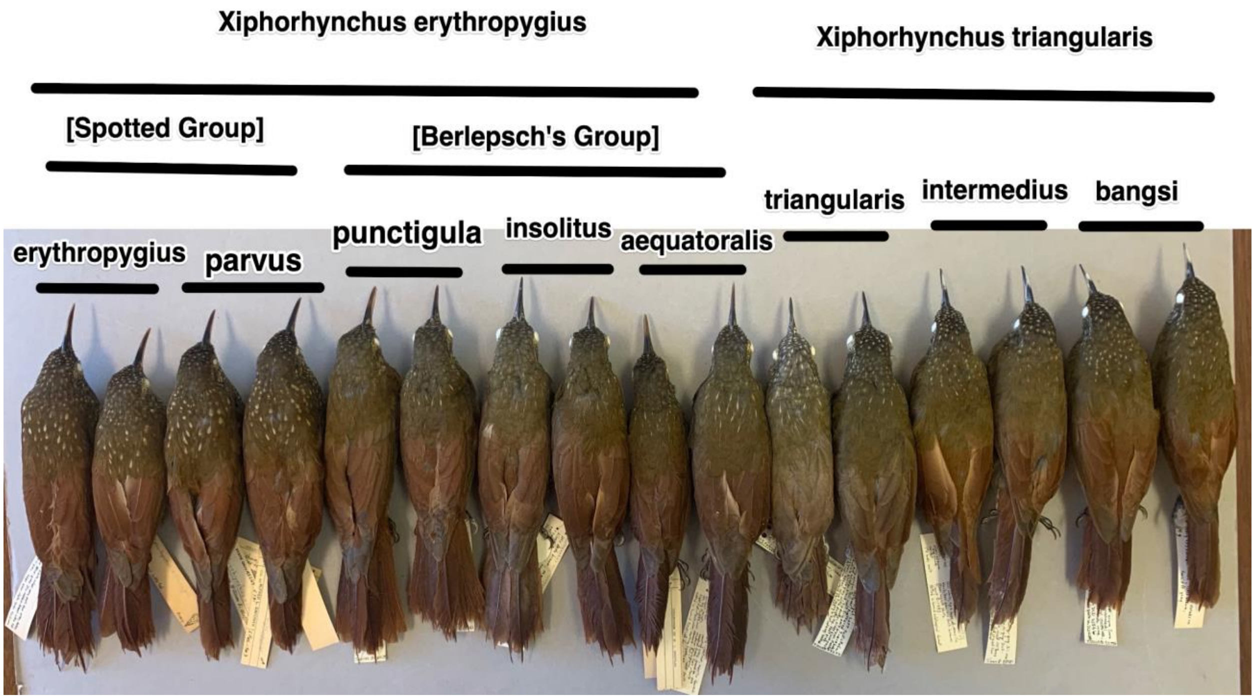

Figure 1: Dorsal view of LSUMNS specimens of *X. erythropygius* and *X. triangularis.*

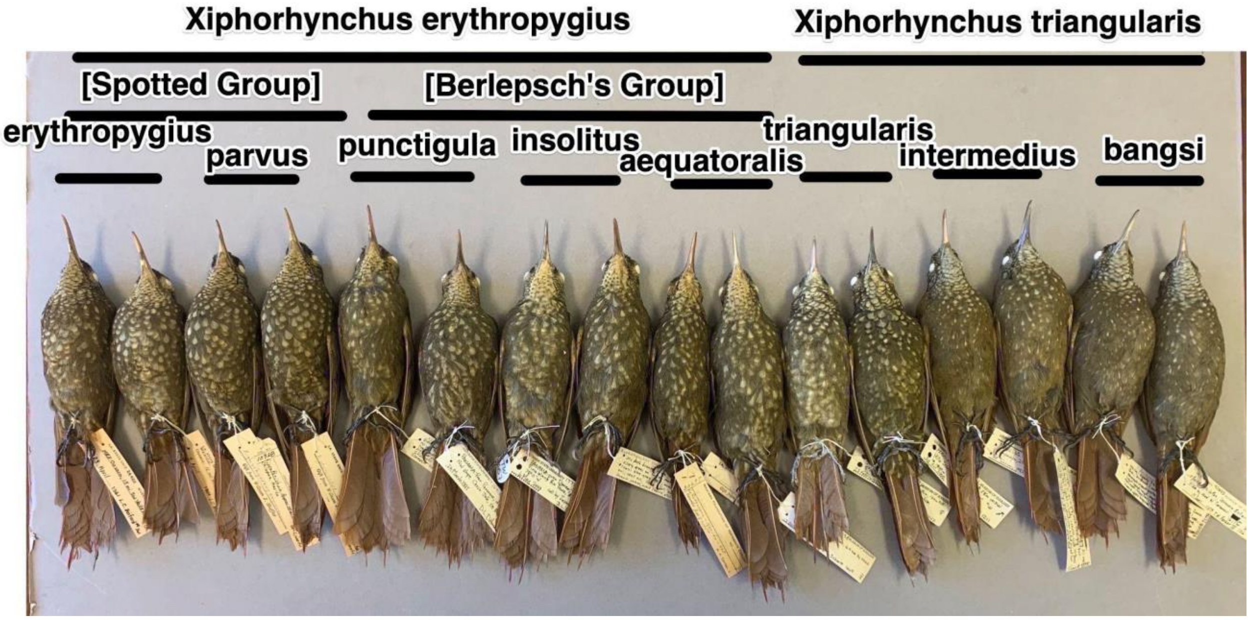

Figure 2: Ventral view of LSUMNS specimens of *X. erythropygius* and *X. triangularis.*

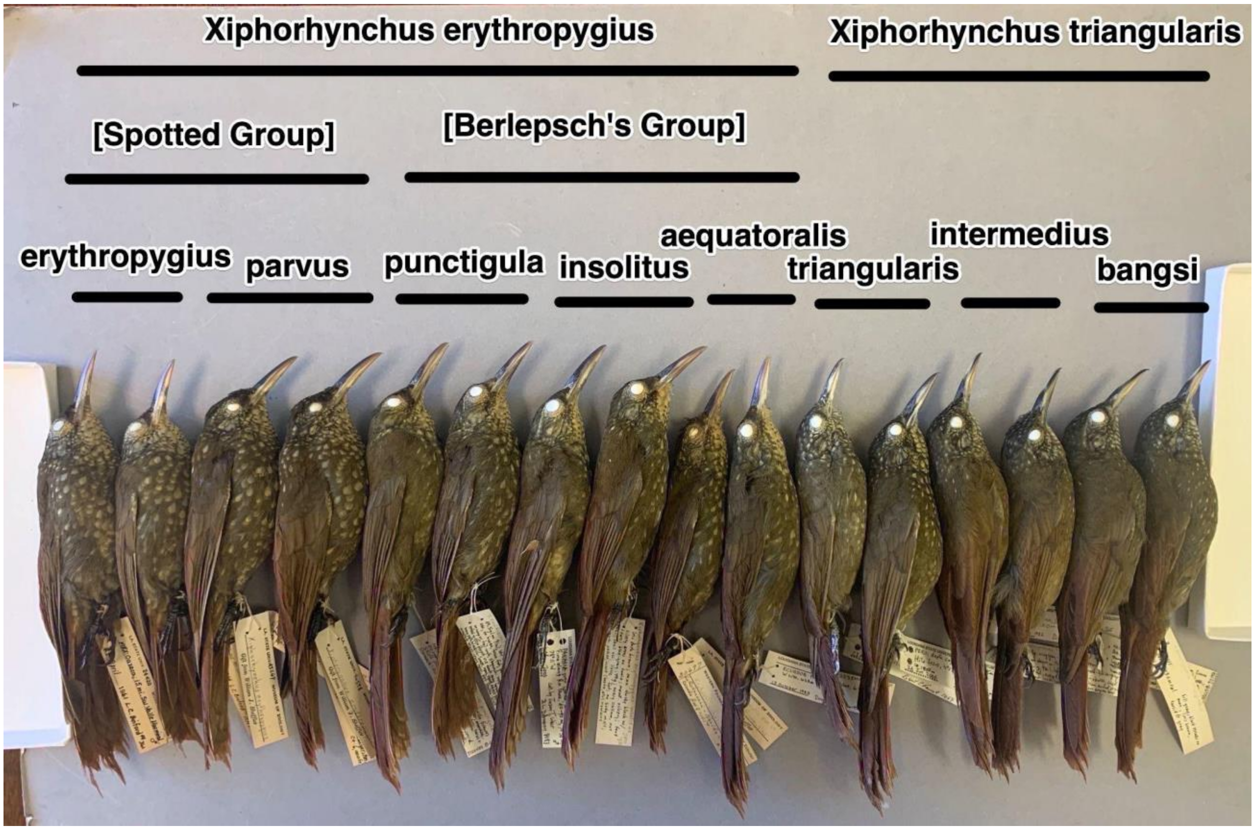

Figure 3: Lateral view of LSUMNS specimens of *X. erythropygius* and *X. triangularis.*

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emit a similar series of 2-4 whistles each of approximately 0.5–1.0 s in length. However, the *erythropygius* / *parvus* group has little to no frequency modulation in these whistles and is slightly lower in pitch, starting at ~2.5 kHz and descending to ~1.5 kHz. Among the Berlepsch's group of *punctigula / insolitus / aequatorialis*, the nearest neighbor *X. e. punctigula* in Costa Rica has a similar structure in the series of whistles to the *erythropygius* / *parvus* group, but the first *punctigula* note has considerably more frequency modulation and higher pitch overall, starting at ~3.5 kHz and descending to ~2.5 kHz. The songs of *X. e. aequatorialis* are the most distinct among these in having much more frequency modulation in each of the notes, giving them much more of a 'quavering' tone compared to the pure 'whistled' tone of those in Costa Rica or north of Nicaragua. The quavering tone seems to extend to the west of the Canal Zone in Panama, but then becomes decidedly more clear east of the Canal Zone. The type locality of *insolitus* is in Coclé, Panama, so *insolitus* would be of the northern vocal type. Please note that these observations are qualitative and may not stand up to a more rigorous quantitative analysis of larger sample sizes for vocal variation within the group.

Boesman (2016) divided *X. erythropygius* into two vocal groups, a northern one (comprised of *erythropygius* and *parvus*) and a southern one (comprised of *punctigula*, *insolitus*, and *aequatorialis*), and his results largely agree with what we describe above. Additionally, he described the *erythropygius* group as having downslurred notes, whereas the *aequatorialis* group has overslurred notes. This difference is quite subtle to our ears, and the strong frequency modulation of *aequatorialis* (not present in *punctigula* and *insolitus*) and lower pitch of the *erythropygius* group seem like more distinct characters. Boesman (2016) stated that the quavering songs change gradually from north to south, but it seems to us that there may be a clear break between pure-toned and quavering songs near the canal zone of Panama. However, some examples even from the northern group seem to have a quavering tone to some songs.

Macaulay Library holdings for *erythropygius* / *parvus* songs from N of Nicaragua:
https://search.macaulaylibrary.org/catalog?taxonCode=spowoo2&mediaType=audio&view=list
https://search.macaulaylibrary.org/catalog?taxonCode=spowoo1&mediaType=audio&regionCode=MX

Macaulay Library holdings for *punctigula / insolitus* / *aequatorialis* song from S of Nicaragua:
https://search.macaulaylibrary.org/catalog?taxonCode=spowoo3&mediaType=audio&tag=song&view=list

An example of the quavering song immediately east of the canal zone in Panama: https://xeno-canto.org/253672

But songs of birds immediately west of the canal zone in Panama are whistled like those from Costa Rica:
https://xeno-canto.org/127316
https://xeno-canto.org/128320

However, some recordings of *parvus* are somewhat quavering, but otherwise match typical *parvus* songs in pattern and lower pitch:
https://macaulaylibrary.org/asset/527388

Because *X. triangularis* has been considered part of the same species, we have here provided some recordings from the nearest populations in Colombia. However, there are not many recordings of the song of this species, and recordings from farther south in the Andes sound quite different from those in the north. The short descending whinny of these northern birds is quite different from the songs of any of the taxa currently considered part of *X. erythropygius*.
https://xeno-canto.org/320708
https://xeno-canto.org/148021
https://xeno-canto.org/251788

Schulenberg et al. (2007) described the song of the northern Peruvian populations of *X. triangularis* as a “mellow, decelerating, descending series of musical whistled notes: “*whi’we-we-we-we we we wur*”, which agrees with the recordings linked to above, but they noted that the southern Peruvian (Pasco south) *X. t. bangsi* has an additional song, a wiry insistent rising-falling series of nasal whines: “*WHEEEW who-WHI-WHI-whi-whi-whi*” suggesting some vocal variation within *X. triangularis*. An example of that latter song is here: https://xeno-canto.org/746087 All song recordings available online from south of the Marañón Valley seem to match this latter nasal song type.

Very few examples of *hylodromus* are available online, all in Macaulay, and it is not clear if these refer to natural songs:
https://media.ebird.org/catalog?taxonCode=olbwoo1&mediaType=audio&regionCode=VE

Effect on AOS-CLC area:

Splitting *X. aequatorialis* from *X. erythropygius* would result in one additional species for the AOS area. Splitting *X. aequatorialis* and *X. punctigula* from *X. erythropygius* would result in two additional species for the AOS area.

Recommendation:

We recommend a **NO** on any splits in this group at this time.

Although we suspect that multiple species may be involved within what is currently treated as *X. erythropygius*, it is not clear where best to split taxa as the different data types are not concordant in their clustering. Vocal data suggest three song groups within *X. erythropygius*, a low-pitched group with clear whistles (*erythropygius* / *parvus*), a higher-pitched group with clear whistles (*punctigula* / *insolitus* west of the canal zone) and a quavering song group (*aequatorialis* east of the canal zone). The vocal aspect of the BirdLife split is based on song pitch and downslurred vs overslurred notes but minimized the diagnosability of the distinctive quavering songs of *aequatorialis*. However, quantitative analyses are likely necessary to ascertain whether there is a gradual change in clear-noted to quavering songs as suggested by Boesman (2016). The differences between the songs of these groups do not seem as drastic as the differences between *X. erythropygius* and *X. triangularis*, and the songs of the southern *X. triangularis* (*bangsi*) seem more distinct than do the three groups within *X. erythropygius*.

Plumage data support the distinctiveness of the *erythropygius* / *parvus* group based on their extensive mantle and crown streaking. However, the two southern groups (*punctigula* and *aequatorialis*) show ventral streaking similar to the northern taxa in *X. triangularis*, although they differ from *X. triangularis* in throat pattern. We are unable to find consistent plumage differences between *punctigula*/*insolitus* and *aequatorialis* (which agrees with comments by Cory and Hellmayr 1925, see above) despite apparent differences in song.

This complex is an excellent candidate for future work. Quantitative analysis of song, plumage, and genetic variation (the latter of which is lacking) would go a long way towards resolving species limits in the group.

If any of these splits gain traction, an English name proposal should be drafted to address the new names. Cory and Hellmayr (1925) provided some options to work with, which adapted for modern conventions would be:

Spot-throated Woodcreeper for *punctigula* (which would include *insolitus*).
Spotted Woodcreeper for *erythropygius* (although this has now been used for *X. erythropygius s.l.*, so a new name may be necessary)
Pacific Woodcreeper for *aequatorialis s.s.*

AOU (1983, 1998) used Spot-throated Woodcreeper for the *aequatorialis* group (when separated from *X. erythropygius*, although we note that both groups have spotted throats). Clements/eBird gives Berlepsch's Woodcreeper as the English name for this group.

Please vote on the following:

1) Elevate *aequatorialis* (with *punctigula* and *insolitus*) to species rank (BirdLife treatment)
2) Elevate both *punctigula* (with *insolitus*) and *aequatorialis* to species rank

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Submitted by: Oscar Johnson, The University of Texas at El Paso, and Nicholas A. Mason, Louisiana State University

Date of proposal: 1 December 2022

Revise the taxonomy of Black-necked Stilt *Himantopus mexicanus*: (a) treat it as a subspecies of Black-winged Stilt *H. himantopus*, or (b) treat current subspecies (i) *melanurus* and (ii) *knudseni* as separate species

Effect on NACC (and SACC):

This would change our treatment of the Black-necked Stilt (*Himantopus mexicanus*) of North and South America (a) by treating it as conspecific with the Black-winged Stilt (*H. himantopus*) of Eurasia and Africa, or (b) by elevating *H. mexicanus knudseni* and/or *H. mexicanus melanurus* to species status.

Background:

We are revisiting this species limits issue in association with the effort to harmonize world lists, and treatment of *H. mexicanus* (and stilts worldwide) is a point of disagreement.

Species limits in the globally distributed *Himantopus* stilt complex have long been controversial. All members of the genus might be one species (Peters 1934), or they might be a superspecies with as many as eight species (Mayr & Short 1970, AOU 1998). They are generally considered to represent from two to five species (e.g., Hayman et al. 1986, Pierce 1996, Dickinson & Remsen 2013, del Hoyo & Collar 2014). HBW-Birdlife considered that there could be two to five species-level taxa but treated the complex as just two: *H. himantopus* and *H. novaezelandiae*. These latter two taxa hybridize extensively; more on this below.

H. mexicanus has been recognized as a distinct species by the *Check-list* in every edition since the first. In the 7th edition, AOU (1998) considered that *H. mexicanus* comprises three subspecific groups, *H. m. mexicanus* (North and South America), *H. m. knudseni* (Hawaii), and *H. m. melanurus* (South America).

Hybrids are known in the genus, most frequently between *H. m. mexicanus* and *H. m. melanurus* and between *H. h. leucocephalus* and *H. novaezelandiae* (McCarthy 2006). Hybridization of a single (presumed) escaped female *H. mexicanus* with a male *H. himantopus* occurred in Europe, and they have also hybridized in captivity, but these atypical crossings are not informative of species limits given that intergeneric *Himantopus* × *Recurvirostra* have also occurred (McCarthy 2006).

H. m. mexicanus and *H. m. melanurus* intergrade where their ranges abut in Peru and perhaps also in Brazil, but species limits might be involved (e.g., Short 1975, Blake 1977). The degree of hybridization has been described as extensive (McCarthy 2006), but the levels of hybridization here remain uncertain. For example, Schulenberg et al. (2007:128) stated only that the two "may intergrade," and noted that their vocalizations differ. Phenotypically, evidence for hybridization seems fairly strong, suggesting intergradation to a degree that has typically been viewed as warranting subspecies-level designation (e.g., Peters 1934, Hellmayr & Conover 1948, Blake 1977, Hayman et al. 1986, Robinson et al. 1999, McCarthy 2006, Harvey et al. 2014).

Pierce's (1996) treatment of all the pied forms as one species (*H. himantopus*) and the black-plumaged *H. novaezelandiae* as the second species in the genus was followed by Dickinson & Remsen (2013) and del Hoyo and Collar (2014). Here is the reasoning of the latter in the HBW-Birdlife checklist (http://datazone.birdlife.org/species/taxonomy).

> *Himantopus himantopus* (del Hoyo and Collar 2014) was previously split as *H. himantopus*, *H. leucocephalus* and *H. mexicanus* and following AOU (1998) and SACC (2006). Prior to that, *H. melanurus* had been split from *H. mexicanus* following Sibley and Monroe (1990, 1993). Original note from Illustrated Checklists: Closely related to *H. novaezelandiae*, with which known to hybridize and which is sometimes considered conspecific. Subspecies often considered to warrant recognition of 2–5 distinct species. Subspecies can be split into three groups (nominate; "pied" subspecies *leucocephalus*; and "black-necked" subspecies *knudseni, mexicanus* and *melanurus*); four groups (as preceding one, but with *melanurus* separated out as a full species); or five monotypic groups (as indicated here). One recent author (Livezey 2010) treated each of the forms *himantopus*, *leucocephalus*, *knudseni* and *mexicanus* (but not, puzzlingly, *melanurus*) as a separate species, but provided no supporting evidence. Patterns of differentiation on the head are notable but thematically recurrent (e.g. similar between *knudseni* and *mexicanus*, and between *leucocephalus* and *melanurus*), and typical calls of nominate and *leucocephalus* apparently differ, latter giving lower-pitched, shorter notes (Bakewell 2012b). With the (current) limited availability of vocal evidence indicating differences between taxa, however, the case for treating this complex as anything but a single species with variations in the amount and distribution of black on the head and neck is hard to make. Geographical variation also claimed in S Africa and Sri Lanka, in respective forms *meridionalis* and *ceylonensis*, but both exhibit considerable overlap with other populations of nominate *himantopus*. Five subspecies normally recognized.

The Clements list (Clements et al. 2022) splits this group into four species (*H. himantopus*, *H. leucocephalus*, *H. novaezelandiae*, and *H. mexicanus*), and recognized three subspecific groups in *H. mexicanus* (*mexicanus*, *knudseni*, and *melanurus*).

The IOC list (Gill et al. 2022) splits this group into five species, raising *H. mexicanus melanurus* to species status. The details for the latter split were "*Himantopus melanurus* is split from *H. mexicanus* (Sibley & Monroe 1990; Ridgely & Greenfield 2001); SACC awaits more study."

SACC (Remsen et al. 2022) stated this:

> *Himantopus mexicanus* was formerly (e.g., Peters 1934, Pinto 1938, Hellmayr & Conover 1948b, Phelps & Phelps 1958a, Vaurie 1965c, Meyer de Schauensee 1970, Blake 1977, Haverschmidt & Mees 1994) considered a subspecies of Old World *H. himantopus* ("Common Stilt") and was so treated by Dickinson (2003). Many authors continue to treat them as conspecific, e.g., Pierce (1996), Christidis & Boles (2008), and Dickinson & Remsen (2013). Some authors have treated southern South American *melanurus* as a separate species (e.g., Sibley & Monroe 1990, Ridgely & Greenfield 2001). The six taxa in the genus *Himantopus* form a near-globally

> distributed superspecies (Mayr & Short 1970, Sibley & Monroe 1990, Pierce 1996), and with from one to six species-level taxa recognized by various authors. Virtually no data are available relevant to taxon-ranking of allopatric populations. The contact between *mexicanus* and *melanurus* in South America, where at least some hybridization occurs, affords one of the best opportunities for such study; preliminary data indicate substantial hybridization (Harvey et al. 2014). Dickinson & Remsen (2013) and del Hoyo & Collar (2014) treated all New World taxa as subspecies of a broadly distributed species, *H. himantopus* (as "Black-winged Stilt"). SACC proposal needed. [We have not tracked down all these references.]

H. m. knudseni is apparently a recent colonist from North America, as supported both by phenotypic and genetic evidence (e.g., Pierce 1996, Fleischer and McIntosh 2001). Although its plumage divergence indicates that it is a species under the PSC (Pratt and Pratt 2001), it has rarely been treated as a separate species and the evidence for such treatment is scant. Pratt and Pratt (2001: 72) noted plumage differences and habitat adaptations, and they stated that the evidence of Fleischer and McIntosh (2001) "shows large genetic divergence." Fleischer and McIntosh (2001: 59) interpreted their own evidence quite differently: "The endemic subspecies of the Black-necked Stilt differs from North American Black-necked Stilts (*H. m. mexicanus*) by only about 1.5 + 0.6% sequence divergence [0.6% is the standard error] in 447 bp of mtDNA control region (R. Fleischer et al., unpubl. data)."

Wallis (1999) stated that *H. himantopus leucocephalus* and *H. novaezelandiae* differ in mtDNA control region by about 5% or a million years. No details were provided, however, and this divergence estimate is quite high compared with other estimates (see below).

In sum, species limits in this group are a mess.

New Information:

Because *H. mexicanus* and *H. himantopus* are allopatric, what occurs in contact zones in the genus can help us infer species-level differences under the biological species concept.

Steeves et al. (2010) used mtDNA and microsatellites (nuDNA) to find that, despite substantial levels of hybridization between *H. himantopus leucocephalus* and *H. novaezelandiae*, the latter had achieved a degree of reproductive isolation that apparently prevented extensive introgression of *H. h. leucocephalus* into *H. novaezelandiae*. However, this isolation is incomplete and is based in part on active management, and although there is some reduced fitness in hybrid females (Haldane's rule; see evidence in Wallis 1999), one of their hypothesized mechanisms for this isolation included small population size (Steeves et al. 2010, Brumfield 2010). Notably, *contra* Wallis (1999), Steeves et al.'s (2010) mtDNA (291 bp of cyt*b*) showed a shallow difference between these two taxa of just one fixed difference (~0.34%; see also below).

Forsdick et al. (2021), following up on the earlier efforts of Steeves et al. (2010), used genomic data to investigate hybridization between *H. novaezelandiae* and *H. himantopus leucocephalus*. Using genotyping by sequencing (GBS) on a total of 145 birds (130 *novaezelandiae*, 6 *leucocephalus*, and 9 hybrids), they found no introgression from *himantopus* into *novaezelandiae*, by which they meant that all apparent non-hybrid *novaezelandiae* were genetically diagnosable with >95% accuracy. However, hybrids clearly contained mixed genomes and maintaining the genetic integrity of *H. novaezelandiae* appears to require human intervention (Steeves et al. 2010, Forsdick et al. 2021). The secondary contact between these taxa apparently stems from a natural range expansion stimulated by human habitat alteration. Hybridization before direct human intervention was extensive, with almost 20% of non-*leucocephalus* individuals considered hybrids, and, with genetic evidence, Steeves et al. (2010:5096) confirmed that "hybridization is indeed extensive and bidirectional". The general lack of nuDNA gene flow from *leucocephalus* into *novaezelandiae* is hypothesized to be the result of moderate outbreeding depression and small population size (Steeves et al. 2010). Forsdick et al. (2021) further credited the intensive management program for preventing introgression of *leucocephalus* into *novaezelandiae* (they cull the non-*novaezelandiae* individuals of wild mixed pairs and exclude any but pure *novaezelandiae* from the captive breeding program). From a biological species perspective, this continued contact, if unchecked, would likely result in the reticulation of the two lineages. It's a fascinating situation, both from the conservation and speciation perspectives (Steeves 2010, Brumfield 2010, Forsdick et al. 2021).

In addition to the evidence for hybridization between *H. m. mexicanus* and *H. m. melanurus* noted above, hybridization also seems to occur between *H. h. himantopus* [Black-winged Stilt] and *H. h. leucocephalus* [White-headed Stilt] (McCarthy 2006, Bakewell 2012). We don't have access to Bakewell (2012), but some of the information there is relevant to our developing understanding of hybridization in this group, which might be substantial where they both occur in Malaysia and the Philippines (text quoted from Ramos and Perez 2014):

> Amongst these winter influxes have been several birds showing plumage characteristics associated with White-headed Stilt. Birds with a full, well-developed black nuchal mane and pure white head are relatively rare, and have always occurred singly in flocks of more typically plumaged Black-winged Stilts. However, birds with poorly marked dark nuchal manes are not uncommon; perhaps 5% show this feature, some of which have pure white heads, while others have variable amounts of black on the crown and ear coverts. Some birds appear to have a white head at a distance but, on close inspection, have some darker markings on the crown or ear-coverts. The birds showing White-headed Stilt plumage characters which I have observed in Malaysia have not been distinguishable vocally from Black-winged Stilts. This, and the fact that they occur at times of year typical for northern hemisphere migrants, has led me to conclude that these birds are variant-plumaged Black-winged Stilts, rather than White-headed…"
>
> …A cursory survey of photographs on the internet reveals that the extent and pattern of black on the nape and head of Black-winged Stilts occurring in Asia is far more variable than most literature suggests. Danny Rogers (in litt.) has suggested that black feathering on the hindneck might be some kind of ancestral plumage character that is occasionally expressed in stilts, and might therefore be part of the normal variation in Black-winged—even in the case of birds which look virtually identical to White-headed. Another possibility is that it is the result of hybridisation in areas where the two taxa have now met. In view of the apparent expansion in the breeding ranges of both taxa, hybridisation may be increasing. Whatever the

> case, I suggest that there is sufficient evidence for the existence of Black-winged Stilts showing White-headed Stilt plumage characteristics for extra-limital sightings of apparent White-headed Stilts to be treated with great caution, particularly if such birds occur singly and in the company of Black-winged Stilts during the northern winter.

What does all this suggest for other members of the superspecies complex? Using mtDNA sequence data (COI) from GenBank, one of us (KW) reconstructed a phylogeny for those members of the group for which data were available, using *Recurvirostra avosetta* as an outgroup (Fig. 1). This topology indicates that *H. h. leucocephalus* and *H. novaezelandiae* are the most closely related members and that the other members of the group have been diverging longer (Table 1). Overall, however, they are remarkably similar in mtDNA. The maximum COI divergence within the group is below 1.5%. Converting this into a time estimate is difficult, however. Although Lavinia et al. (2016) found that COI has a substitution rate ~14% less than cyt-*b,* at COI divergence levels below ~2.5% estimates of divergence become decidedly unreliable. Notably, however, they stated that “most species pairs do not fall into the ‘danger zone’ of low divergence” (Lavinia et al. 2016:89). This stilt complex is deeply within this ‘danger zone.’

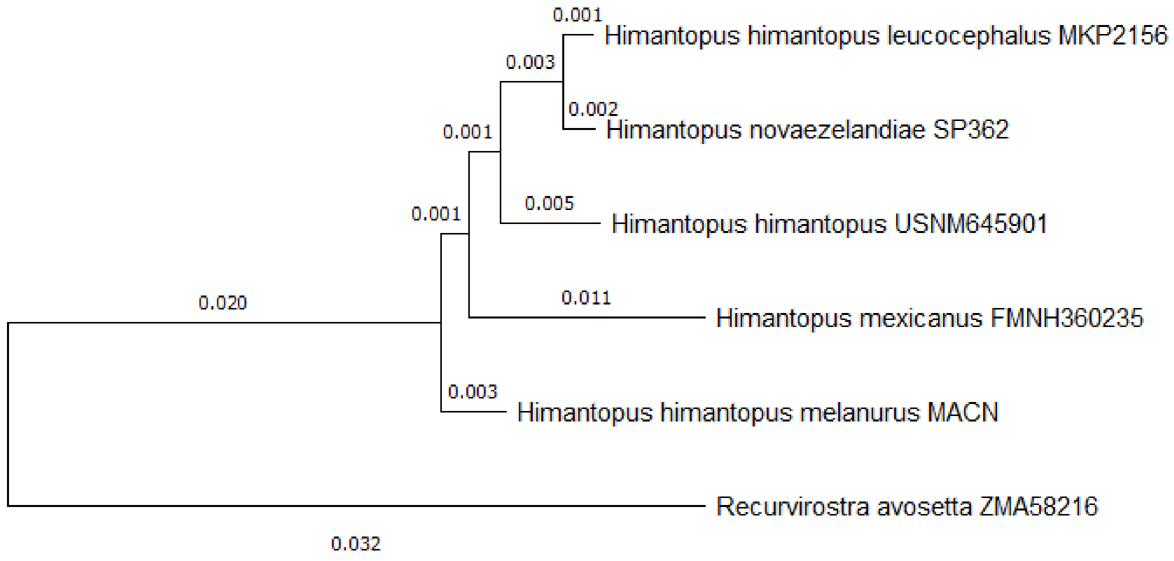
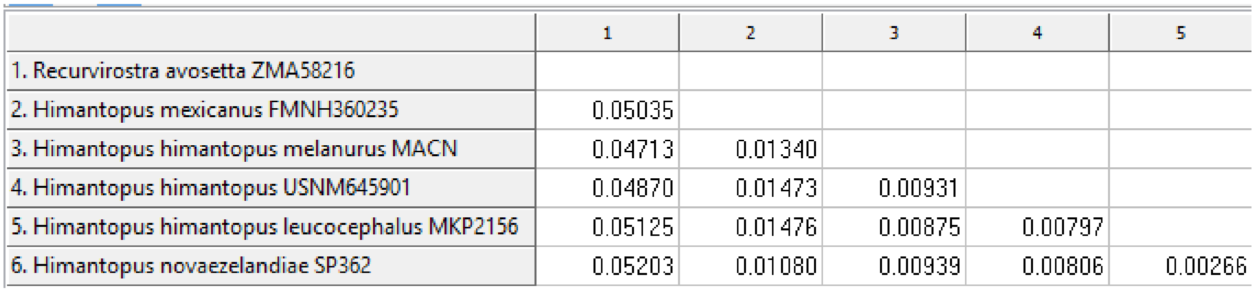


Figure 1. Maximum likelihood tree of ~900 bp of mtDNA COI sequence data from GenBank. Numbers below branches are substitutions per site along that branch. Sequences aligned using Clustal Omega (https://www.ebi.ac.uk/Tools/msa/clustalo). Analyses after Tamura & Nei (1993) and Kumar et al. (2018).

Table 1. Pairwise genetic distance matrix of ~900 bp of mtDNA COI sequence data between *Himantopus* taxa present on GenBank (*Recurvirostra* is the outgroup; see also Fig. 1).



	1	2	3	4	5
1. Recurvirostra avosetta ZMA58216					
2. Himantopus mexicanus FMNH360235	0.05035				
3. Himantopus himantopus melanurus MACN	0.04713	0.01340			
4. Himantopus himantopus USNM645901	0.04870	0.01473	0.00931		
5. Himantopus himantopus leucocephalus MKP2156	0.05125	0.01476	0.00875	0.00797	
6. Himantopus novaezelandiae SP362	0.05203	0.01080	0.00939	0.00806	0.00266

Taxonomy and nomenclature:

If part (a) of this proposal is approved, *Himantopus mexicanus* (Black-necked Stilt) would become *H. himantopus mexicanus* (Black-winged Stilt), with its subspecies retaining subspecific status. Other issues we're asked to consider are in the opposite direction: not only retention of *H. mexicanus* as a species, but also elevation of current subspecies *melanurus* and/or *knudseni* to species status.

Recommendation:

We are not close to the end of the controversy over species limits in this group. The differing taxonomic treatments seem to be largely due to disagreements among authors about how to interpret very limited evidence. More comparative work on the complex is needed to resolve species limits. Some level of reproductive isolation occurs between *H. h. leucocephalus* and *H. novaezelandiae*, but while it has reached a level that apparently causes lowered hybrid fitness, it is incomplete enough to not meet the 'essentially reproductively isolated' criterion of the biological species concept. With these two taxa being each other's closest relatives in mtDNA (Fig. 1, Table 1), it might be inferred that more distantly related taxa in the complex could have more effective reproductive isolating mechanisms. However, the distances involved are small (Table 1), and *mexicanus* and *melanurus* show intergradation where their ranges overlap in South America, where species limits might be involved (e.g., Short 1975, Blake 1977, Harvey et al. 2014). Similarly, the Asian contact between *himantopus* and *leucocephalus* also seems to be causing intergradation, though species limits might be involved there as well (Bakewell 2012, Ramos and Perez 20140, Gill et al. 2022). Having only a small mtDNA dataset and no modern comparative study of the complex leaves many open questions. To us it seems reasonable on present evidence to lump them all as one biological species (e.g., Peters 1934), but we'd be uncomfortable changing our current taxonomy (in any aspect) without better evidence to do so. Because we are reluctant to make a change with no new compelling evidence, we recommend voting no on every aspect of this proposal.

Please vote on the following:

(a) Recognize *H. mexicanus* as a subspecies of *H. himantopus* (i.e., *H. himantopus mexicanus*) (b, part i) Recognize *H. melanurus* as a species separate from *H. mexicanus* (note that this is primarily a SACC issue, so this is a provisional vote)

(b, part ii) Recognize *H. knudseni* as a species separate from *H. mexicanus*

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Submitted by: Kevin Winker and Terry Chesser

Date of Proposal: 2 December 2022

Treat *Chlorophonia sclateri*, *C. flavifrons*, or both as separate species from Antillean Euphonia *C. musica*

Effect on NACC: This proposal would modify our treatment of *Chlorophonia musica* to include as many as three species, thereby adding up to two species to the NACC checklist.

Background:

Species limits within *Chlorophonia* (previously part of *Euphonia)* vary considerably among taxonomic authorities. In particular, the "blue-hooded" euphonias (*C. cyanocephala*, *elegantissima*, and *musica*) have been treated as a single wide-ranging species, *C. musica* (e.g., Hellmayr 1936, Meyer de Schauensee 1970, Storer 1970), although most recent classifications have followed AOU (1983) in treating them as three species despite a lack of published analysis. A recent phylogeny based on UCEs and mitochondrial genomes found that the "blue-hooded" euphonias formed a monophyletic group sister to *Chlorophonia* (Imfeld et al. 2020), which led to a taxonomic revision that transferred the "blue-hooded" euphonias to *Chlorophonia* (Chesser et al. 2021). The UCE phylogeny of Imfeld et al. (2020) included a single individual from the *C. musica* complex from Puerto Rico (*C. m. sclateri*) and found that this individual was sister to *C. cyanocephala*. These two individuals were in turn sister to *C. elegantissima*, such that the "blue-headed" euphonias formed a well-supported clade (Fig. 1).

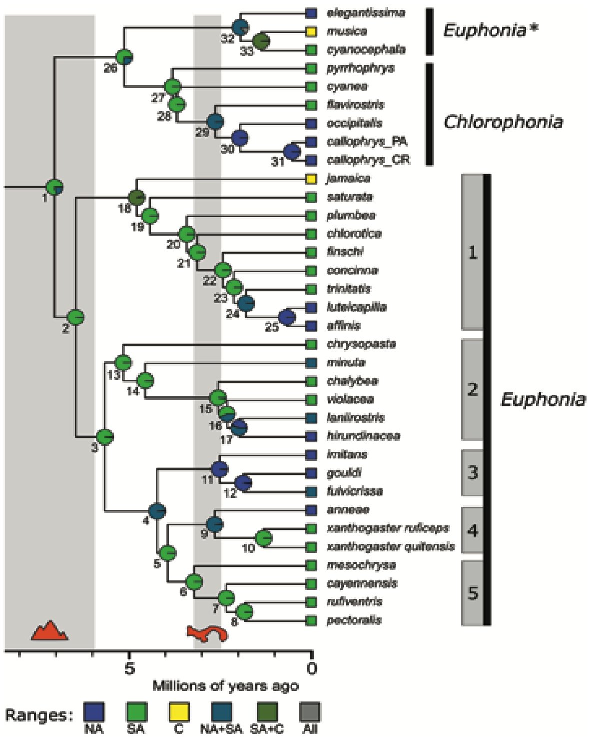

Figure 1: UCE-based phylogeny from Imfeld et al. (2020). Note sister relationship (at top) between *musica* (sample was from Puerto Rico) and *cyanocephala*.

Within the Antillean Euphonia (*Chlorophonia musica*), three subspecies (*musica, sclateri,* and *flavifrons*) were originally described as separate species (Greeney 2021) and have been treated as separate species as recently as 2018 (Greeney 2021), but are currently considered a single polytypic species by the Clements checklist v2022 (Clements et al. 2022), the IOC v12.2 (Gill et al. 2022), and the The Howard & Moore Complete Checklist of Birds of the World v4 (Dickinson and Christidis 2014). We present a summary of taxonomic treatments for this group in Table 1. Distributed across the Greater and Lesser Antilles, each subspecies occupies its own discrete geographic area: Puerto Rico (*sclateri*), Hispaniola (*musica*), and the Lesser Antilles (*flavifrons*). These allopatric subspecies vary considerably in plumage, but have yet to undergo a comprehensive study of genetic and phenotypic variation.

Table 1: Summary of taxonomic treatments of the “blue-hooded” euphonias. If cells are merged, then those taxa were recognized as a single species by a given authority. “NA” indicates that the given taxon was not treated by the corresponding taxonomic reference.

<table>
<tr><th>Reference</th><th>*cyanocephala*
South America</th><th>*elegantissima*
Central America</th><th>*musica*
Hispaniola</th><th>*sclateri*
Puerto Rico</th><th>*flavifrons*
Lesser Antilles</th></tr>
<tr><td>Cory (1889)</td><td>NA</td><td>NA</td><td></td><td></td><td></td></tr>
<tr><td>Ridgway (1911)</td><td>NA</td><td></td><td></td><td></td><td></td></tr>
<tr><td>Peters (1945)</td><td colspan="5"></td></tr>
<tr><td>Eisenmann (1955)</td><td>NA</td><td></td><td colspan="3"></td></tr>
<tr><td>Bond (1956)</td><td>NA</td><td colspan="4"></td></tr>
<tr><td>AOU (1957)</td><td>NA</td><td>NA</td><td>NA</td><td>NA</td><td>NA</td></tr>
<tr><td>Mayr and Short (1970)</td><td>NA</td><td>NA</td><td>NA</td><td>NA</td><td>NA</td></tr>
<tr><td>AOU (1983)</td><td>NA</td><td colspan="4"></td></tr>
<tr><td>AOU (1998)</td><td>NA</td><td></td><td colspan="3"></td></tr>
<tr><td>Collar in HBW (2001)</td><td></td><td></td><td colspan="3"></td></tr>
<tr><td>Dickinson and van Remsen (2003)</td><td></td><td></td><td colspan="3"></td></tr>
<tr><td>Del Hoyo et al. (2018)</td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Clements et al. (2022)</td><td></td><td></td><td colspan="3"></td></tr>
<tr><td>Gill et al. (2022)</td><td></td><td></td><td colspan="3"></td></tr>
</table>

This proposal has been prompted by the WGAC and an attempt to reconcile discrepancies among major global avian taxonomies. In particular, the Handbook of Birds of the World recently recognized three species within the Antillean *Euphonia* complex, based on distinct color differences between patches in both sexes, scored according to the Tobias et al. (2010) point system:

> [*E. sclateri*] hitherto treated as conspecific with *E. musica* and *E. flavifrons*, but differs from latter in characters given under that species and from former in its bright yellow

> vs orange underparts and lower rump (upper rump yellow in both) (2); bright yellow vs black throat (3); powder blue vs royal blue crown to nape (2); steel blue vs deep purplish gloss on mantle, back and wings (ns1); and smaller overall size, with notably shorter tail (effect size –4.02, score 2)." *E. flavifrons* "Hitherto treated as conspecific with *E. musica* and *E. sclateri*, but differs from both by its green vs yellow underparts (3); pale yellow vs black or yellow throat (ns2); bright yellow vs orange frons (ns2); bottle green vs glossy steel-blue mantle, back and wings (3); reduced dull yellowish-green vs bright yellowish-orange rump (3); and somewhat larger size (effect size for tail vs *E. sclateri* 6.6, score 3; for bill vs *E. musica* 2.9, score 2).

New Information:

Unfortunately, little to no information has been published for phenotypic or genetic variation within the *C. musica* complex. Imfeld et al. (2020)'s UCE-based phylogeny inferred *musica* as sister to *cyanocephala* with an estimated divergence time between them of approximately 1.5 mya (estimated by eye by NAM from Fig. 1). However, there have been no genetic or phenotypic data collected for the nominate *C. m. musica* nor *C. m. flavifrons*, precluding comparisons within the *musica* complex. Here, we summarize plumage and vocal differences among the group to consider species limits.

Plumage differences within the *C. musica* complex are striking. The males of nominate *musica* more closely resemble the mainland *cyanocephala* and *elegantissima* than other Caribbean taxa currently within *musica*. Within *C. musica*, the nominate *C. m. musica* and *C. m. sclateri* differ in crown (darker blue in *musica*), black throat patch (present in *musica*, absent in *sclateri*), and hue of the belly (more orange in *musica*). The subspecies of the Lesser Antilles, *C. m. flavifrons*, is arguably the most distinct of the three: it has a green dorsum and yellow-green belly, and lacks the black throat patch present in *musica*.

Figure 2: Phenotypic variation among males within the "blue-hooded" euphonia lineage. From top to bottom: males of *C. m. flavifrons, C. m. sclateri, C. m. musica, C. cyanocephala,* and *C. elegantissima*. At one point all were lumped under the single species *C. musica* or each taxon was considered a separate species (Table 1), the tags in the image above have not been updated to the current taxonomy.

These plumage differences are mostly consistent within each of the three taxa, but some variation does exist within each of these forms (Figure 3). Within *C. m. musica* and *C. m. sclateri* the hue of belly varies, such that some individuals are more orange while others have more yellow.

Figure 3: Variation of males within each subspecies of the *C. musica* complex: top two are *C. m. flavifrons*, middle three are *C. m. sclateri*, and bottom two are *C. m. musica*.

Females across the complex are more similar, but also have substantial color differences. Females of the nominate *C. m. musica* have a more russet-orange forehead patch, compared to a yellow forehead in *C. m. sclateri* and *C. m. flavifrons*. Females of *C. m. flavifrons* of the Lesser Antilles have much more green on their bellies and ventral plumage overall.

Here are some examples of female plumages from the mainland congeners and the three subspecies within the *C. musica* complex:
C. elegantissima https://macaulaylibrary.org/asset/125408301
C. cyanocephala https://macaulaylibrary.org/asset/204562281
C. musica musica https://macaulaylibrary.org/asset/254471251
C. musica sclateri https://macaulaylibrary.org/asset/276833781
C. musica flavifrons https://macaulaylibrary.org/asset/140599201

Vocal differences among the “blue-hooded” euphonias have not yet been quantified. Del Hoyo et al. (2018) stated that “[*elegantissima, cyanocephala*, and *musica*] do not differ greatly in voice or behavior”, suggesting that there is little to no vocal variation within the *musica* complex as well. To my [NAM’s] ear, the three subspecies within *musica* sound largely similar with no obvious consistent difference between the subspecies.

C. m. musica recordings:
Macaulay Library

C. m. sclateri recordings:
Macaulay Library

C. m. flavifrons recordings:
Macaulay Library

Xeno-canto recordings

The three subspecies are largely similar in morphology, but there are some slight differences: *C. m. flavifrons* is larger overall, while *C. m. sclateri* has a proportionately smaller tail. These differences do not seem to translate to any differences in ecology or natural history. Each of the three subspecies within *C. musica* and their mainland congeners are frugivorous and eat mostly mistletoe berries. They also all seem to prefer forest borders, second-growth woodland, or partially open habitats.

Summary and Recommendations:

In summary, we have relatively little data on which to base this decision. If the *C. musica* complex is monophyletic, the crown age is > 1.5 mya (Imfeld et al. 2020), and we can expect some level of genetic divergence between the subspecies due to geographic isolation on islands. Given that the island forms are inherently allopatric, genetic data wouldn't tell us much about reproductive isolation, but could potentially estimate how frequent gene flow is among the taxa (*flavifrons* is known to disperse across islands at least occasionally; Greeney 2021). Morphology, ecology, and song do not differ appreciably across the *C. musica* complex, but male coloration differs substantially, and female coloration differs as well—albeit to a lesser extent.

A comparative approach could be illustrative here: plumage is largely conserved within the subfamily Euphoniinae with many species pairs differing in color of only a single plumage patch. The plumage differences here are substantial and commensurate or greater than species-level differences among closely related taxa. Given the considerable divergence in plumage, we recommend a **YES** vote to recognize *C. m. sclateri* as a separate species from *C. m. musica* and a **YES** vote to recognize *C. m. flavifrons* as a separate species from *C. m. musica.*

Please vote on the subproposals listed below. Vote NO on all subproposals to maintain the current taxonomy, in which *C. musica* consists of the three subspecies *musica*, *sclateri*, and *flavifrons*.

(a) Treat *C. sclateri* as a separate species from *C. musica*, retaining *flavifrons* as a subspecies of *C. musica* (two-species treatment, version 1);
(b) Treat *C. flavifrons* as a separate species from *C. musica*, retaining *sclateri* as a subspecies of *C. musica* (two-species treatment, version 2);
(c) Treat both *C. sclateri* and *C. flavifrons* as separate species (three-species treatment).

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Submitted By: Nicholas A. Mason, Samantha L. Rutledge, and David Vander Pluym, Louisiana State University

Date of Proposal: 9 December 2022

Treat *Corvus minutus* as a separate species from Palm Crow *C. palmarum*

Description of the problem:

The islands of Cuba and Hispaniola each have two species of *Corvus*, one larger and one smaller. The larger species are the relatively distinctive and large Cuban Crow *Corvus nasicus* of Cuba (and Turks and Caicos) and the White-necked Crow *Corvus leucognaphalus* of Hispaniola (now extinct on Puerto Rico), both of which have relatively long bills and upswept narial bristles that do not cover the nares, reddish irides (brighter in *leucognaphalus*), and highly varied, often parrot-like vocalizations.

The smaller crows inhabiting these two islands, *Corvus palmarum* of Hispaniola and *C*. [*palmarum*] *minutus* of Cuba, which have shorter bills but long, thick narial bristles closely covering the nares, and dark irides, are much more similar to each other morphologically; their vocalizations are more typical for the genus; and they have been more variably treated taxonomically. As is so often the case, earlier authors treated *minutus* and *palmarum* as separate species (e.g. Ridgway 1904 and many authors listed in the synonymy therein), whereas most later authors lumped them with each other and even with other species. This has included their treatment as conspecific with American Crow *Corvus brachyrhynchos* (Meinertzhagen 1926, which was considered erroneous by Wetmore and Swales 1931) or Fish Crow *C. ossifragus* (Meise 1928, Hellmayr 1934, Dorst 1947). For many years, however, the predominant treatment (e.g. Wetmore and Swales 1931, Cory 1934, Peters 1962, Wolters 1977, Sibley and Monroe 1990, Monroe and Sibley 1993, Dickinson 2003, Clements et al. 2021) and that of the AOS (AOU 1998) has been as *Corvus palmarum*, with two subspecies, the Cuban nominate and Hispaniolan *minutus*.

However, some authorities (Raffaele et al. 1998, 2020; followed by e.g. BirdLife International 2000, Gill and Wright 2006, Gill et al. 2021, Dickinson and Christidis 2014) maintain that they should be considered separate species largely on the basis of Garrido et al. (1997), who considered the first available sound recordings to demonstrate differences commensurate with species status. At the other extreme, Johnston (1961), despite demonstrating that Cuban males have longer tarsi, disputed putative color sheen differences mentioned by some previous authors and considered *C. palmarum* to be a monotypic species.

New information:

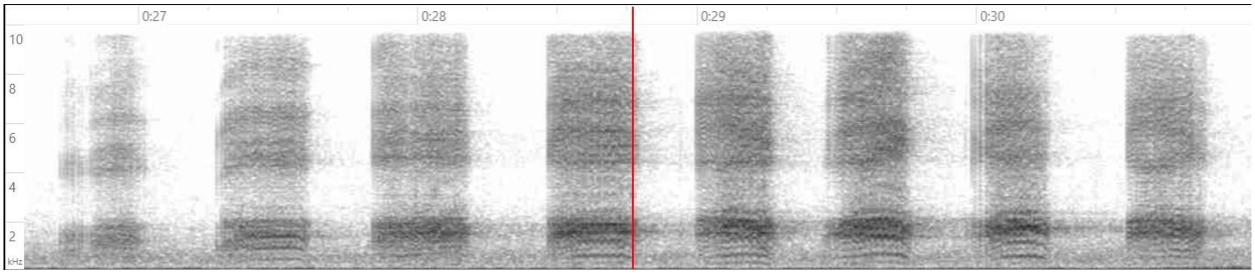
Vocalizations

Garrido et al. (1997) emphasized the shorter, more rapidly delivered, harsher, more grating, complaining, rising and falling notes of Hispaniolan *palmarum*, which they paraphrased as '*aaar*' (the vowel as in 'fast') vs. the longer, more slowly delivered, more abruptly rising notes with more apparent harmonics of Cuban *minutus*, paraphrased as '*craa-aao'*. However, the latter recordings were of only a single *minutus* from a noisy flock.

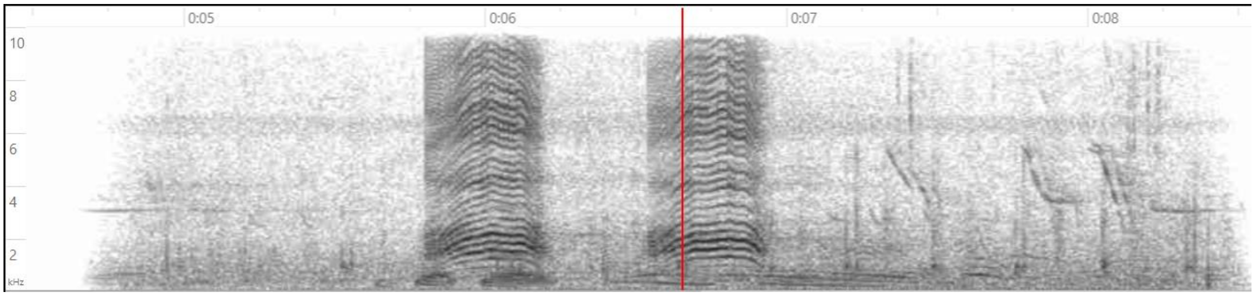
Boesman's (2016) summary of the apparent differences between xeno-canto recordings of *minutus* and *palmarum* was based on more examples of each, although sample size was not given. He emphasized especially the fact that *palmarum* has a distinctly 'vibrating' voice, unlike *minutus*. He also suggested that *minutus* has more drawn-out notes but with some overlap, and that more samples would be needed for quantification. Boesman (2016) stated that "this may well be an important distinguishing feature" and he estimated the vocal score as about 3. del Hoyo and Collar (2016) cited Boesman (2016) but nevertheless lumped *minutus* into *palmarum*, stating "vocal differences minor", and Marzluff and Sharpe (2020) stated that "their vocalizations are rather similar".

There are many more online recordings of both available now, and in my opinion sonagrams are consistently identifiable at a glance, with Hispaniolan *palmarum* making gruff vibrato calls that appear as broadband noise showing hardly any harmonics, and Cuban *minutus* making more nasal, more inflected calls that show little or no vibrato and many clear harmonics. Both also show relatively little vocal variation in the now substantial number of available recordings. (Note that ML236111 has contributions from *C. nasicus*.) I don't think there is any doubt that *minutus* and *palmarum* differ at least as much in vocalizations from each other as do some other congenerics—e.g. the "Indian Jungle" Crow *Corvus* [*macrorhynchos*] *culminatus* vs. House Crow *Corvus splendens*, which are broadly sympatric and have never been considered conspecific.

Here are sonagrams of typical examples of each:



palmarum, ML 145646, Mark Robbins



minutus, ML 183549, Tim Burr

Behavior

Wetmore and Swales (1931) noted that Wetmore in 1927 had observed calling nominate *palmarum* “jerking their drooping wings and elevated tails conspicuously”. Holyoak (1983), on a visit to Haiti, also noted that the nominate frequently produced a “peculiar ‘tail-flicking’ movement”…”quite different to displays…for other *Corvus* species. The tail was slowly raised to slightly above horizontal and then sharply flicked down to a position where it pointed downwards about 45° below the horizontal. The wing tips were held slightly lowered throughout. The ‘tail-flicks’ were seen to be given at short intervals during a long bout of cawing (but not in time with the calls) as well as by birds that did not call.” Garrido et al. (1997) quoted Holyoak’s (1983) observations and stated that this behavior “has not been observed so far among Cuban birds”. Raffaele et al. (1998) mentioned that *palmarum* “characteristically flicks tail downward”, while not mentioning tail-flicking for *minutus*. Likewise, Kirwan et al. (2019) stated that *palmarum* “often flicks tail downwards when calling”, and again did not mention this behavior for *minutus*. Raffaele et al. (2020) stated that Cuban *minutus* “flicks tail upward on alighting”, whereas Hispaniolan nominate *palmarum* “flicks tail downward.” Madge and Burn (1994) appeared to attribute the behavior to both taxa but do not explicitly distinguish between them in most of their species account.

The single video clip on ML of *palmarum*, ML 201617481 shows this exaggerated behavior repeatedly, but none of the nine videos of *minutus* now on ML, which include several bouts of calling, show anything but the most minor tail movements. Numerous ML photos (including my own) of the nominate race vocalizing appear to show phases of this behavior as well. Of over 100 ML photos of Cuban *minutus*, such behavior is not obvious like it is in *palmarum*.

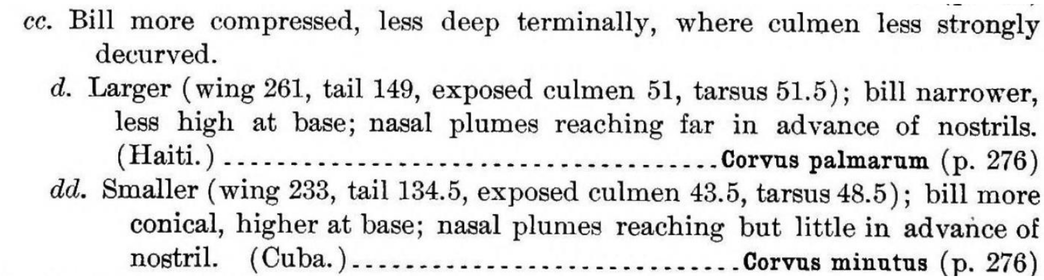
In my view the above is good evidence that the pronounced tail-flicking behavior is limited to *palmarum*, and I suggest committee members watch the videos for themselves. However, I have not found a comparative study specifically on this behavior nor any firsthand source stating that *minutus* does not engage in this behavior.

Habitat

Although named *palmarum* by Württemberg (1835), who stated (in Gothic script) that it lives in palm trees (rough Google translation), the nominate is typical of pine forests in Hispaniola, but is also found in xeric woodland, around royal palms, and more open country (Danforth 1929, Wetmore and Swales 1931, Marzluff and Sharpe 2020). Conversely, Cuban *minutus*, formerly known as the “Little Pine Crow” or “Cao Pinalero” (Barbour 1923) is now found mainly in open farmland with royal palms but at least sometimes also with scattered pines. Thus, their habitats do overlap, but *minutus* is mostly now associated with open country with palms, whereas *palmarum* is a woodland bird mainly associated with pine forest.

Morphology

I have not studied specimens, and online photographs have proven a minefield. This is largely due to the co-occurrence of Cuban Crow *Corvus nasicus* with *minutus*; local people have even claimed that *nasicus* is the male and *minutus* the female of the same species (Cañizares Morera 2017). Misidentifications of photos of nominate *palmarum* seem less of a problem, although Wetmore and Swales (1931) mentioned that misidentifications were frequent, and that experience is necessary for confident identification of *palmarum* vs. *leucognaphalus*. Confidence can be placed in identifications of photos of *minutus* and *palmarum* in which the narial bristles are clearly visible to be profuse and to cover the nares, and rictal bristles are prominent at the gape, as opposed to the unfeathered nares and gapes of *nasicus* and *leucognaphalus*. Comparing such unequivocally correctly identified photographs suggests to me that Ridgway (1904) may have been right about some of the differences he listed between *minutus* and *palmarum*, especially bill size and shape, and narial feathering:



cc. Bill more compressed, less deep terminally, where culmen less strongly decurved.

d. Larger (wing 261, tail 149, exposed culmen 51, tarsus 51.5); bill narrower, less high at base; nasal plumes reaching far in advance of nostrils. (Haiti.) .... **Corvus palmarum** (p. 276)

dd. Smaller (wing 233, tail 134.5, exposed culmen 43.5, tarsus 48.5); bill more conical, higher at base; nasal plumes reaching but little in advance of nostril. (Cuba.) .... **Corvus minutus** (p. 276)

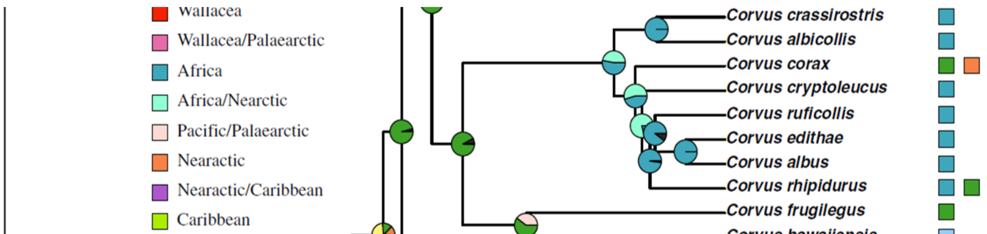
However, most recent authors have discounted any morphological differences except the longer tarsus of male *minutus* found by both Johnston (1961) and Garrido et al. (1997). The latter authors nevertheless maintained, on the basis of study of specimens, that “in general, the Cuban birds are blacker and less lustrous with a violet sheen”, as was mentioned by many earlier authors (e.g. Meise 1928).

Eggs

Wetmore and Swales (1931) described a clutch of four eggs from Haiti thus: “light Niagara green, covered rather evenly with diffuse spots of clove brown and dark olive, the spots being moderately large and somewhat uneven in outline.” Raffaele et al. (1998) gave identical statements for both *minutus* and *palmarum*: “Eggs (3-4) pale green, evenly speckled or blotched with olive-brown and dark brown.” However, Kirwan et al. (2019) stated that “their eggs also differ (pale blue with well-defined marking in present species [*minutus*] vs. pale green with diffuse markings [*palmarum*], P. Regalado).” To my knowledge data demonstrating differences in egg pigmentation have not been published.

Genetics

Analysis of mtDNA and two nuclear genes places *palmarum* and *minutus* as sister taxa that are sister to a clade that includes Sinaloa *C. sinaloae*, Tamaulipas *C. imparatus*, and Fish crows *C. ossifragus* (Jønsson et al. 2012). Estimated time of divergence of *palmarum* and *minutus* of 1-2 mya is similar to some other congeneric species pairs, notably *sinaloae* and *imparatus*, and White-necked Crow *C. leucognaphalus* and Jamaican Crow *C. jamaicensis* (Fig. 2 from Jønsson et al. 2012 below).



On a side note, results of Haring et al. (2012) on the basis of mtDNA (mainly sampled from skin specimens) agree with those of Jønsson et al. (2012) in that *C. palmarum* (based on two samples of the nominate) falls in the *C. ossifragus* clade (but *sinaloae* and *imparatus* were not included), suggesting that our linear sequence should be changed. This should be addressed in another proposal.

Effect on AOS-CLC area:

Acceptance of the split of *minutus* would add another species to the AOS area. *Corvus minutus* would thus be a species-level endemic to Cuba, whereas *palmarum* occurs in both Haiti and the Dominican Republic. The range of *minutus* is now highly restricted and, when split by BirdLife International (2000), it was considered a threatened species, although a new population was recently discovered (Cañizares Morera 2017).

Recommendation:

I recommend splitting *minutus* from *palmarum* primarily on the basis of their consistently different vocalizations. In addition, minor morphological differences do exist; extravagant tail-flicking behavior appears to be limited to *palmarum*; *minutus* typically occurs in open palm country and *palmarum* in pine forest or xeric woodland; and egg pigmentation differences have been reported, but all of these require further study or substantiation. Available genetic evidence is consistent with and suggestive of species status but of course is not definitive. On balance, in my opinion the preponderance of evidence favors species status for *Corvus minutus*.

English names:

Cuban Palm Crow and Hispaniolan Palm Crow have already been used in several sources, and thus are recommended as English names should this proposal pass.

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

Date of proposal: 12 December 2022

Treat *Cyanocorax luxuosus* as a separate species from Green Jay *C. yncas*

Background:

The AOS currently recognizes *Cyanocorax yncas* (Green Jay) as a single species with two groups, each of which is comprised of multiple subspecies: the *luxuosus* group, resident from southern Texas to northern Honduras, and the *yncas* group, which occurs in South America from Colombia and Venezuela to central Bolivia. These two groups were originally described as separate species: *Garrulus luxuosus* (Lesson, 1839) and *Corvus yncas* (Boddaert, 1783). Both species were later transferred to the genus *Xanthoura* before being placed in *Cyanocorax* (American Ornithologists' Union 1955). The two groups were recognized as a single species by Hellmayr (1934:34), who wrote: "Though widely separated geographically, the Central American Green Jays are clearly conspecific with *X. yncas.* Certain specimens of [subspecies] *guatimalensis* with bright yellow under parts so closely resemble the Venezuelan *X. y. caeruleocephala* as to be almost indistinguishable in coloration." The species listed in the Checklist was *luxuosus* through the 4th edition (1931), but became *yncas* as of the 5th edition (1957), evidently following Hellmayr.

Ridgely and Greenfield (2001) recognized the *yncas* group as a separate species (*C. yncas*, Inca Jay) on the basis of "distinct differences in habitat and social behavior, as well as plumage and vocal distinctions" (no references cited). Hilty (2003) also recognized that group as a separate species without comment other than "Previously called Green Jay, a name now applied to C. Amer. birds." On the basis of those guides, the IOC World Bird List (https://www.worldbirdnames.org) elevated the two groups to species in 2009 with a note that "AOU may review." Other sources (Gayou 2020, Clements et al. 2022) continue to recognize the two groups within a single species. Gayou (2020) stated that "South American Green Jays [are] distinct in color, vocalizations, and montane distribution; potentially deserve separation as different species."

The HBW-Birdlife list also treats the two as a single species based on the following rationale:

> Subspecies fall into two groups, "*luxuosus* group" in Central America, and "*yncas* group" in Andes; these sometimes treated as two separate species, the *luxuosus* group differing in its shorter frontal tuft (2); smaller overall size (allow 1); green-tinged underparts in some but not all subspecies (ns); dark iris in some but not all subspecies (ns); more clear-cut colour transition from crown to mantle (1); and possibly higher pitch to the typical rapid series of cracking notes (ns).

The following photos show some variation in plumage as well as size. In the top set of photographs, from MVZ specimens, birds in the *luxuosus* group (left specimen, Texas) have a blue crown/nape and greenish belly, whereas birds in the *yncas* group (right specimen, Colombia) are noticeably larger, have a whitish crown/nape, and are yellow ventrally.

We also took photos of USNM specimens from southern Central America and Venezuela for comparison in light of Hellmayr's (1934) statement about the lack of distinction in ventral

coloration. The bird on the left end in the last two photos is from Guatemala (unsexed) followed by one unsexed bird and two males from Honduras, then five males from Venezuela on the right. The Venezuelan birds are very similar to those from Central America, although they are slightly more yellow ventrally than those from Central America. Dorsal coloration does not differ much in this series, except for the more gradual transition between mantle and crown in the Central American birds mentioned in the Birdlife-HBW note, and in contrast to the comparison of birds from Texas versus Colombia. Note especially the wide variation in crown color within the *yncas* group, varying from whitish in the Colombian birds to blue in the Venezuelan birds, and the wide variation in ventral plumage within the *luxuosus* group, varying from green to yellow.

Like other jays, these birds have a rich vocal repertoire (Hardy 1969, Gayou 2020). Thus, it is important to compare vocalizations used in the same context. You can listen to audio recordings of both groups here: https://birdsoftheworld.org/bow/species/grnjay/cur/multimedia?media=audio. To my (CC's) ear, ML105549 (*luxuosus* group) and ML69973 (*yncas* group) appear to be similar type of calls but with distinctly different pitches (see also the Birdlife-HBW comment above). However, we are not aware of any quantitative analyses of vocal variation in the two groups.

Habitats and elevational ranges seem to overlap (Gayou 2020): "In s. Texas prefers open woodland, dense secondary growth, and brushy thickets dominated by mesquite (*Prosopis glandulosa*), huisache (*Acacia farnesiana*), Texas ebony (*Pithecellobium flexicaule*), and anaqua (*Ehretia anacua*), as well as citrus groves. Less common in open areas. In remaining range in Middle America, humid forest, rain forest, lowlands, plantations, and mountains to 1,500 m. In South America, humid montane forest and forest borders, clearings, and secondary woodland, as well as disturbed areas from near sea level in Venezuela to (most commonly) 900-3,000 m."

New Information:

There is no really "new" information. A genetic study of *Cyanocorax* jays (Bonaccorso et al. 2009) sequenced two mitochondrial genes and three nuclear genes for all species in the genus plus related genera and outgroups. Multiple samples were sequenced for some species including *C. yncas* (Texas-1, Mexico-2, Ecuador-1, Peru-1). Although the placement of *C. yncas* in the overall phylogeny was unstable, results consistently separated the samples into two distinct groups corresponding to their geographically disjunct distributions. Although they suggested that these populations might represent distinct species, in line with other authors, they stated that “Further analysis of populations from across the range of the species, particularly in Central America and northern South America, will be crucial in assessing their validity as independent evolutionary lineages.” They further stated that “the geographic gap between Mesoamerican and South American populations of *C. yncas*…could represent the early stage of a geographic gap produced by local extinction.”

Recommendation:

Although the *luxuosus* and *yncas* groups appear to show phenotypic, genetic, and possibly vocal differences, a study of geographic variation that samples populations across their disjunct distributions is lacking. Especially needed is a detailed analysis of plumage variation within and among populations. The genetic data are suggestive but insufficient to justify a split because of limited sampling (as noted by Bonaccorso et al. 2009). Finally, although vocal differences may exist, no quantitative data are available, and such a study must account for behavioral contexts of the different types of calls (Gayou 2020). For these reasons, we recommend maintaining the status quo (two groups of a single species) pending additional data.

Please vote on the following:

a) Split the two groups into separate species.
b) If split, then vote on the English names currently in use: “Green Jay” for “*C. luxuosus*” and “Inca Jay” for “*C. yncas*.”

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Submitted by: Carla Cicero and Terry Chesser

Date of proposal: 16 December 2022

Transfer Tiny Hawk *Accipiter superciliosus* to the newly described genus *Microspizias*

Background:

The Tiny Hawk, *Accipiter superciliosus* (Linnaeus, 1766), has been placed in *Accipiter* on the AOS-NACC checklist since the sixth edition (AOU 1983), when coverage expanded to include Middle America, and it has been treated in *Accipiter* on the AOS-SACC checklist since its inception. All four major global checklists today place the species in *Accipiter*, as did most if not all authors throughout the 20th century (including Peters 1931, Hellmayr and Conover 1949, Friedmann 1950, and more recent authors cited in the following paragraph). For at least the half-century before, many authors had placed the species (under the name *Accipiter tinus* (Latham, 1790), which was in more widespread use than *superciliosus* until as recently as 1910) in an *Accipiter* (or synonym thereof) that was roughly equivalent to the small and medium-sized species of today's *Accipiter* (the larger ones often being separated in *Astur*). Some placed *tinus* in *Hieraspiza* Kaup, 1844, variously ranked as a subgenus of *Accipiter* or as a distinct genus, along with a varying selection of primarily Old World species, including *Accipiter virgatus* and *A. minullus*; *tinus* was at times considered to be the type species of *Hieraspiza*, but this was incorrect (see New Information). The species was seemingly never placed in a genus or subgenus of its own, nor a (sub)genus comprising Tiny Hawk and Semicollared Hawk *Accipiter collaris* (after that species's 1860 description) to the exclusion of other taxa.

The Semicollared Hawk, *Accipiter collaris* Sclater, 1860, mainly a species of Andean cloud forest, closely resembles the slightly smaller Tiny Hawk. The two species are similar in overall coloration, including the presence of two juvenile color morphs (although the relative abundance of each morph differs between the two species), and are "virtually identical" in structure; compared with other *Accipiter* species, they have very heavy legs/feet and bills for their small size, and are also distinctive in having barred underparts in juvenile plumage (Wattel 1973, Ferguson-Lees and Christie 2001). However, *collaris* was described by Sclater as a relative of *A. castanilius* (at the time mistakenly believed to be a Neotropical species), and as being more similar in appearance to the African *A. minullus* than any American *Accipiter*. Gray (1869) added *collaris* to the subgenus *Hieraspiza*, directly following *tinus*, but Sharpe (1874), who did not delineate subgenera, separated the two species in his *Accipiter* sequence. Gurney (1875), perhaps the first to comment in print on the close similarities in plumage coloration between *collaris* and *tinus* (=*superciliosus*), did not consider the two to be closely related; he judged *collaris* to be so distinctive that it might not fit into any then-recognized subgenus (although he did not name a new one for it at the time), and considered *tinus* to form a group with a few small African species (including *minullus*). As late as Peters (1931), *superciliosus* and *collaris* were not listed adjacently, but Hellmayr and Conover (1949) did place them next to each other in their sequence, and Amadon (1964) even entertained (and rejected) the possibility that *collaris* might simply be a subtropical/temperate zone subspecies of *superciliosus*. Amadon (in Stresemann and Amadon 1979) considered *superciliosus* and *collaris* to form a superspecies, as did Sibley and Monroe (1990), Thiollay (1994), and Ferguson-Lees and Christie (2001). Wolters (1975–1982) listed *superciliosus* and *collaris* together as "(Subgenus -)", presumably alluding to the lack of an available name.

New Information:

Olson (2006) found that *A. superciliosus* (henceforth *superciliosus*) differed strongly from all other examined *Accipiter* species in several major details of its skeletal anatomy, and accordingly recommended that it be removed from *Accipiter*.* Subsequently, several molecular studies (Kocum 2006, Hugall and Stuart-Fox 2012, Oatley et al. 2015, and Mindell et al. 2018) corroborated the distant relationship between *superciliosus* and *Accipiter* proper. Mindell et al. (2018) also sampled *A. collaris* (henceforth *collaris*), and their tree suggested a sister relationship between the two species (albeit only weakly supported, with posterior probability <0.95). These two species appeared to fall within a grade of superficially *Accipiter*-like taxa near the base of the clade comprising Accipitrinae and Buteoninae (sensu Mindell et al. 2018). Relationships of taxa near the base of the Accipitrinae/Buteoninae are as yet unclear, with each study finding a different topology in that part of the accipitrid tree, none with strong support. In the tree of Mindell et al. (2018), *superciliosus* and *collaris* are sister to the Lizard Buzzard *Kaupifalco monogrammicus*, but the lack of branch support coupled with biogeographical implausibility and phenotypic dissimilarity all argue against a congeneric relationship with this African species. Regardless of the precise relationships of *superciliosus* and *collaris*, however, and whether or not they are truly sister species, it is clear that they are not closely related to *Accipiter* proper and should be removed from that genus, and on morphological and molecular grounds they do not fit into any other currently recognized genus.

The main obstacle to removing *superciliosus* (and *collaris*) from *Accipiter* has been confusion regarding the applicable generic name. Olson (2006) used the generic name *Hieraspiza* Kaup, 1844 for *superciliosus*, following G. R. Gray's (1855) selection of *Falco tinus* Latham, 1790 as the type species of that genus as reported by Hellmayr and Conover (1949: 48). Mindell et al. (2018) recommended following suit. However, *Falco tinus* was not among the species originally included in *Hieraspiza* (Kaup first included it in *Hieraspiza* in an 1847 publication), so it is ineligible as the type species of that genus (per ICZN Article 67.2), and accordingly Gray's designation of it as the type is irrelevant (Dickinson and Remsen 2013, Sangster et al. 2021). (For additional details on the history of the name *Hieraspiza*, the type species of which has been fixed as *Falco virgatus* Temminck, 1822 (= *Accipiter virgatus*) for nomenclatural stability, see Sangster et al. 2021.)

Sangster et al. (2021) reviewed the history of the name *Hieraspiza* and compiled all generic names applicable to species currently placed in *Accipiter*, and confirmed that *Hieraspiza* cannot be applied to *superciliosus* and *collaris* and (as implied by Wolters 1975–1982) that no previously existing genus name is applicable to these two species. As a result, they named a new genus (with *Falco superciliosus* Linnaeus, 1758 as its type species): *Microspizias*, which appropriately translates to "tiny hawk."

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*Olson (2006) did not expressly mention *A. collaris*, leading to subsequent confusion in the literature. Olson had not examined skeletal material of the species (per Olson 1988), so accordingly statements that the 2006 study refuted a close relationship between *superciliosus* and *collaris* were erroneous.

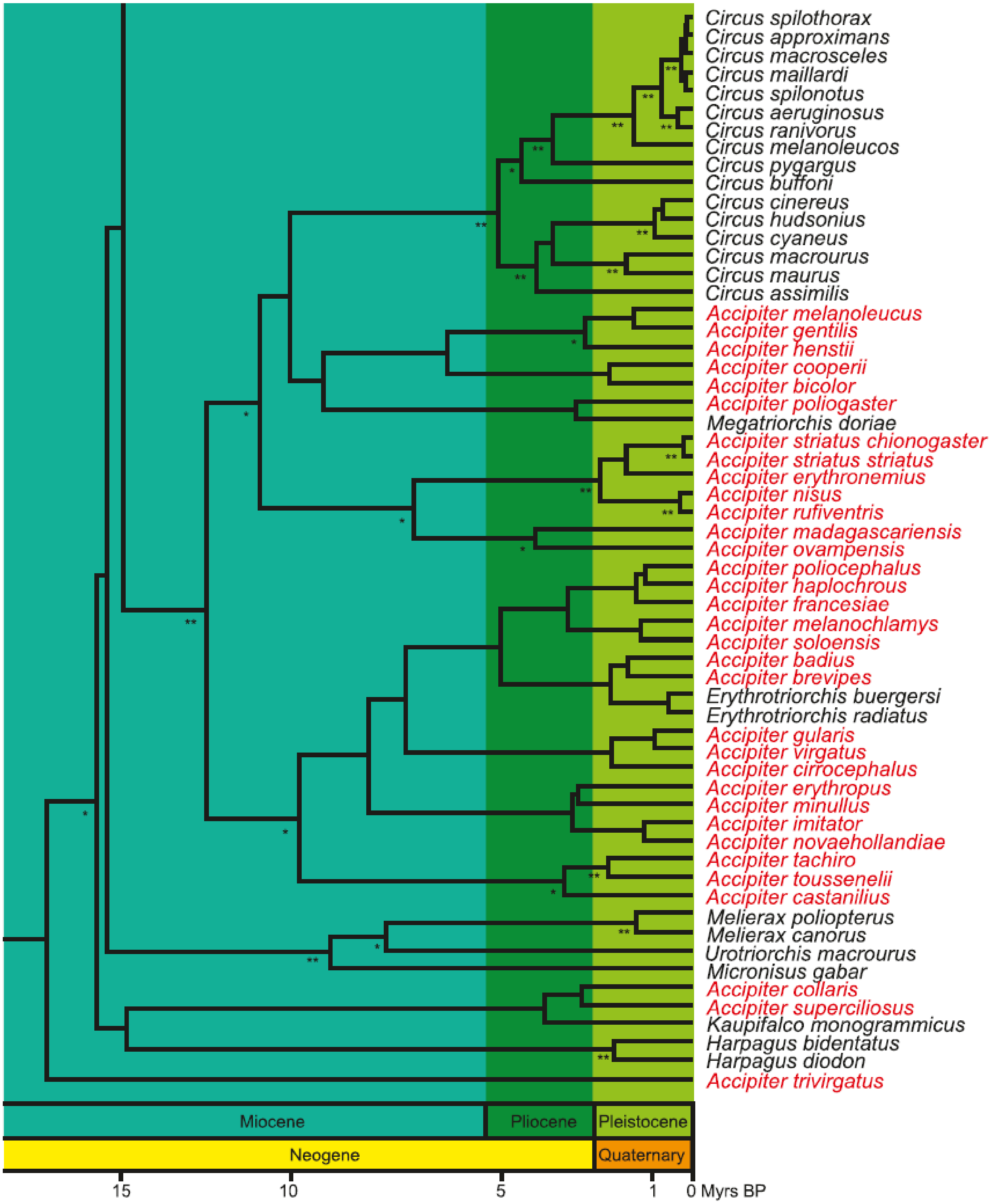

Figure 1. Phylogeny of the Accipitriformes based on published DNA sequence datasets (from Mindell et al. 2018). *Accipiter* species in red; * indicates posterior probability of 0.95–0.99; ** indicates posterior probability of 1.0.

Note that even with the removal from *Accipiter* of *A. superciliosus* and *A. collaris*—as well as two Asian species even more distantly related to the rest of *Accipiter*, *A. trivirgatus* and its presumed close relative *A. griseiceps*, for which the generic name *Lophospiza* Kaup, 1844 is available—*Accipiter* remains paraphyletic with respect to harriers (*Circus*), as well as the Australasian genera *Erythrotriorchis* and *Megatriorchis*; a generic revision of the remainder of *Accipiter* awaits more comprehensive sampling.

Recommendation:

Given the molecular and morphological data and the nomenclatural conclusions of Sangster et al. (2021), we strongly recommend a YES vote to move Tiny Hawk from *Accipiter* to the new genus *Microspizias*, as *Microspizias superciliosus*. As for the location of *Microspizias* in the linear sequence of the checklist, placing it between *Harpagus* and *Circus* would be consistent with the results of Mindell et al. (2018) (leaving *Circus* adjacent to *Accipiter*).

Note: While this proposal was in preparation, an independently prepared proposal (https://www.museum.lsu.edu/~Remsen/SACCprop942.htm) was submitted to SACC, with the same recommendation and with (as of 18 Dec 2022) unanimous approval.

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Submitted by: Max T. Kirsch and Pamela C. Rasmussen

Date of Proposal: 20 June 2022, revised 19 December 2022

Treat *Accipiter atricapillus* as a separate species from Northern Goshawk *A. gentilis*

Background:

As currently recognized by most global authorities, *Accipiter gentilis*, the Northern Goshawk, has a Holarctic distribution. In the Palearctic region, it is found across Europe and northern Asia, with populations also in Japan, the Himalayas, and northern Morocco. In the Nearctic region, it occurs through northern North America, south through the Rocky Mountains and into the mountains of western Mexico. Northern Goshawk forms a superspecies with Meyer's Goshawk (*Accipiter meyerianus*) of New Guinea and surrounding islands, Henst's Goshawk (*Accipiter henstii*) of Madagascar, and Black Goshawk (*Accipiter melanoleucus*) of Africa. Northern Goshawk is broadly comprised of two subspecies groups, the Palearctic *gentilis* group and the Nearctic *atricapillus* group, which differ in a number of morphological characteristics, including upperparts color (including contrast between crown and mantle), barring pattern on the underparts, and eye color (Sangster 2022), although underparts and eye color do vary somewhat.

In North America, *A. gentilis atricapillus* was originally described as a separate species, as *Falco atricapillus* Wilson, 1812. It was treated as a separate species until at least 1918 by many authorities, including by the first through fourth editions of the AOU *Check-List* (1886, 1895, 1910, 1931) and Ridgway (1874, 1887). It appears that Hartert (1914) was the first to include *atricapillus* as a subspecies of a broader *gentilis*, a view that was supported by Oberholser (1918), who noted that "the latter [*atricapillus*] differs from *Astur [Accipiter] gentilis* in its more mottled or irregularly barred lower parts; individual variation in each of the two races bridges." This treatment was followed by most subsequent authorities, including Peters (1931), the fifth edition of the AOU *Check-List* (1957) (as well as all subsequent versions), Dickinson and Remsen (2013), the HBW/BirdLife International taxonomy (del Hoyo and Collar 2014), and the IOC World Bird List (Gill et al. 2022).

New Information:

Several studies have recently investigated the phylogeography and systematics of the Northern Goshawk. In one study investigating the status of populations of Northern Goshawk on Haida Gwaii (Geraldes et al. 2019), European and North American birds were found to be highly divergent using genotyping by sequencing (GBS) data. Geraldes et al. (2019) estimated the divergence time between the North American and European birds at about 247,000 years before present based on mitochondrial sequence data, and about 346,000 years before present based on the GBS dataset. In another study looking at the *Accipiter gentilis* superspecies using only mitochondrial sequence data, deep divergence was again recovered between North American *atricapillus* and Palearctic *gentilis*, with uncorrected mean distance at the control region at 4.3%; divergence within Palearctic subspecies was 2.6–3.2% (Kunz et al. 2019). In addition to finding relatively deep divergence between Nearctic and Palearctic birds, Kunz et al. (2019) also found that Nearctic *atricapillus* was not sister to Palearctic *gentilis*, with the Palearctic *gentilis* group instead sister to the remaining Old World taxa, including Meyer's

Goshawk, Henst’s Goshawk, and Black Goshawk, although relationships within this Old World clade were not strongly supported (Fig. 1).

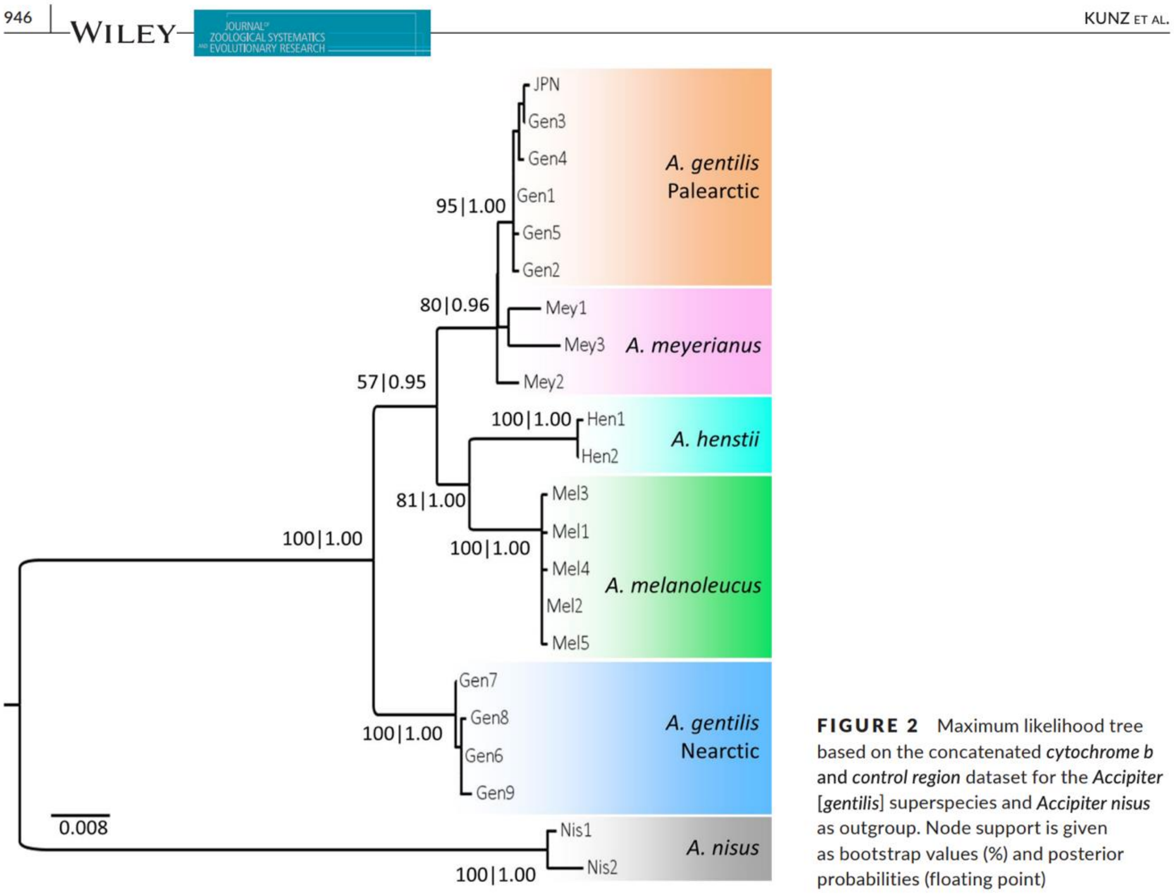

FIGURE 2 Maximum likelihood tree based on the concatenated *cytochrome b* and *control region* dataset for the *Accipiter* [*gentilis*] superspecies and *Accipiter nisus* as outgroup. Node support is given as bootstrap values (%) and posterior probabilities (floating point)

Figure 1. From Kunz et al. (2019). Phylogenetic tree of mitochondrial sequence data (concatenated *cyt-b* and *control region*), showing Nearctic *atricapillus* as sister to entire clade of Old World taxa, including Palearctic *gentilis*, Meyer’s Goshawk (*Accipiter meyerianus*), Henst’s Goshawk (*Accipiter henstii*), and Black Goshawk (*Accipiter melanoleucus*).

In addition to genetic data showing deep divergence and even paraphyly between Palearctic and Nearctic groups of Northern Goshawk, Sangster (2022) analyzed vocal data and found significant differences between the two groups consistent with differences between Henst’s Goshawk and the other two taxa. Although there are few studies of vocal differences among hawks, and its importance as an indication of species-level divergence is uncertain, Sangster (2022) argued that vocalizations are important in mate choice, suggesting that they could play an important role as an isolating barrier, and that vocal differences are not learned, and so likely have a genetic basis that can be useful in diagnosing species-level differences. Sangster (2022) analyzed what he called the “chattering” call, which is used for display and pair-bond purposes. A total of 75 Palearctic, 37 Nearctic, and 7 Henst’s Goshawk individuals were included in the analyses, and each of the three groups showed consistent differences in vocalizations that allowed them to be classified with 100% accuracy using Discriminant Function Analysis. In addition, Nearctic Northern Goshawk were as different from Palearctic Northern Goshawk as each were from Henst’s Goshawk, with Nearctic Northern Goshawk vocalizations differing significantly from Palearctic Northern Goshawk in 5 vocal variables, including duration of the median note (longer in *atricapillus*), call duration (longer in *atricapillus*), and note rate (lower in *atricapillus*; Figure 2).

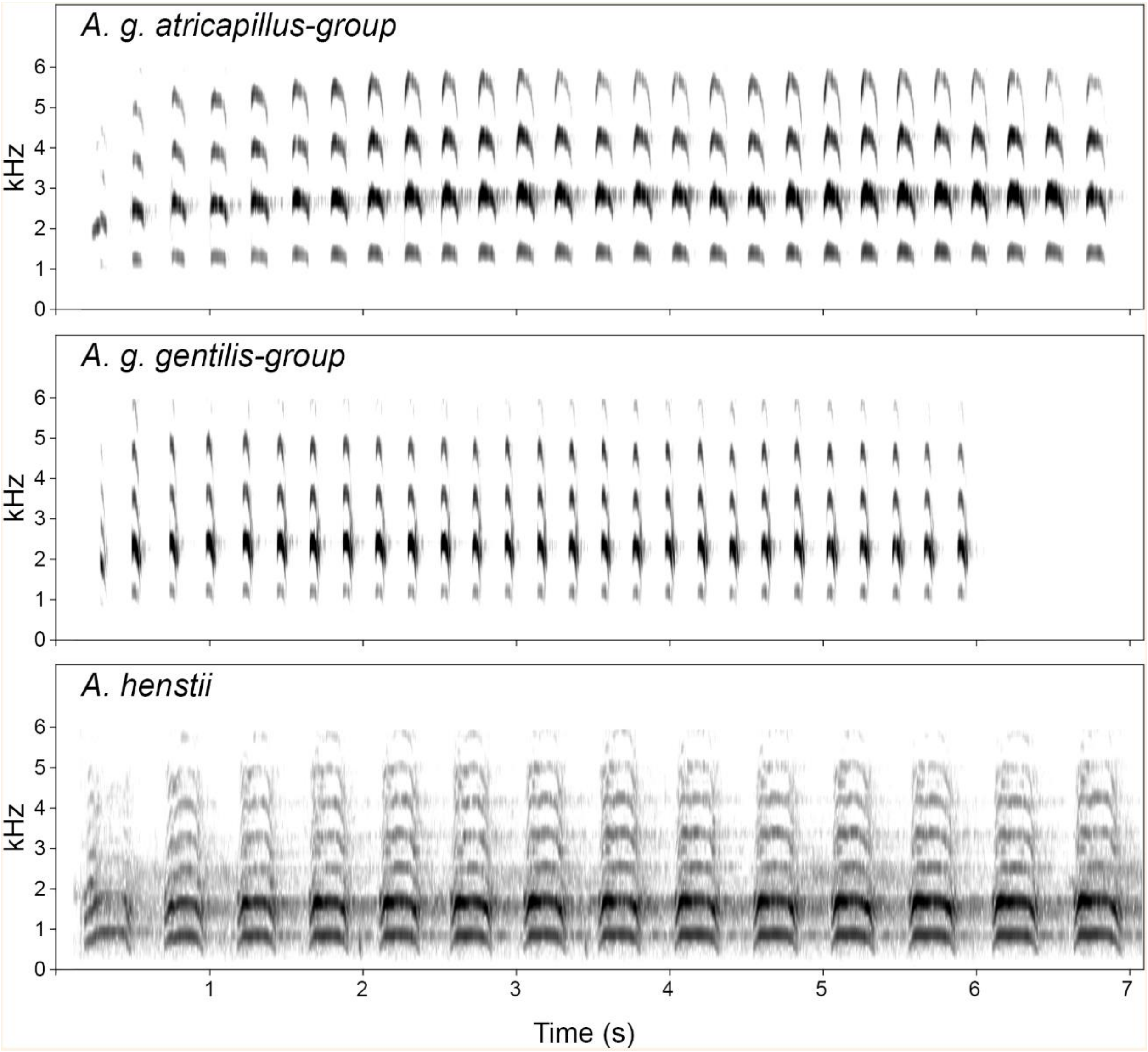

Figure 2. From Sangster (2022). Sonograms of the “chatter” call of Nearctic Northern Goshawk (top), Palearctic Northern Goshawk (middle), and Henst’s Goshawk (bottom).

Recommendation:

I recommend voting YES to split North American Northern Goshawk populations from Palearctic populations as *Accipiter atricapillus*. Based on the strong genetic divergence between Nearctic and Palearctic populations, apparent in both mitochondrial and nuclear DNA, and the apparent paraphyly of Northern Goshawk using mitochondrial DNA, as well as vocal differences that are consistent with species-level divergence, North American goshawks appear to be a separate species from Northern Goshawks in Europe and Asia.

If the committee votes to split these taxa, I recommend the following common English names for the resulting taxa:

Accipiter atricapillus – American Goshawk. This name was in use by the AOU and other authors prior to it being lumped with Palearctic taxa (see AOU 1886, 1895, 1910, and 1931), and it was suggested by Sangster (2022) in his recommendation to re-split Northern Goshawk.

Accipiter gentilis – Eurasian Goshawk. This name was suggested by Sangster (2022) for the Palearctic taxa if North American taxa are split. Although it seems that "Northern Goshawk" was in use prior to North American taxa being lumped together with Palearctic birds, I think its widespread use for the entire species across North America would lead to confusion if this name was still in use for only Palearctic taxa.

Effect on the AOS Checklist:

This split would potentially add a species to the AOS *Check-List*, pending acceptance of a specimen of *A. g. gentilis* from Labrador (UMMZ) or records (subspecies *albidus*) from Shemya Island in the Aleutians.

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Submitted by: Shawn M. Billerman, Cornell Lab of Ornithology

Date of Proposal: 19 December 2022

Treat *Aphelocoma sumichrasti* as a separate species from Woodhouse's Scrub-Jay *A. woodhouseii*

Background:

The taxonomy of the scrub-jay species complex has been a longstanding subject of debate, with recognition of two to four species throughout history. The comprehensive treatment of the entire *Aphelocoma* complex by Pitelka (1951) identified as many as five distinct phenotypic groups which are all allopatric or parapatric. The first molecular phylogenetic reconstruction of the group with comprehensive geographic sampling (Gowen et al. 2014) identified five deeply divergent genetic clades, despite only three recognized species at the time of publication. Notably, the phylogenetic reconstructions performed by Gowen et al. (2014) revealed a sister relationship between the coastal lineage of Western Scrub-Jay (*Aphelocoma californica*) and the Island Scrub-Jay (*Aphelocoma insularis*). This result rendered the Western Scrub-Jay paraphyletic, leading to the subsequent split of Western Scrub-Jay into California Scrub-Jay (*Aphelocoma californica*) and Woodhouse's Scrub-Jay (*Aphelocoma woodhouseii*; Chesser et al. 2016). This taxonomic split was supported despite the known hybrid zone between California and Woodhouse's Scrub-Jays near the California/Nevada border, just east of the Sierra Nevada mountains. The prevailing logic of this proposal leaned on the evidence of a sigmoidal transition zone between these lineages, indicating a measure of reproductive isolation between the parental populations that is likely due to reduced fitness of hybrid offspring (Gowen et al. 2014, Irwin 2020). This outcome was an encouraging example demonstrating the power of taxonomy and molecular phylogenetics/phylogeography to reciprocally inform one another, with taxonomy guiding the sampling scheme of the molecular project and novel information from the resulting phylogenies being used to inform taxonomy.

Despite the split of Western Scrub-Jay, significant genetic structuring remained within the lineage designated as Woodhouse's Scrub-Jay (Figure 1). A phylogeny built using mitochondrial DNA (mtDNA) revealed that the Woodhouse's Scrub-Jays sampled from southern Mexico (subspecies *A. w. sumichrasti/remota*) formed a deeply divergent, reciprocally monophyletic clade that was sister to all other individuals from throughout the entire range of Woodhouse's Scrub-Jay (Figure 2; Gowen et al. 2014). In fact, the mtDNA split between the *A. w. sumichrasti/remota* clade and the rest of Woodhouse's Scrub-Jay was estimated to have occurred before the divergence between the currently recognized sister species California Scrub-Jay and Island Scrub-Jay (Figure 2). This deep divergence led Gowen et al. (2014) to propose that the *A. w. sumichrasti/remota* clade, which has long been recognized as a phenotypically distinct group (Pitelka 1951), ought to be recognized as a distinct species. Despite the compelling evidence accumulated by Gowen et al. (2014), a formal proposal to split the *A. w. sumichrasti/remota* clade from the rest of Woodhouse's Scrub-Jay was put on hold pending further investigations with both genomic and quantitative phenotypic data.

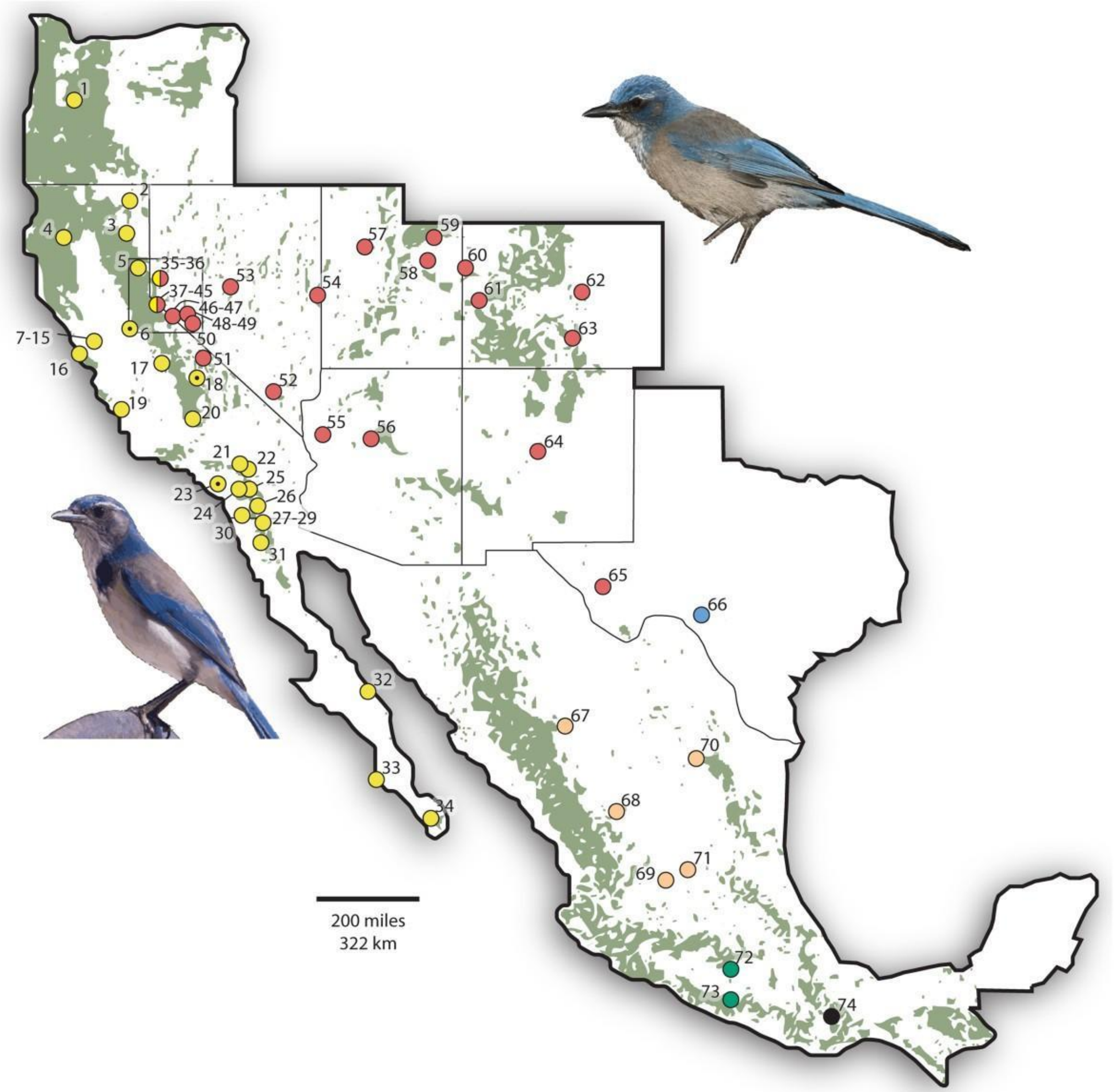


Figure 1. Sampling map from Gowen et al. (2014). Dot colors correspond to nuclear genetic clusters identified by the program Structure. Yellow represents the newly recognized (2016) California Scrub-Jay, whereas all other genetic clusters were lumped into Woodhouse's Scrub-Jay.

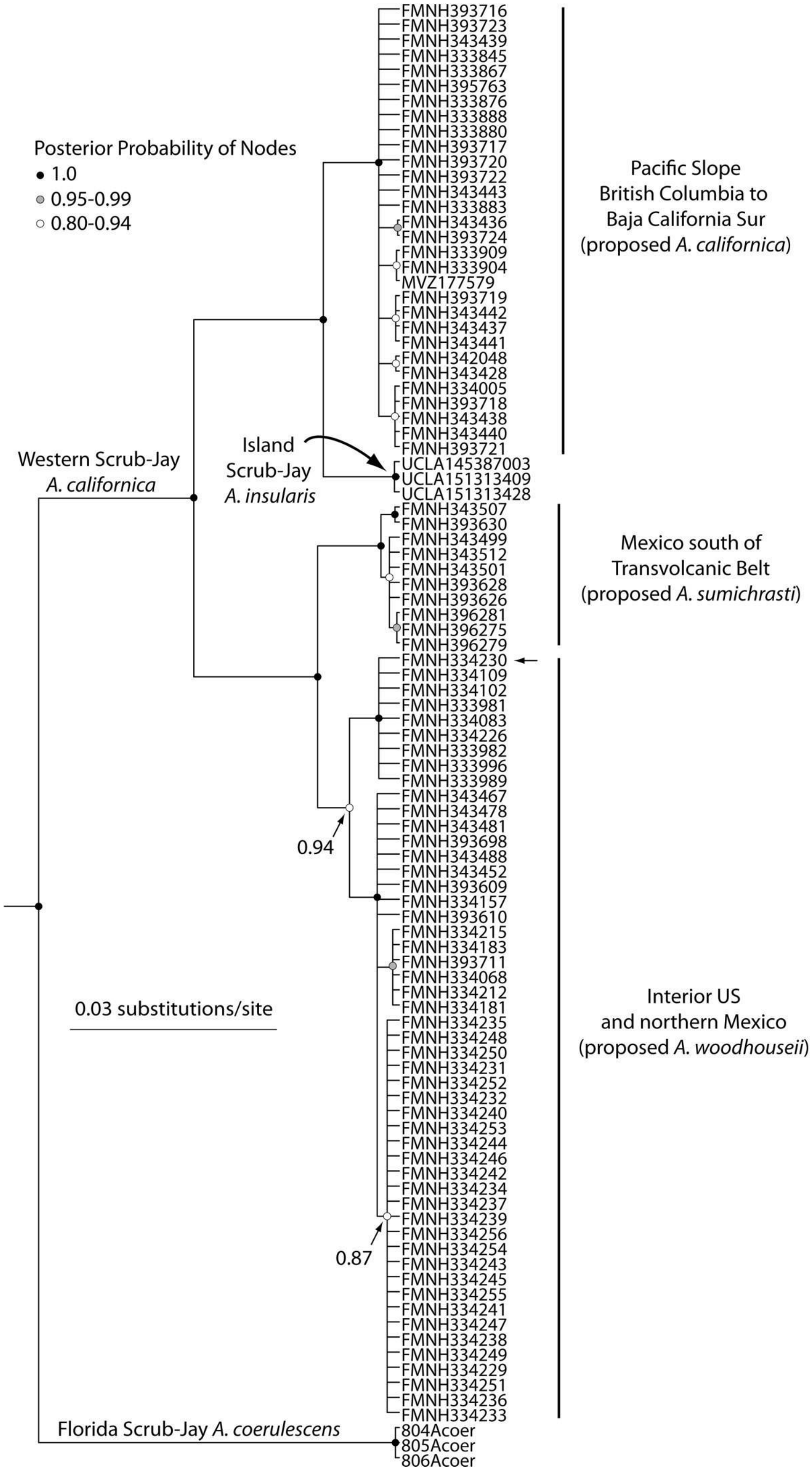


Figure 2. Mitochondrial phylogeny from Gowen et al. (2014) showing the reciprocal monophyly of the *A. w. sumichrasti/remota* clade and its deep break relative to the rest of Woodhouse's Scrub-Jay.

New information:

Genomic data

Genomic data strongly support the species status of the *A. w. sumichrasti/remota* clade regardless of methodological approach. Sequence data from genome-wide RADseq markers confirm that the *A. w. sumichrasti/remota* clade is sister to and deeply divergent from all other populations of Woodhouse's Scrub-Jay throughout the genome (Figure 3). Additionally, measures of relative genomic divergence (i.e., F_{ST}) between the *A. w. sumichrasti/remota* clade and parapatric Woodhouse's Scrub-Jay populations is nearly twice the relative divergence between parapatric populations of Woodhouse's and California scrub-jays in the western U.S. (Figure 4). These results are further supported by a range of modern species delimitation algorithms, which unanimously identify the *A. w. sumichrasti/remota* clade as a unique species (Figure 5).

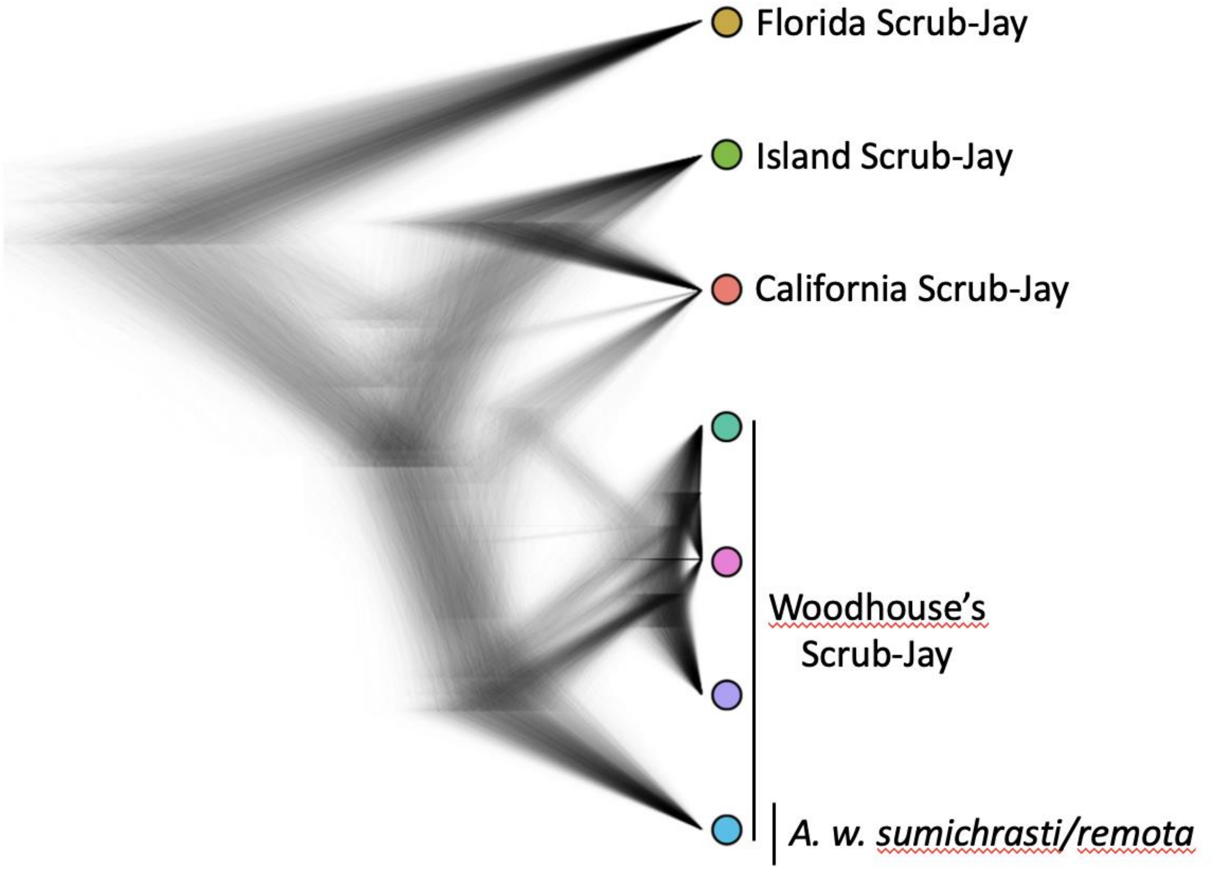
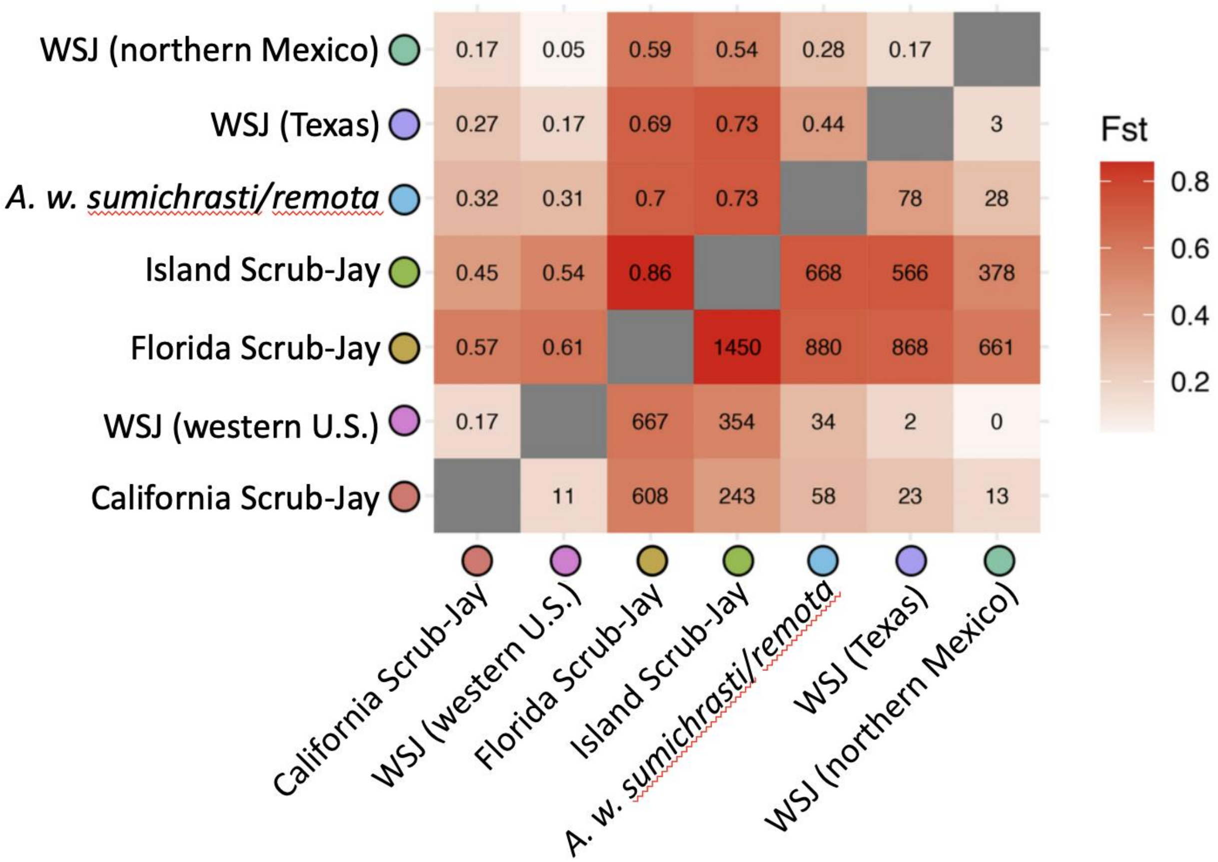


Figure 3. Species phylogeny from DeRaad et al. (2022) based on thousands of RAD loci. The phylogeny shows the deep break between the *A. w. sumichrasti/remota* clade and the rest of Woodhouse's Scrub-Jay. Green, pink, and purple dots represent samples from northern Mexico, the western U.S., and the Edward's Plateau in Texas, respectively.



	California Scrub-Jay	WSJ (western U.S.)	Florida Scrub-Jay	Island Scrub-Jay	*A. w. sumichrasti/remota*	WSJ (Texas)	WSJ (northern Mexico)
WSJ (northern Mexico)	0.17	0.05	0.59	0.54	0.28	0.17	
WSJ (Texas)	0.27	0.17	0.69	0.73	0.44		3
A. w. sumichrasti/remota	0.32	0.31	0.7	0.73		78	28
Island Scrub-Jay	0.45	0.54	0.86		668	566	378
Florida Scrub-Jay	0.57	0.61		1450	880	868	661
WSJ (western U.S.)	0.17		667	354	34	2	0
California Scrub-Jay		11	608	243	58	23	13

Figure 4. Heatmap from DeRaad et al. (2022) showing pairwise divergence between identified clades of Scrub-Jays. Above the gray diagonal is F_{ST} and below the diagonal is the number of fixed differences for the given comparison.

Although the new genomic data consistently support the genetic differentiation of the *A. w. sumichrasti/remota* clade, this is ultimately just a recapitulation of the results of Gowen et al. (2014), albeit with genome-wide coverage and updated statistical methods. In this light, the most important consequence of adding thousands of additional loci to investigate species limits in DeRaad et al. (2022) was not the ability to analyze population structure with greater statistical power, but rather the ability to perform statistical tests for gene flow between non-sister lineages. These tests require a number of loci to search for cases of excess allele sharing between non-sister taxa, i.e., statistical signatures of gene flow, which can reveal incomplete reproductive isolation between non-sister taxa even when no clearly admixed individuals are present in the sample (e.g., ABBA/BABA tests; Malinsky et al. 2021). In DeRaad et al. (2022), tests for gene flow revealed a statistically significant signature of gene flow between California Scrub-Jay and Woodhouse's Scrub-Jay, despite not sampling intermediate individuals from near the contact zone (Figure 6). In comparison, with a similar sampling scheme (i.e., no sampling from the contact zone), no statistical signatures of gene flow were detected between the non-sister parapatric populations of Woodhouse's Scrub-Jay in northern (*A. w. grisea/cyanotis*) and southern (*A. w. sumichrasti/remota*) Mexico. Stated plainly, there is currently no detectable genomic evidence for gene flow between the *A. w. sumichrasti/remota* clade and any other populations of Woodhouse's Scrub-Jay, barring future sampling from inside the contact zone in central Mexico. Further, tests for gene flow suggest that the barriers

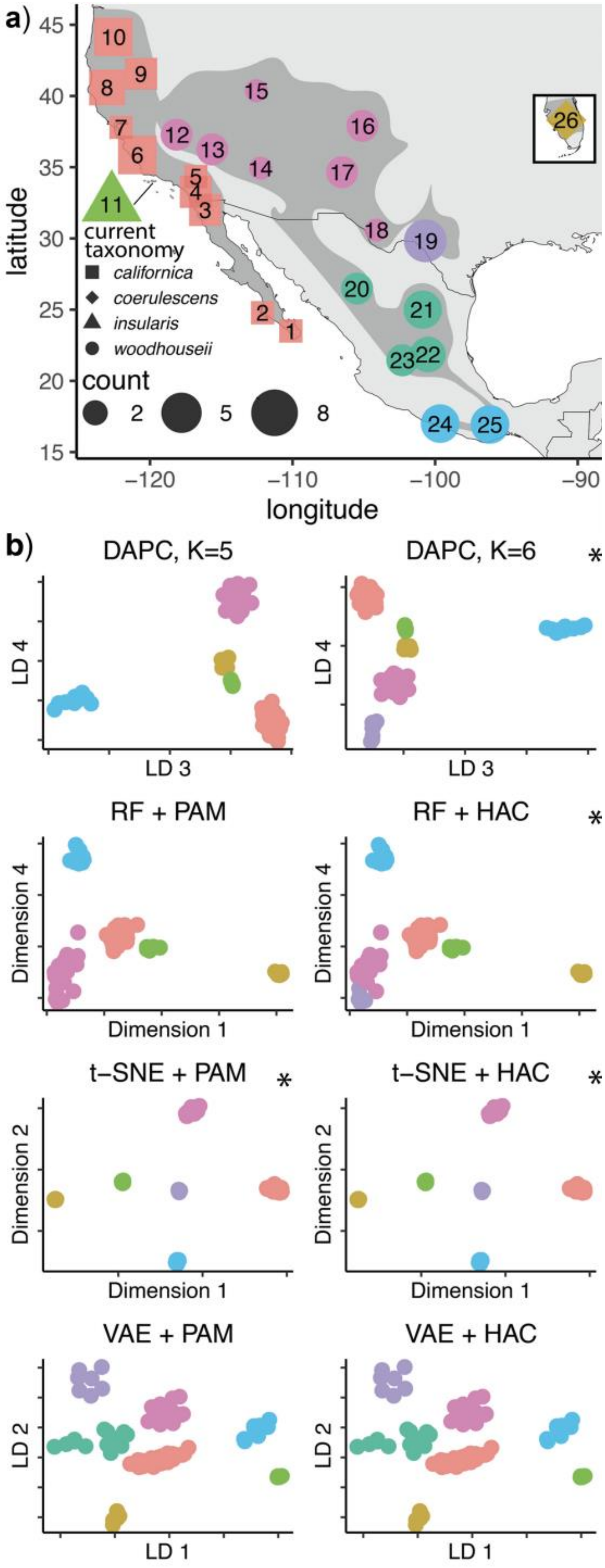


Figure 5. (A) Sampling map color coded according to the most aggressive species delimitation scheme (k=7). (B) Unsupervised clustering algorithms used to identify species groups from genomic data without *a priori* sample assignments. Asterisk indicates the most commonly recovered species delimitation scheme (k=6). Reproduced from DeRaad et al. (2022).

enforcing reproductive isolation between Woodhouse's Scrub-Jay populations in northern and southern Mexico are more complete than the barriers to gene flow between California Scrub-Jays and Woodhouse's Scrub-Jays in the western U.S.

Quantitative phenotypic data

Although the new genomic data presented above strongly support the species status of the *A. w. sumichrasti/remota* clade, a major limitation is the lack of genomic data from central Mexico where the *A. w. sumichrasti/remota* clade is presumably parapatric with non-sister populations of Woodhouse's Scrub-Jays from northern Mexico (*A. w. grisea/cyanotis*). The genomic sampling gap in this putative contact zone results from an unfortunate lack of fresh tissue samples from this region. Nonetheless, a series of 20th century museum specimens exist that document comprehensively the phenotype of Woodhouse's Scrub-Jay from throughout its entire distribution in Mexico (Pitelka 1951; DeRaad et al. 2019). Quantification of body size and the color of the mantle plumage reveals that samples from outside of the contact zone have mostly non-overlapping distributions in both characteristics (Figure 7), whereas the *A. w. sumichrasti/remota* clade is characterized by larger body size and brown mantle plumage, compared to the blue mantle and small body size of Woodhouse's Scrub-Jays from northern Mexico.

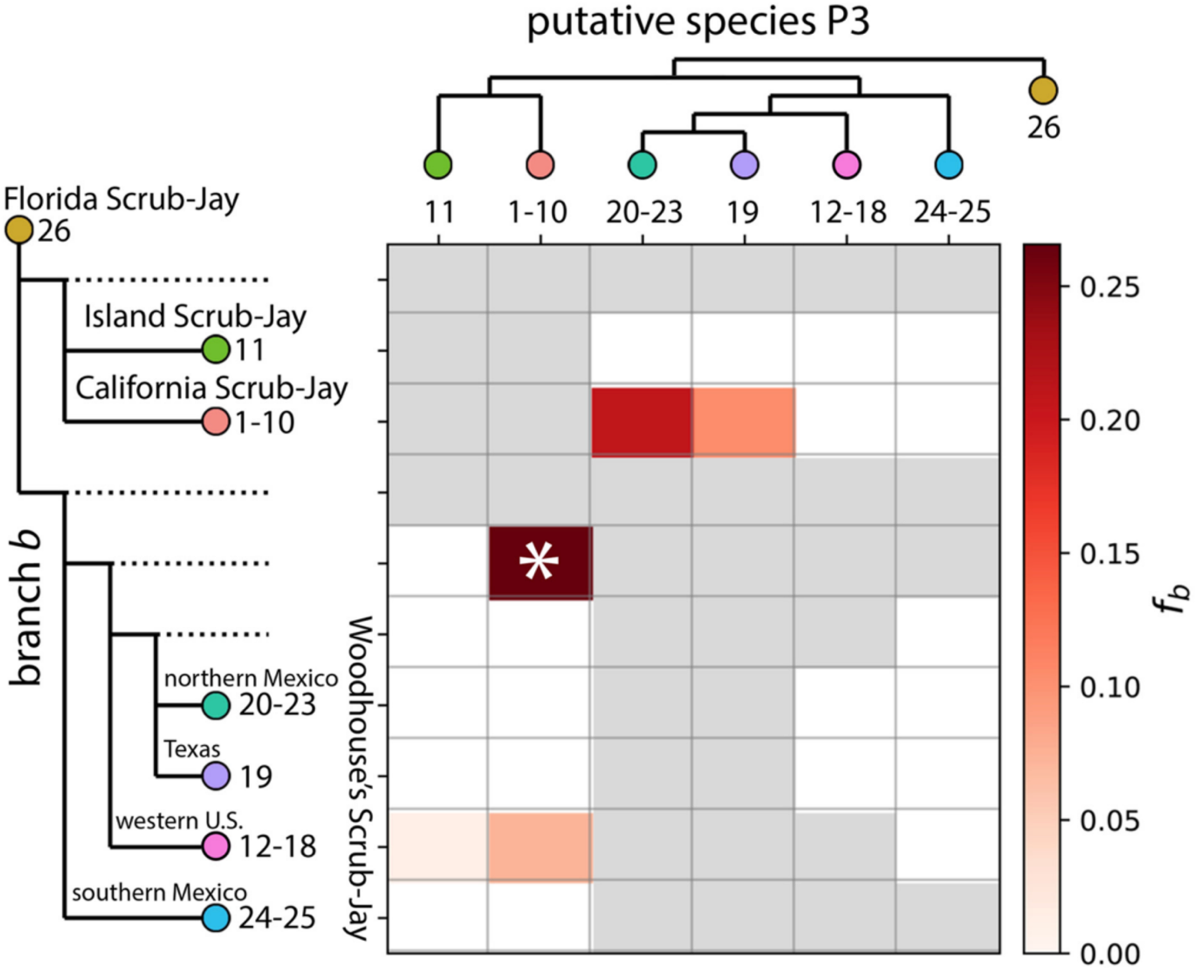


Figure 6. Heatmap from DeRaad et al. (2022) showing the f-branch statistic which quantifies the probability of gene flow for a given pairwise comparison. Gray squares indicate pairwise comparisons that cannot be made under an ABBA/BABA framework. Note the high values (and the single statistically significant value noted by a white asterisk) in comparisons involving California and Woodhouse's Scrub-Jays, compared to the consistent zero values in comparisons involving the *A. w. sumichrasti/remota* clade (populations 24-25).

Visual observation of all specimens reveals a handful of individuals from near the putative contact zone in central Mexico that appear intermediate in both body size and back color, suggesting the possibility of hybridization (Figure 8). Sigmoidal clines are well fit to the quantitative phenotypic data, indicating a relatively rapid transition in phenotype centered on the putative contact zone in central Mexico (Figure 9). The transition in mantle plumage color is especially rapid, with an estimated cline width of just 257 km, which could be explained by assortative mating according to plumage, or reduced fitness in phenotypically intermediate individuals (Irwin and Schluter 2022). Overall, the phenotypic evidence is best explained by a model of secondary contact between two phenotypically distinct lineages resulting in a narrow hybrid zone, which is likely maintained by some form (unable to distinguish between intrinsic vs. extrinsic) of selection against hybrid offspring (DeRaad et al. 2019).

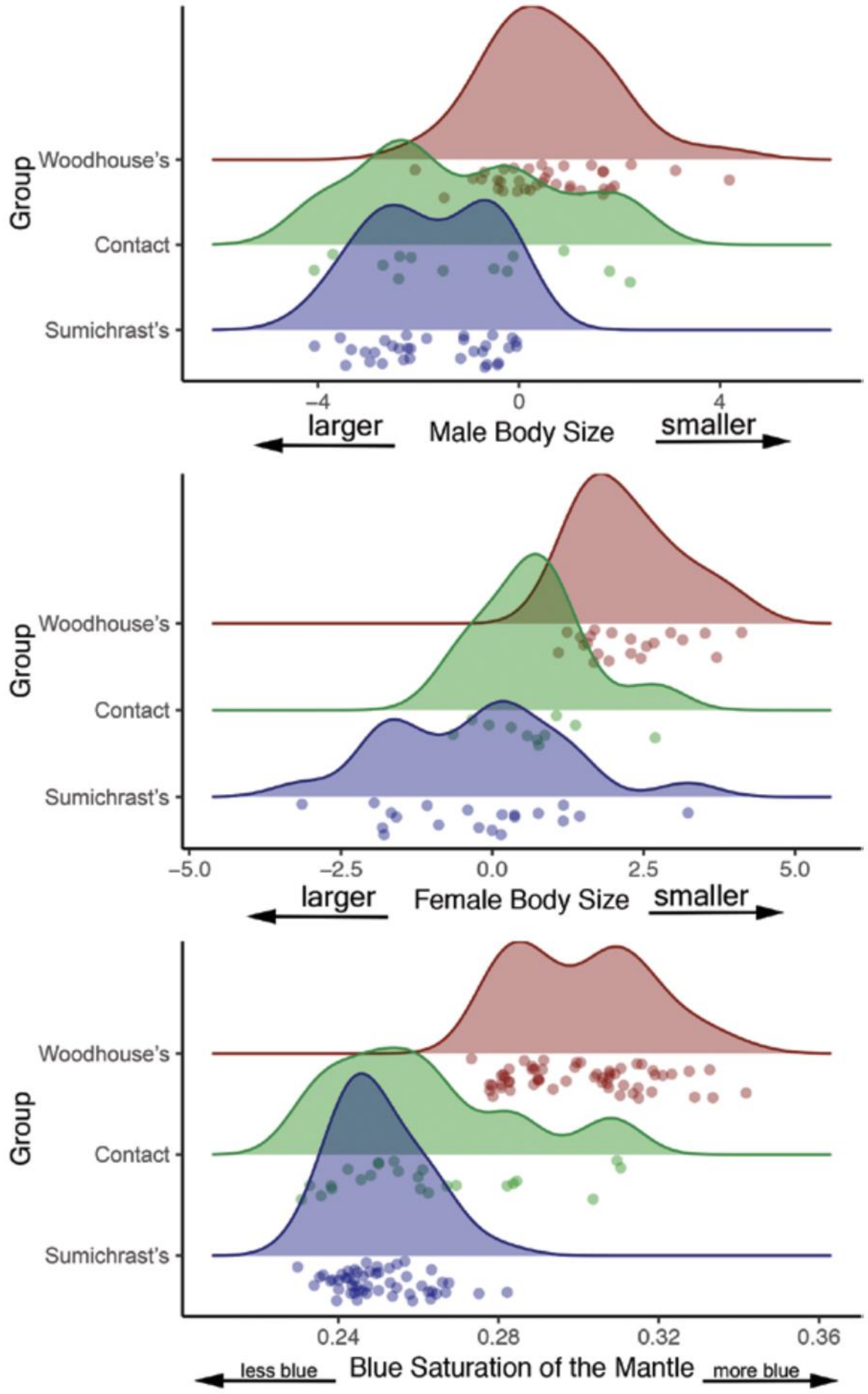


Figure 7. Histograms from DeRaad et al. (2019) showing the distribution of body size (split by sex) and mantle color for specimens from the core range of each species and specimens collected within the contact zone.

Figure 8. Photos of specimens from DeRaad et al. (2019) showing the entire phenotypic range from small birds with blue mantles in northern Mexico, to large birds with brown mantles in southern Mexico.

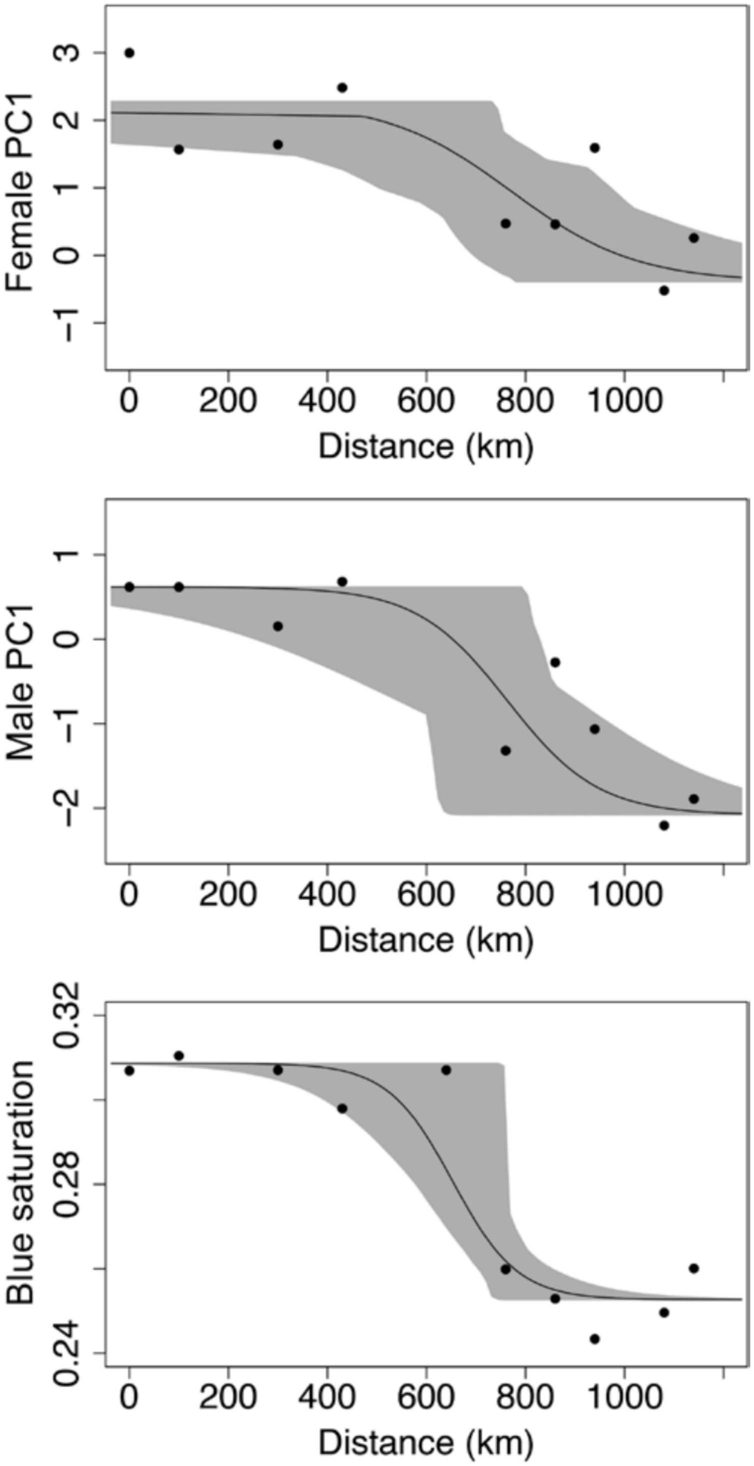


Figure 9. Geographic clines fit to body size (split by sex) and mantle color across the sampling transect from northern to southern Mexico show sigmoidal transitions indicating geographically bounded regions of intermediacy. Reproduced from DeRaad et al. (2019).

Summary:

A recent, comprehensive genomic analysis of the scrub-jay species complex found unanimous support for species status of the *A. w. sumichrasti/remota* clade from southern Mexico (DeRaad et al. 2022), confirming previous results from mtDNA and microsatellite loci (Gowen et al. 2014). Beyond simply supporting the genetic distinctiveness and reciprocal monophyly of this lineage (good evidence for species status under a phylogenetic species concept; Donoghue 1985), genomic data also reveal no evidence for gene flow from other lineages permeating the genome of the *A. w. sumichrasti/remota* clade. This novel evidence supports genome-wide reproductive isolation of the *A. w. sumichrasti/remota* clade.

The genomic evidence presented in DeRaad et al. (2022) does require the caveat that it does not include sampling from central Mexico, the site of a putative contact zone between the *A. w. sumichrasti/remota* clade and parapatric *A. woodhouseii* populations from northern Mexico. Luckily, this genomic sampling gap can be filled with quantitative phenotypic data from museum specimens (DeRaad et al. 2019). Phenotypic data from this putative contact zone indicate that hybridization between the *A. w. sumichrasti/remota* clade and parapatric populations is both rare (implying a degree of assortative mating) and geographically restricted. The geographic transition in body size and plumage across the contact zone are well fit by sigmoidal clines, conforming to a classic tension zone model (Barton and Hewitt 1989) where selection against hybrids maintains species boundaries despite incomplete reproductive isolation upon secondary contact.

But how can we square the potentially conflicting results of a genome-wide lack of evidence for gene flow involving the *A. w. sumichrasti/remota* clade (DeRaad et al. 2022) with phenotypically intermediate putative hybrid individuals from central Mexico (DeRaad et al. 2019)? One potential explanation could be a severe reduction (or even total absence) of fertility in F1 hybrid offspring produced between *A. w. sumichrasti/remota* birds and *A. woodhouseii* birds from northern Mexico. Even a moderate intrinsic reduction in hybrid fertility would reduce backcrossing and the sharing of divergent alleles between scrub-jays in northern and southern Mexico. An alternative explanation could be strong natural selection against hybrid offspring with a phenotype intermediate between the two hybridizing populations. Strong divergent natural selection could reduce the fitness of hybrid offspring such that long term survival and successful reproduction is a rarity. In this circumstance, divergent natural selection would function similarly to an intrinsic genomic incompatibility, severely reducing allele sharing between scrub-jays from northern and southern Mexico.

Needless to say, the exact mechanisms maintaining the strong (albeit incomplete) reproductive isolation of the *A. w. sumichrasti/remota* clade will require further detailed studies integrating ecological and genomic approaches to fully understand the key evolutionary forces maintaining the species boundaries. However, regardless of the exact mechanism conferring reproductive isolation in this system, the evolutionary implications of this isolation are clear. Distantly related parapatric populations of Scrub-Jays in northern and southern Mexico do not share alleles at any detectable frequency, maintaining their divergent phenotypes, genomes, and evolutionary histories, despite opportunity for extensive interbreeding in central Mexico. Here, we present novel genomic and phenotypic evidence that clinches support for the species status of the *A. w. sumichrasti/remota* clade under both phylogenetic (reciprocal monophyly, deep divergence; Donoghue 1985) and biological (reproductive isolating barriers upon secondary contact; Mayr 1982) species concepts.

Recommendation:

We recommend elevating the *A. w. sumichrasti/remota* clade to species status by splitting *Aphelocoma woodhouseii* into two species. Populations across the western U.S. and northern Mexico would retain the specific epithet *Aphelocoma woodhouseii*. We recommend that *A. woodhouseii* be assigned the English name Western Scrub-Jay, reverting to historical precedent.

The subspecies group *A. w. sumichrasti/remota* would be recognized under the specific epithet *Aphelocoma sumichrasti*. Possibilities for the English name of this species include:

Oaxaca Scrub-Jay: This name recognizes the Mexican state of Oaxaca, which encompasses a large portion of the distribution of *A. w. sumichrasti/remota.* This name is consistent with the Oaxaca Sparrow (*Aimophila notosticta*), which inhabits a similar range.

Puebla Scrub-Jay: This name recognizes the Mexican state of Puebla, which encompasses a large portion of the distribution of *A. w. sumichrasti/remota.*

Tehuacan Scrub-Jay: This name recognizes the Tehuacán-Cuicatlán Biosphere, a richly biodiverse habitat found in southern Mexico, in the heart of the range of *A. w. sumichrasti/remota.* It also recognizes the city of Tehuacán within the state of Puebla.

Aztec Scrub-Jay: This name recognizes the Aztec peoples who inhabited central Mexico, in a similar region to the current distribution of *A. w. sumichrasti/remota.* The name is consistent with the Aztec Thrush (*Ridgwayia pinicola*) and the Aztec Rail (*Rallus tenuirostris*) which have similar distributions in central Mexico.

Mixtec Scrub-Jay: This name is consistent with another species from the region, *Calothorax pulcher*, which is colloquially known as 'Colibrí Mixteco', for the indigenous Mesoamerican Mixtec peoples who inhabited regions of modern Oaxaca, Puebla, and Guerrero.

The drawback to all these names is that none of them perfectly align with the distribution of the new species. Despite being phenotypically distinct from other lineages of Woodhouse's Scrub-Jay, there are unfortunately no obvious phenotypic characteristics unique to the *A. w. sumichrasti/remota* lineage, relative to all other scrub-jays, that could provide a common name.

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Date of proposal: 19 December 2022

Treat *Delichon lagopodum* as a separate species from House Martin *D. urbicum*

Description of the problem:

The genus *Delichon* is variously treated as two to four species, with the Nepal House-Martin (*D. nipalense*) universally being treated as a separate species, at least in recent years. The Asian House-Martin has been treated as a subspecies of Common House-Martin (e.g. Vaurie 1972 and other references summarized in Dickinson and Dekker 2001), but on the basis of “close approaches and probable sympatry at several locations in eastern Asia” (Sibley and Monroe 1990), it is now generally recognized as a species (e.g., Smythies 1953, Mayr and Greenway 1960, Wolters 1980, Monroe and Sibley 1993, Dickinson 2003, Gill and Wright 2006, Dickinson and Christidis 2014, Gill et al. 2021, Clements et al. 2022). Tebb and Ranner (2002) cited multiple sources as indicating that *D. dasypus* breeds sympatrically with *D. urbicum lagopodum*, but in Buryatia (southeastern Siberia, on the southern and eastern sides of Lake Baikal) the former is limited to breeding among rocks in the alpine zone, whereas the latter breeds at low elevations and on anthropogenic structures.

In Buryatia, Tebb and Ranner (2002) saw *Delichon urbicum* on most days and noted that both *urbicum* and *lagopodum* were found in close proximity. Tebb and Ranner (2002) noted the ease of identification of the two taxa in the field and detailed the separating features. On the east side of the lake (in Ulan-Ude and the steppes around Petropavlovka), they found only *urbicum*, whereas on the south side they found only *lagopodum,* breeding on bridges over the rivers running into Lake Baikal and in a large colony on a water tower near Tankhoy railway station. They found the two taxa as close as some 90 km apart and stated: “The observation so close together of two distinct forms without any evidence of interbreeding, or of co-occurrence, suggests that the forms are parapatrically separated” (Tebb and Ranner 2002). They clarified that “J. Haffer (in Glutz von Blotzheim and Bauer 1985) and C. S. Roselaar (in Cramp 1988) both cited Sushkin (in Hartert 1910) as saying that forms between *D. urbica urbica* and *D. urbica lagopoda* have been reported from the Yenisey basin. Stepanyan (1990) also reported that the two forms intergrade, although without giving details of his source. Sushkin wrote exactly the opposite, claiming that the two forms occur in close proximity without any evidence of interbreeding. His statement concurs with our observations in Buryatia. We believe the distinction between *D. urbica urbica* and *D*. (*urbica*) *lagopoda* merits further investigation” (Tebb and Ranner 2002). On this basis as well as the Tobias et al. 7-point scoring system (which amounted to 7 in this case), del Hoyo and Collar (2016) treated *lagopodum* as a separate species. Shirihai and Svensson (2018) noted that *lagopodum* “is suspected to locally overlap with *urbicum* in NW China and possibly in some areas of NW Mongolia and Russian Altai, but this needs to be confirmed and better studied. It would have obvious taxonomic consequences if established.”

New Information:

Leader et al. (2021) found both nominate *urbicum* and *lagopodum* breeding at the same location, even on the same structures, in early June 2013 in Respublika Buryatia, southeastern Siberia, hence providing the first published evidence of sympatry. This site was at a large village/holiday camp near Tunka next to River Irkut, some 90 km west of the southwestern end of Lake Baikal. Leader et al. (2021) found no sign of interbreeding, either mixed pairs or birds showing intermediate characters. They estimated 40 pairs of *lagopodum* and 15 pairs of *urbicum*, of which five *lagopodum* and one *urbicum* were trapped, allowing both taxa to be examined in the hand simultaneously.

On 23 June 2018 an additional site where both *lagopodum* and *urbicum* occur was found at Baganuur, Kherlen River, Hentiy, Mongolia, around 100 km east of Ulaanbaatar, Mongolia (Leader et al. 2021). At this site more than 100 *Delichon* martins were gathering mud at the river's edge as they approached potential nest sites under a road bridge. Although estimates of each taxon were approximate, *lagopodum* seemed to predominate. At other sites Leader et al. (2021) visited in Mongolia at Hövsgöl (Mörön and Hövsgöl Nuur) and in the Russian Federation in Irkutskaya Oblast (Kultuk) and Respublika Buryatia (Tankhoy) they found only *lagopodum.*

Leader et al. (2021) indicated that in Buryatia, *D. dasypus* is parapatric to *D. u. urbicum* and both parapatric and sympatric with *D. u. lagopodum*. The separation is elevational, with *D. dasypus* found at higher elevations, and generally not using human structures for nest sites. Farther east in Primorskiy Kray, Russian Federation in May-June 2011, Leader et al. (2021) observed *D. u. lagopodum* breeding in a mixed colony with *D. d. dasypus* underneath a road bridge crossing the River Zhigitouka on the main road between Plastun and Tefnei. They found no mixed pairs nor any that could not be identified to each taxon. Four Asian House-Martins were trapped, and the vocalizations of both taxa were recorded.

Morphology

Leader et al. (2021) detailed the features that separate *lagopodum* from *urbicum* as well as features that separate *D. dasypus* (Asian House-Martin). All three were illustrated in a color plate by Manuel Schweizer, and numerous color photos of the three taxa were included. The most striking feature that separates *lagopodum* from *urbicum* is the size of the white rump patch. In *lagopodum* the white feathering extends farther up onto the lower back and extends down to include all the upper tail coverts. The longest upper tail coverts are black in *urbicum.* In addition, *urbicum* has a longer and more deeply forked tail, giving *lagopodum* a more compact appearance (as with *dasypus*). In particular, the tail of *urbicum* averages about 9 mm longer than that of *lagopodum*, with the tail fork averaging nearly 8 mm deeper (see Table 2 from Leader, below). The combined effect of a longer tail and a deeper tail fork with the more extensive white in the rump region of *lagopodum* makes field identification fairly straightforward. The underwing coverts of *urbicum* average paler in comparison to *lagopodum*, but there is overlap. The wing/tail ratio of *urbicum* is lower and non-overlapping with that of *lagopodum* (see Table 2 and Figure 4 from Leader, below).

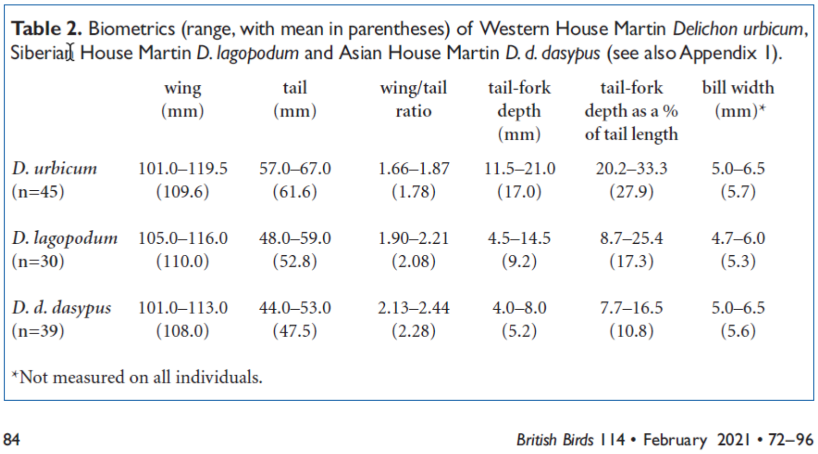

Table 2. Biometrics (range, with mean in parentheses) of Western House Martin *Delichon urbicum*, Siberian House Martin *D. lagopodum* and Asian House Martin *D. d. dasypus* (see also Appendix 1).

	wing (mm)	tail (mm)	wing/tail ratio	tail-fork depth (mm)	tail-fork depth as a % of tail length	bill width (mm)*
D. urbicum (n=45)	101.0–119.5 (109.6)	57.0–67.0 (61.6)	1.66–1.87 (1.78)	11.5–21.0 (17.0)	20.2–33.3 (27.9)	5.0–6.5 (5.7)
D. lagopodum (n=30)	105.0–116.0 (110.0)	48.0–59.0 (52.8)	1.90–2.21 (2.08)	4.5–14.5 (9.2)	8.7–25.4 (17.3)	4.7–6.0 (5.3)
D. d. dasypus (n=39)	101.0–113.0 (108.0)	44.0–53.0 (47.5)	2.13–2.44 (2.28)	4.0–8.0 (5.2)	7.7–16.5 (10.8)	5.0–6.5 (5.6)

*Not measured on all individuals.

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Table 2 from Leader et al. (2021).

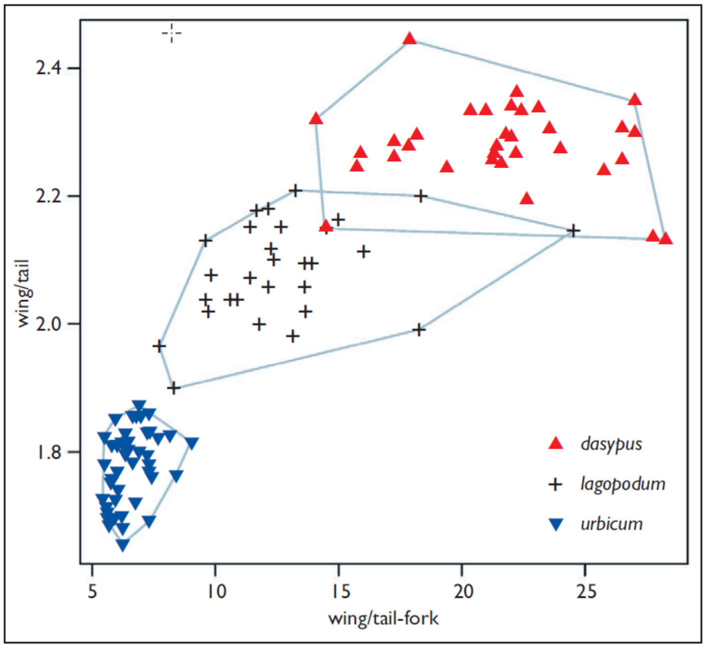

Fig. 4. The best two ratios found by the LDA ratio extractor to separate Western House Martin *Delichon urbicum*, Siberian House Martin *D. lagopodum* and Asian House Martin *D. dasypus* are based on wing length and tail length as well as depth of tail-fork.

Fig. 4 from Leader et al. (2021).

Vocalizations

Leader et al. (2021) detailed the vocal differences and provide spectrograms of *urbicum, lagopodum* and *D. dasypus*. They measured the contact call of *lagopodum* as lower-pitched than that of *urbicum* or *D. dasypus*, with peak frequency at 4,126 Hz in *lagopodum* vs. 4,535 Hz for *urbicum* and 4,510 Hz for *D. dasypus.* (However, this does not seem like a major difference especially given the difficulty of measuring such characters accurately in a broadband vocalization.) They stated: “The contact call of *lagopodum* has a slightly slower delivery, while the number of main elements is greater (Table 3)” (see below for Table 3 from Leader et al. 2021).

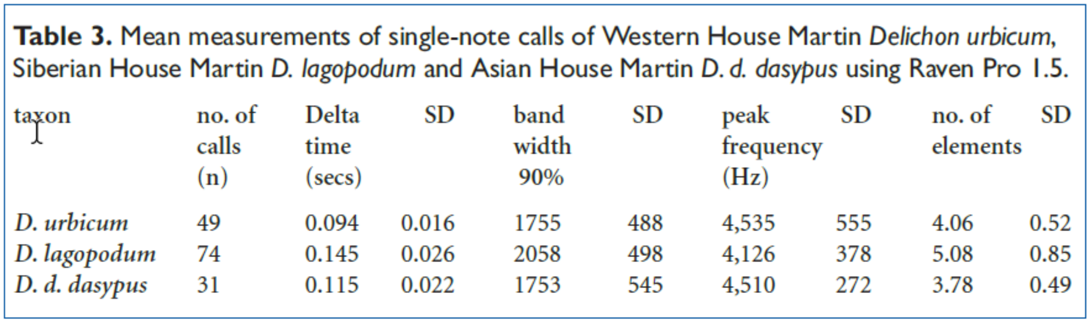

Table 3. Mean measurements of single-note calls of Western House Martin *Delichon urbicum*, Siberian House Martin *D. lagopodum* and Asian House Martin *D. d. dasypus* using Raven Pro 1.5.

taxon	no. of calls (n)	Delta time (secs)	SD	band width 90%	SD	peak frequency (Hz)	SD	no. of elements	SD
D. urbicum	49	0.094	0.016	1755	488	4,535	555	4.06	0.52
D. lagopodum	74	0.145	0.026	2058	498	4,126	378	5.08	0.85
D. d. dasypus	31	0.115	0.022	1753	545	4,510	272	3.78	0.49

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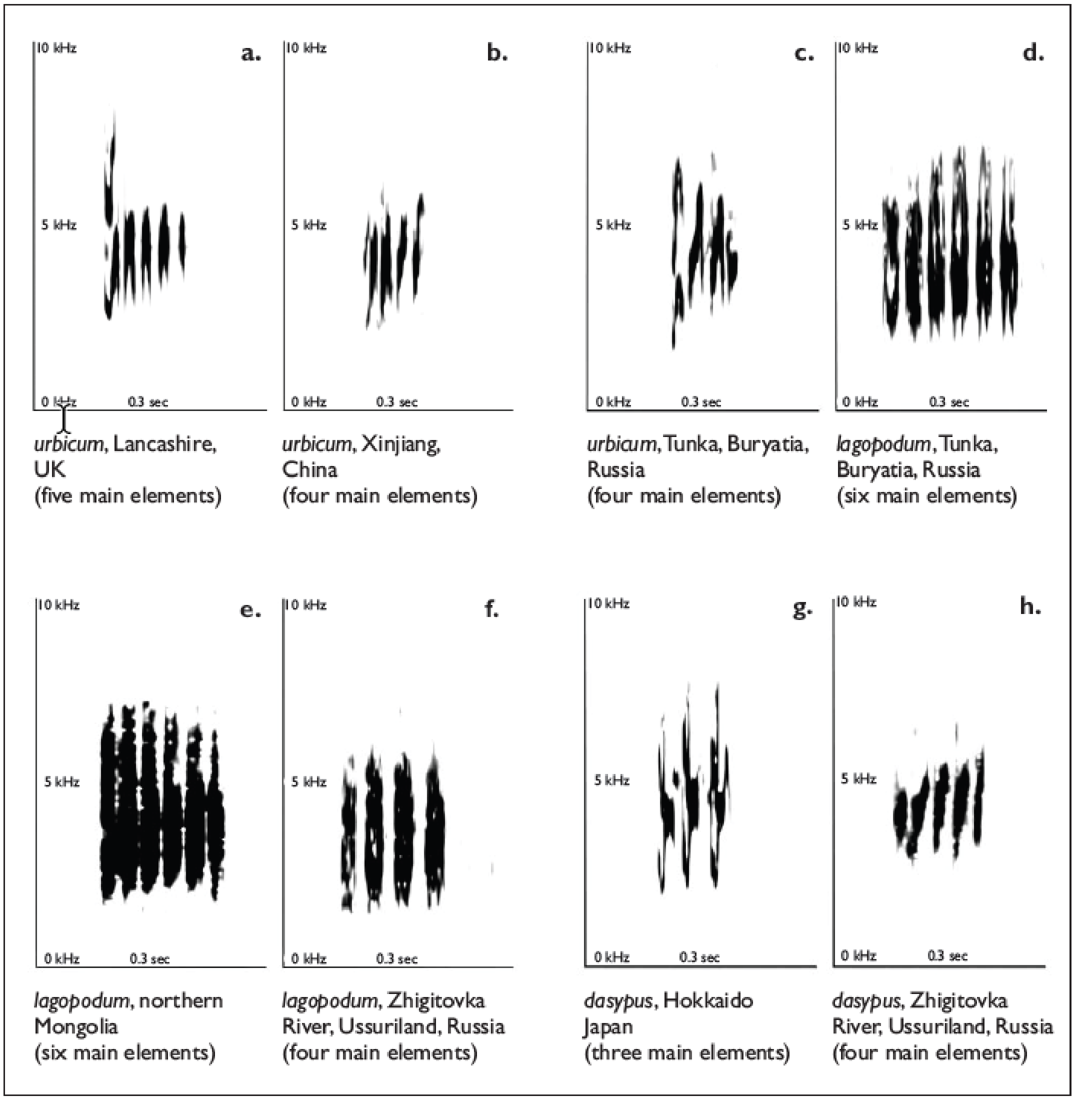
Leader et al. (2021) concluded: “Thus, single contact calls of a vagrant *lagopodum* in Europe would sound lower-pitched, have a more uniform quality and be of a slightly longer duration than those typically uttered by *urbicum.* The appearance in a sonogram is very different. The contact call of a vagrant *dasypus* would sound very similar to that of *urbicum*, but might be identified because of a more consistent slight increase in pitch and a less flat or hard quality. The appearance in a sonogram may differ noticeably” (see Fig. 5 below for sonograms in Leader et al. 2021).



urbicum, Lancashire, UK (five main elements)

urbicum, Xinjiang, China (four main elements)

urbicum, Tunka, Buryatia, Russia (four main elements)

lagopodum, Tunka, Buryatia, Russia (six main elements)

lagopodum, northern Mongolia (six main elements)

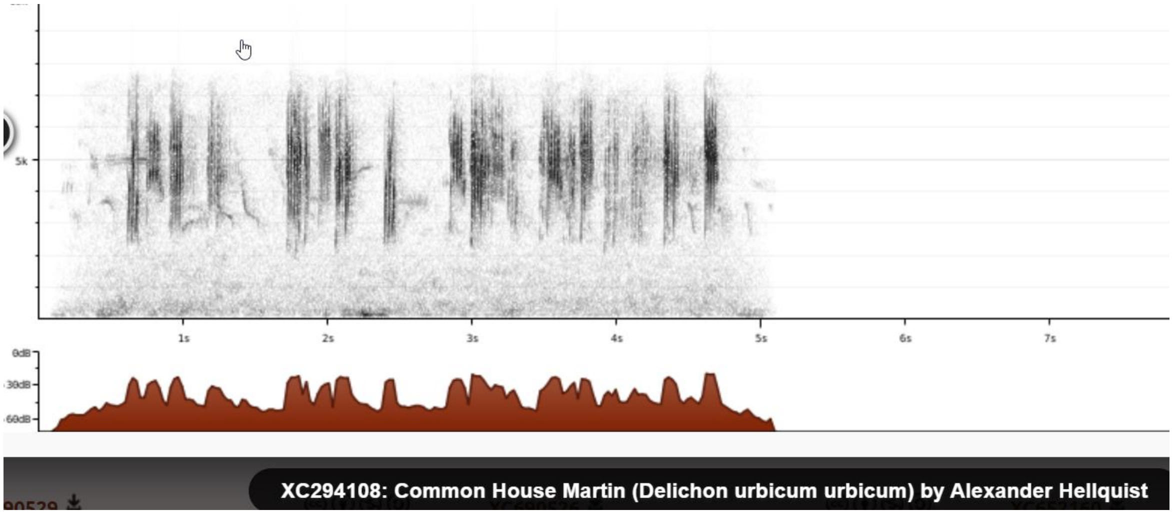
lagopodum, Zhigitovka River, Ussuriland, Russia (four main elements)

dasypus, Hokkaido Japan (three main elements)

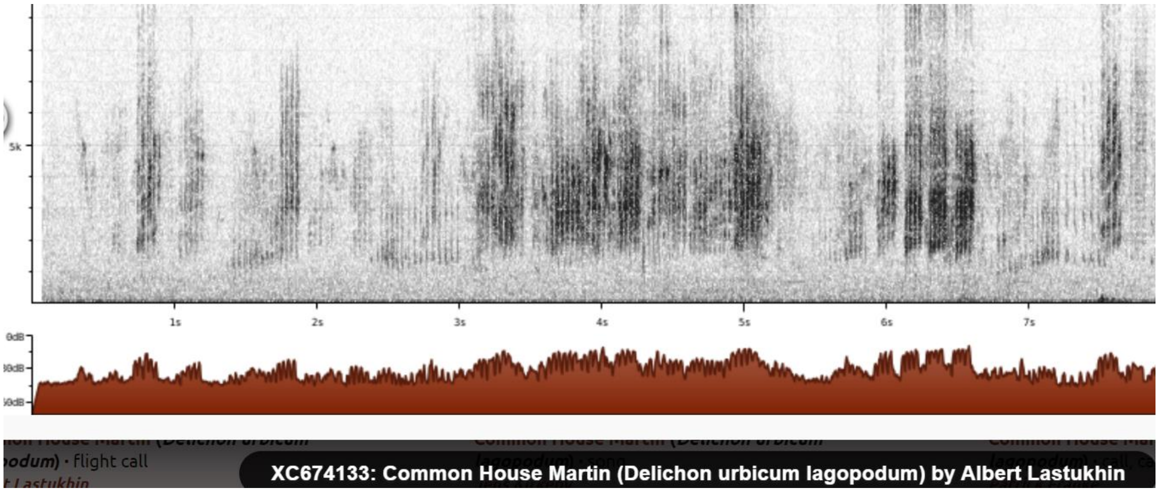
dasypus, Zhigitovka River, Ussuriland, Russia (four main elements)

Fig. 5. Sample sonograms of single-note calls of Western House Martin *Delichon urbicum*, Siberian House Martin *D. lagopodum* and Asian House Martin *D. dasypus*.

Although PCR considers this difficult to verify from the sonagrams in Leader et al. (2021), inspection of online sonagrams indeed suggests that each “main element” of *lagopodum* seems to be composed of more and longer trilled “minor” elements, which can be readily visualized on the waveform (see below). Here is a selection of xeno-canto sonograms (with waveforms below) of fairly typical recordings to show the apparent differences in frequency, length of notes, and degree of rolling or trilling, the latter especially apparent in the waveform.



XC294108: Common House Martin (Delichon urbicum urbicum) by Alexander Hellquist



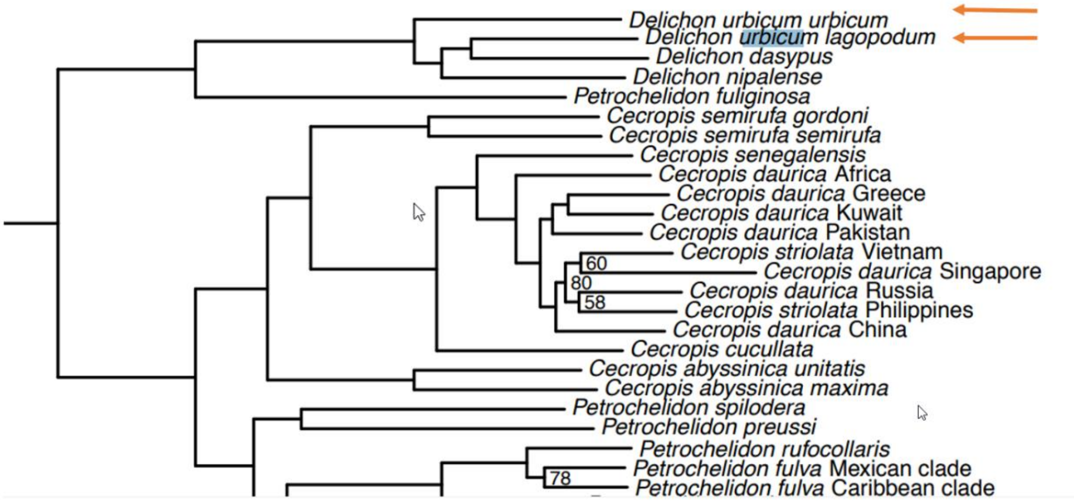
XC674133: Common House Martin (Delichon urbicum lagopodum) by Albert Lastukhin

Given the variation in vocalizations evident among online recordings, it seems that a more detailed analysis of homologous vocalizations with more useful sonograms is needed to definitively establish differences. However, the demonstrated sympatry between *urbicum* and *lagopodum* is obviously maintained by some feature or combination of features, and perhaps this includes such seemingly minor differences, given that at least some birds have much better temporal resolution of vocalizations than do humans (Dooling and Prior 2017). On the basis of findings of sympatry by Leader et al. (2021), as well as the reported morphological and vocal differences, the IOC World Bird List accepted the split of *lagopodum* (Gill et al. 2021).

Genetics

Sheldon et al. (2005) analyzed mitochondrial and nuclear DNA, finding deep genetic differences within *Delichon*. They found that *D. dasypus* and *D. nipalense* are most closely related with an average difference of 4.1% in cytochrome b; together they form the sister clade to Western House-Martin *D. urbicum*, which differed by 8% in cyt-b. This is despite the fact that *D. dasypus* and *D. urbicum* were often formerly treated as conspecific owing to limited differences in plumage and morphology, and predominantly allopatric distribution.

Leader et al. (2021) indicated that to date there had been no genetic studies of *D. u. lagopodum*. However, an overlooked, unpublished online dissertation by Brown (2019; https://www.proquest.com/pagepdf/2665131856?accountid=12598) included single individuals of both *urbicum* and *lagopodum* in a UCE phylogeny, along with single individuals of *dasypus* (Russia) and *nipalensis* (Nepal; skin specimen). In this phylogeny, well-supported nodes place *lagopodum* as sister to *dasypus* rather than *urbicum*, with *nipalensis* sister to that clade and *urbicum* sister to these clades. Brown (2019) stated: "…all three inference methods tentatively support the divisions in HBW and BirdLife International (2017) of *Delichon urbicum* into *D. urbicum* and *D. lagopodum*, …"



Relevant part of Figure 3.2 of Brown (2019), showing the sister relationship of *lagopodum* and *dasypus* (arrows) based on UCE data.

Effect on AOS-CLC Area:

Both taxa of Common House-Martin, *urbicum* and *lagopodum*, are recorded from the AOS area, so approval of this proposal would add one species to the *Checklist.*

Status of Common House-Martin in North America

Aaron Lang (in preparation for an article for Western Birds with JLD and D. D. Gibson) has tallied 28 records from Alaska, most from the Bering Sea region, but one (sight record) from Thetis Island, off the Coleville Delta on the North Slope. There is a sight record of one identified at close range in 1983 on St. Matthew Island (Winker et al. 2002). A sight record from Buldir Island, western Aleutians, on 13 June 1990, was treated as *Delichon* sp. and placed on the hypothetical list (not substantiated by photo/specimen) by Gibson and Byrd (2007), who by their treatment indicate that *D. dasypus* was not eliminated as a possible ID.

The first record for Alaska was one at Nome, 6-7 June 1974, and it is the only record documented with a specimen; it was identified (and confirmed to subspecies by M. Ralph Browning) as *lagopodum* (Hall and Cardiff 1978). Another bird was found by the same tour group that found the Nome bird, this one at Webster Lake, St. Paul Island, Pribilof Islands, on 12 June 1974: "this bird appeared to have the same amount of white on the upper tail coverts as the bird at Nome, and was doubtless the same race" (Hall and Cardiff 1978). Seven others are documented with photos; some, perhaps all, will be identifiable to *lagopodum* and it would seem the likely taxon to occur in the northern Bering Sea region, given the proximity of the breeding range of *lagopodum*. Lehman (2019) cites Tomkovich (2007) and Arkhipov et al. (2013) for breeding of the species east, at least irregularly, to western and central Chukotka**.** The Buldir record (western Aleutian Islands) is perhaps as likely to be *D. dasypus* as *lagopodum* given the relative proximity of breeding *dasypus* in the southeastern portion of the Russian Far East, so we consider that Gibson and Byrd (2007) treated the Buldir Island record appropriately.

Delichon urbicum lagopodum, 2 June 2022, at Gambell, St. Lawrence Island, AK (photo by J. L. Dunn)

Records of *urbicum* in the eastern NACC region are as follows: Boertmann (1994) listed three records of Common House-Martin from Greenland, at least two of which are substantiated by specimens. Boertmann (1994) indicated that Salomonsen (1963) assigned the first two records (1902 and 1937) to *urbica* (= *urbicum*). The records are from West, Northeast, and Southeast Greenland. The appearance of *urbicum* in Greenland is hardly surprising as, just to the east of the NACC region, there are hundreds of records from Iceland, where they have bred sporadically (Howell et al. 2014, Turner and Rose 1989). Moreover, the Common House-Martin (presumably all *urbicum*) has been annual in the Azores in recent years, mainly in spring (Howell *et al*. 2014). Elsewhere in the NACC region, one was collected from Bermuda (Devonshire Parish) on 9 August 1957 (Wingate 1958), the identification as nominate *urbicum* being confirmed by Charles Vaurie at the AMNH. Buckley et al. (2009) listed three records from Barbados: eight at Harrison Point 30 October-6 November 1999 ("photographs examined") and single individuals at Fosters on 11 November 2000 and St Bernard's Village 9-11 June 2002. They also listed an April 2002 record from Tobago (in the SACC area). The only other record, and the only one from the ABA area, was one photographed from 26 May-1 June 1989 at Saint-Pierre, Saint-Pierre & Miquelon (Etcheberry 1998). One of the two published color photos seems to show a long tail with a deep tail fork, thus *urbicum*, not *lagopodum.* Subspecies *urbicum* is not yet recorded for the United States.

<u>Range expansions of *D. u. urbicum and D. d. lagopodum*</u>

There have been apparent range extensions of both *urbicum* and *lagopodum* in northern Asia. Leader et al. (2021) indicated that the presence of breeding *urbicum* in Respublika Buryatia is some 1000 km farther east than the breeding range in Russia as detailed by Turner and Rose (1989), who placed the eastern limit as the upper Yenisei. Vaurie (1958) placed the eastern limit in Russia for *urbicum* as "to about the Yenisei and the western limit for *lagopodum* "from the region directly west of the Yenisei (Yelogui and Turu Rivers, north to 69.30' N. Lat.)." Leader et al. (2021) pointed out that both of these taxa nest primarily on human-made structures and that the range of both *urbicum and lagopodum* spread with the completion of the Trans-Siberian and Baikal-Amur railways in the late 19th-early 20th centuries, which required construction of vast numbers of bridges, tunnels, water towers, and other buildings that provide nest sites for both *urbicum* and *lagopodum*. The human population in Siberia and the Russian Far East increased from 500,000 by the end of the 17th century to 30 to 40 million by the early 21st century (Hartley 2014), no doubt leading to an increase in *Delichon* numbers.

Winter range of *lagopodum* in Asia, East Asian records of *urbicum*, and records of *lagopodum* in the Western Palearctic

The winter range of *lagopodum* is relatively poorly known. Most are believed to winter in much of Myanmar, northern Thailand, Laos, Cambodia, and parts of Vietnam north to southern China (Leader et al. 2021). Perhaps the uncertainty about the winter range is a result of the lack of awareness of the field separation of *lagopodum* from the various subspecies of *D. dasypus* in addition to nominate *urbicum.* Recently *lagopodum* has been found to be more numerous in the lowlands of northern Thailand than previously realized (Leader et al. 2021), although JLD has yet to record it there in some 25 winter (February) trips. The *Delichon* he has seen in northwestern Thailand have been in the mountains and all appeared to be *D. dasypus.* Leader et al. (2021) stated that in recent years in Hong Kong, *lagopodum* is nearly annual in fall, but was first recorded there in 2009. In Taiwan it is a scarce passage migrant, first recorded in 2013. In India a flock of 30 *Delichon* martins observed in Arunachal Pradesh (northeastern India) on 19 October 2008 included at least three *lagopodum* (Sangha et al. 2009). Leader et al. (2021) indicated that there are two recent records (photographs) of *urbicum* from Chiang Mai in early 2020, the first records from Southeast Asia. They indicated that this is about 2500 km east of the known winter range in southwestern India.

An individual in Israel in December 2016 (Granit 2016) was accepted as the first record of *D. dasypus* for that country (Yoav Perlman, pers. comm to Leader et al. 2021), but Leader et al. (2021) believed it to be a juvenile *lagopodum*, and if so it would be the only record for the Western Palearctic. They (*ibid*) argued that given the larger and more northerly distribution of *lagopodum* compared with that of *D. dasypus, lagopodum* is “more likely to occur in the Western Palearctic, and that it is probably being overlooked.”

Recommendation:

We strongly recommend the elevation of *lagopodum* to species status. It breeds sympatrically with *urbicum*, and thus must be considered specifically distinct under the BSC. In addition, UCE evidence suggests that these taxa are not sisters, but that *dasypus* is sister to *lagopodum* (and these two also breed sympatrically with each other and hence cannot be lumped). The distinct morphology and apparent vocal differences could well explain why there is assortative breeding.

English names

Leader et al. (2021) recommended that *D. urbicum* be named Western House-Martin and *D. lagopodum* be named Siberian House-Martin. (We have added the hyphens to match NACC hyphenation policy.) Their justification is that the type locality of *lagopodum* (Dauria, i.e., Transbaikalia) is in Siberia and also because the breeding range of Asian House-Martin extends farther east in Japan and the Kuril Islands than much of the breeding range of *lagopodum.* We add that *lagopodum* breeds over much of Siberia as well as the Russian Far East, and breeds in fewer Asian countries than does *dasypus*. Hall and Cardiff (1978) used Siberian House Martin for the English name in the title of their paper detailing the first North American records of that taxon, suggesting that the English name of Siberian House Martin has been in use for at least half a century. The IOC World Bird List adopted the names recommended by Leader et al. (2021) in v. 11.2 (July 2021; Gill et al. 2021). However, del Hoyo and Collar (2016) used

Northern and Eastern House-Martins, whereas the Clements et al. (2021) group names are Western and Eastern House-Martins. As Leader et al. (2021) pointed out, Northern House Martin is no more appropriate for *urbicum* than for *lagopodum*. Although *urbicum* occurs in western Siberia, *lagopodum* occurs throughout Siberia. Eastern could equally well apply to *dasypus* as to *lagopodum*.

If this split is accepted, we recommend adopting Leader et al.'s (2021) recommendations of Western House-Martin and Siberian House-Martin as the English names.

Please vote on:

a) Recognize *lagopodum* as a separate species from *urbicum*
b) Adopt Western House-Martin (*urbicum*) and Siberian House-Martin (*lagopodum*) as the English names

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Date of proposal: 21 December 2022