AOS Classification Committee – North and Middle America

Proposal Set 2023-D

20 March 2023, revised 20 April 2023

No. Page Title

Add Bat Falcon *Falco rufigularis* to the U.S. List

Background:

A Bat Falcon (*Falco rufigularis*) was found at Santa Ana National Wildlife Refuge, Hidalgo County, Texas, on 8 December 2021 and was last reliably recorded on 10 March 2022. It was widely seen and photographed, and the ABA Checklist Committee unanimously accepted it (8-0) in June of 2022. The results were published in Pyle et al. (2022), which includes a color photo of the perched bird with its wing spread. The same issue of North American Birds includes an article detailing its discovery and its time at Santa Ana NWR and including many more color photos (Gelernter et al. 2022). In this article, the bird was aged as an adult and was thought possibly to have been a male as it appeared small. Neither Pyle et al. (2022) nor Gelernter et al. (2022) indicated whether the record was accepted by the Texas Bird Records Committee.

Recommendation:

I recommend that Bat Falcon be added to the U.S. list. There is no question about the identification. It showed no signs of being previously held as a captive, and Pyle et al. (2022) noted that it breeds as close in Mexico as 170 km away.

References:

Gelernter, R., M. Gustafson, Z. E. Johnson, and J. R. Ramirez-Garofalo. 2022. First U.S. record of Bat Falcon. North American Birds 73 (2): 4-7.

Pyle, P., M. Gustafson, A. Jaramillo, T. Johnson, A. W. Kratter, A. Lang, M. W. Lockwood, M. Mutchler, and D. Sibley. 33rd Report of the ABA Checklist Committee 2022. North American Birds 73 (2): 18-23.

Date of Proposal: 31 January 2023

Submitted by: Jon L. Dunn

Add Lilac-crowned Parrot *Amazona finschi* to the U.S. List as an established introduced species

Background:

The CBRC added Lilac-crowned Parrot (*Amazona finschi*), a West Mexican endemic, to the California state list in January 2022, and the ABA-CLC agreed that it met the criteria of the ABA for an established introduced species (Pyle et al. 2022). Populations of this species from the coastal slope of Southern California are estimated to number 400-500+ individuals from Ventura to San Diego counties (Allen et al. 2016, Benson et al. 2021; Fig. 3). Pyle et al. (2022) also pointed out that smaller populations are found in Florida and Texas (Pranty and Garrett 2011).

Recommendation:

I see no reason not to add this species to the U.S. list. In Southern California they are not as well established as Red-crowned Parrot (*A. viridigenalis*) and do interbreed with that species, but both the CBRC and the ABA CLC considered that the species was well enough established to be added to their respective lists.

References:

Allen, L. W., K. L. Garrett, and M. C. Wimer. 2016. Los Angeles County Audubon Society, Los Angeles, CA. pp. 282-284.

Benson, T.A., K. L. Garrett, J. S. Feenstra, J. F. Garrett, K. N. Nelson, and A. J. Searcy. 2021. California Bird Records Committee proposal to add Lilac-crowned Parrot to the California state list. California Bird Records Committee, Camarillo.

Pranty, B., and K. L. Garrett. 2011. Under the radar: "Non-countable" exotic species in the ABA Area. Birding 43(5):46-58.

Date of Proposal: 31 January 2023

Submitted by: Jon L. Dunn

Add Red-masked Parakeet *Psittacara erythrogenys* to the Main List as an established introduced species, and change the linear sequence of *Psittacara*

Background:

This South American species has substantial and increasing populations in California. Notable populations occur in San Francisco (250+), Los Angeles (100's), and San Diego (80+), such that the CBRC added it to the state list in June 2022. The ABA Checklist Committee followed suit and unanimously accepted it (8-0) in August 2022. They included citations for the California populations (P; Fig 2). They also pointed out that there are breeding populations in Florida (about 150; Chatfield-Taylor and Epps 2020) and in Hawaii (50-60 on Oahu and Hawaii; Pyle and Pyle 2017), although those populations were not robust enough to be added to the ABA Checklist in 2017 (Pyle et al. 2018). Based on its status in California, the ABA CLC considered that the species met the standard established by Pranty et al. 2008) and added it to the ABA Checklist. Following Clements (2021), they placed it after Mitred Parakeet (*P. mitratus*).

Recommendation and Position on Checklist:

We don't have a firm recommendation, other than we see no compelling reason to differ from the judgments of the CBRC or the ABA CLC, so that means adding the species. The CBRC annual report adding this species to the California list will come out later this year in Western Birds.

This species is placed between *P. mitratus* and *P. finschi* in Remsen et al. (2013), which indicates that our linear sequence of this genus requires a slight modification. *Psittacara mitratus*, which is currently placed last in our linear sequence, should be moved to follow *P. strenuus*, and *P. erythrogenys* should be added following *P. mitratus*, as in this new sequence:

Psittacara holochlorus
Psittacara brevipes
Psittacara strenuus
Psittacara mitratus
Psittacara erythrogenys
Psittacara finschi
Psittacara euops
Psittacara maugei
Psittacara chloropterus

We recommend that we adopt this new linear sequence.

References:

Allen, L. W., K. L. Garrett, and M. C. Wimer. 2016. Los Angeles County Breeding Bird Atlas. Los Angeles Audubon Society, pp. 282-284.

Benson, T. A., K. L. Garrett, J. S. Feenstra, J. F. Garrett, K. N. Nelson, and A. J. Searcy. 2021. California Bird Records Committee proposal to add Red-masked Parakeet to the California state list. California Bird Record Committee, Camarillo.

Chattfield-Taylor, W. E., and S. A. Epps. 2020. Population trends in the exotic Red-masked Parakeet (*Psittacara erythrogenys*) in southern Florida. Florida Field Naturalist 48:33-44).

Clements, J. F., T. S. Schulenberg, M. J. Iliff, S. M. Billerman, T. A. Fredericks, J. A. Gerbracht, D. Lepage, B. L. Sullivan, and C. L. Wood. 2021. The eBird/Clements checklist of birds of the world, v 2021. www.birds.cornell.edu/clementschecklist/download/

Pranty, B., and K. L. Garrett. 2011. Under the radar: "Non-countable" exotic species in the ABA Area. Birding 43(5):46-58.

Pyle, R. L, and P. Pyle. 2017. The Birds of the Hawaiian Islands: Occurrence, History, Distribution, and Status, V. 2 (tinyurl.com/Pyle-Pyle). B.P. Bishop Museum, Honolulu.

Pyle, P., M. Gustafson, T. Johnson, A. W. Kratter, A. Lang, K. Nelson, M. W. Lockwood, and D. Sibley. 2018. 29th report of the ABA Checklist Committee 2018. Birding 51(12):30-40.

Remsen, J. V., Jr., E. E. Schirtzinger, A. Ferraroni, L. F. Silveira, and T. F. Wright. 2013. DNA-sequence data require revision of the parrot genus *Aratinga* (Aves: Psittacidae). Zootaxa 3641(3):296-300.

Date of Proposal: 31 January 2023

Submitted by: Jon L. Dunn and Terry Chesser

Add Rufous-tailed Rock-Thrush *Monticola saxatilis* to the Main List

Background:

A 2nd year male of this species was present at Utqiaġvik (Barrow), Alaska, 24-25 June 2021. It was well-photographed, and photos were published in Pyle et al. (2022). This record was accepted by the Alaska Checklist Committee, the report to be published later in 2023 in their report in Western Birds (Gibson et al. 2023). The ABA Checklist Committee accepted the record unanimously in May of 2022 (8-0).

Recommendation and Position on the Checklist:

The identification of this male to species is very straightforward. It is highly migratory, and there are no questions as to origin. I recommend that it be added to the Main List of the Check-list.

Monticola is placed between *Phoenicurus* and *Saxicola* on the Clements list, and I recommend that we adopt this linear sequence.

References:

Gibson, D. D., S. C. Hinl, T.G. Tobish, Jr., A. J. Lang, L. H. DeCicco, N. R. Hajdukovich, and R. L. Scheer. 2023. Fifth Report of the Alaska Checklist Committee 2018-2022. Western Birds 54: in press

Pyle, P., M. Gustafson, A. Jaramillo, T. Johnson, A. W. Kratter, A. Lang, M. W. Lockwood, M. Mutchler, and D. Sibley. 2022. 33rd Report of the ABA Checklist Committee 2022. North American Birds (2):18-23.

Date of Proposal: 31 January 2023

Submitted by: Jon L. Dunn

Add Lesson's Seedeater *Sporophila bouvronides* to the Main List

Background:

This seedeater is a moderate-distance migrant, with breeding populations (during boreal summer) from eastern Colombia east across Venezuela (mostly north of the Andes) to Trinidad, and the coastal plain from the mouth of the Orinoco east of Guyana and Suriname (Ridgely and Tudor 1984, Jaramillo 2020, eBird), It winters mostly south of the breeding range south through eastern Peru to central Bolivia, and in western Amazonian Brazil and north of the Amazon in eastern Brazil (Jaramillo 2020). The species has appeared about ten times in eastern Panama in Darién Province (Angehr and Dean 2010, eBird). None of these records, however, was photographed (eBird). All of the Panamanian records were of males, and all were in late February to early May. Most were in its preferred cutover scrubby habitats, such as the edges of dirt runways (Jaramillo 2020. eBird).

New AOS Record:

On 25 June 2022, a male was observed and photographed at Tortuguero (10°32'23.9"N, 83°30'06.1"W), Pococí, Limón province, in the lowlands of northeastern Costa Rica (Gatgens-García et al. 2022). The bird was observed with a flock of Variable Seedeaters (*S. corvina*) at a private residence in an open area and lawn.

Discussion:

The published photos in Gatgens-García et al. (2022) clearly document the record. Although some males show much more pronounced black breast markings (extreme illustrated in Jaramillo 2011), most photos on eBird show variable black markings on the breast, with some having very little to no black (e.g., eBird checklist S119225654, Jaramillo 2020). The most similar species is the closely related Lined Seedeater (*S. lineola*), which has a diagnostic white median crown stripe. That species, an austral migrant, has also reached Costa Rica (Chesser et al. 2014).

Trapping *Sporophila* seedeaters is a huge problem in some Caribbean countries, particularly Trinidad and Tobago (ffrench 1991, https://newsday.co.tt/2021/10/28/where-have-all-the-songbirds-gone/). Trapping and keeping seedeaters (*Lonchura. Phonipara*, *Tiaris*, *Melopyrrha*) also has a rich tradition in Cuba and the Cuban diaspora in south Florida. The FOSRC has had difficulties at times distinguishing whether individual out-of-range birds are natural vagrants or escaped cage birds (Greenlaw et al. 2014). This problem appears to not be as extreme in Costa Rica, but I would not be surprised if locals in Tortuguero, which is culturally Caribbean, kept some seedeaters. Nonetheless, without some indication that Lesson's Seedeater is kept in captivity in Costa Rica, I see no reason not to consider that the record herein should not be considered a wild vagrant.

Recommendation:

I recommend that we add Lesson's Seedeater to the Main List. Given the history of several records from Panama (all undocumented), and its migratory habits, this occurrence is not completely unexpected.

Position on Check-list:

Usually placed first in a linear order of *Sporophila* (before *S. lineola*). The SACC account reads:

> *Sporophila bouvronides* was formerly (e.g., Meyer de Schauensee 1970, Paynter 1970) considered a subspecies of *S. lineola*, but see Schwartz (1975) for rationale for treating them as separate species, representing a return to the classification of Hellmayr (1938) and Phelps & Phelps (1950a); this treatment has been followed by subsequent authors; they constitute a superspecies (Sibley & Monroe 1990).

English name:

Universally referred to as Lesson's Seedeater (SACC, IOC, HBW, Clements).

Literature Cited:

Angehr, G. R., & Dean, R. 2010. The Birds of Panama: A Field Guide. Zona Tropical Publications, Ithaca, NY.

Chesser, R.T., R. C. Banks, K. J. Burns, C. Cicero, J. L. Dunn, A. W. Kratter, I. J. Lovette, A. G. Navarro-Sigüenza, P. C. Rasmussen, J. V. Remsen, Jr., J. A. Rising, D. F. Stotz, and K. Winker. 2014. Fifty-fifth Supplement to the American Ornithologists' Union Check-list of North American Birds. Auk 131: CSi–CSxv

ffrench, R. 1991. A Guide to the Birds of Trinidad and Tobago, 2nd ed. Comstock Publ. Assocs., Ithaca, New York.

Gatgens-García, J., Chaves-Sánchez, A. and Sandoval, L. 2022. First record of Lesson's Seedeater *Sporophila bouvronides*. Bulletin of the British Ornithologists' Club 142: 526-528. https://bioone.org/journals/bulletin-of-the-british-ornithologists-club/volume-142/issue-4/bboc.v142i4.2022.a11/First-record-of-Lessons-Seedeater-Sporophila-bouvronides-in-Costa-Rica/10.25226/bboc.v142i4.2022.a11.full

Greenlaw, J. S., B. Pranty, and R. Bowman. 2014. The Robertson and Woolfenden Florida Bird Species: An Annotated List. Special Publication no. 8, Florida Ornithological Society, Gainesville.

Hellmayr, C. E. 1938. Catalogue of birds of the Americas. Field Mus. Nat. Hist. Publ., Zool. Ser., vol. 13., pt. 11.

Jaramillo, A. 2011. Family Emberizidae (Buntings and New World Sparrows), pp. 428-683 in del Hoyo, J., Elliott, A. and Christie, D. A (eds). Handbook of Birds of the World, vol. 16. Lynx Editions, Barcelona.

Jaramillo, A. (2020). Lesson's Seedeater (*Sporophila bouvronides*), version 1.0. In Birds of the World (J. del Hoyo, A. Elliott, J. Sargatal, D. A. Christie, and E. de Juana, Editors). Cornell Lab of Ornithology, Ithaca, NY, USA. https://doi.org/10.2173/bow.lessee2.01

Meyer de Schauensee, R. 1970. A Guide to the Birds of South America. Livingston Publ. Co., Wynnewood, Pennsylvania.

Paynter, R. A., Jr. (Ed.) 1970. Check-list of Birds of the World, Vol. 13. Museum of Comparative Zoology, Cambridge, Massachusetts.

Phelps, W. H., and W. H. Phelps, Jr. 1950. Lista de las aves de Venezuela con su distribución. Parte 2. Passeriformes. Boletín Sociedad Venezolana Ciencias Naturales 12: 1-427.

Ridgely, R. S., and G. Tudor. 1989. The Birds of South America, Vol. 1 Univ. Texas Press, Austin.

Schwartz, P. (1975). Solved and unsolved problems in the *Sporophila lineola/bouvronides* complex (Aves: Emberizidae). Ann. Carnegie Mus. 45: 277-285.

Sibley, C. G., and B. L. Monroe, Jr. 1990. Distribution and taxonomy of birds of the World. Yale Univ. Press, New Haven, Connecticut.

Submitted by: Andrew Kratter

Date of Proposal: 20 February 2023

Change the linear sequence of genera in the Grallariidae

Background:

We recently considered a proposal (2023-C-2) to transfer Thicket Antpitta *Hylopezus dives* to *Myrmothera*, based on the phylogenetic trees in Carneiro et al. (2018) and the taxonomic recommendations in Carneiro et al. (2019). Acceptance of this proposal means that the four species of the family Grallariidae that occur in our area are now placed in four genera: *Grallaria*, *Hylopezus*, *Myrmothera*, and *Grallaricula*.

New Information:

The phylogenetic trees of Carneiro et al. (2018) indicate that our current linear sequence, which is *Grallaria*, *Hylopezus* (incl. *Myrmothera*), *Grallaricula*, does not reflect the evolutionary relationships of genera and species in this family (Fig. 1).
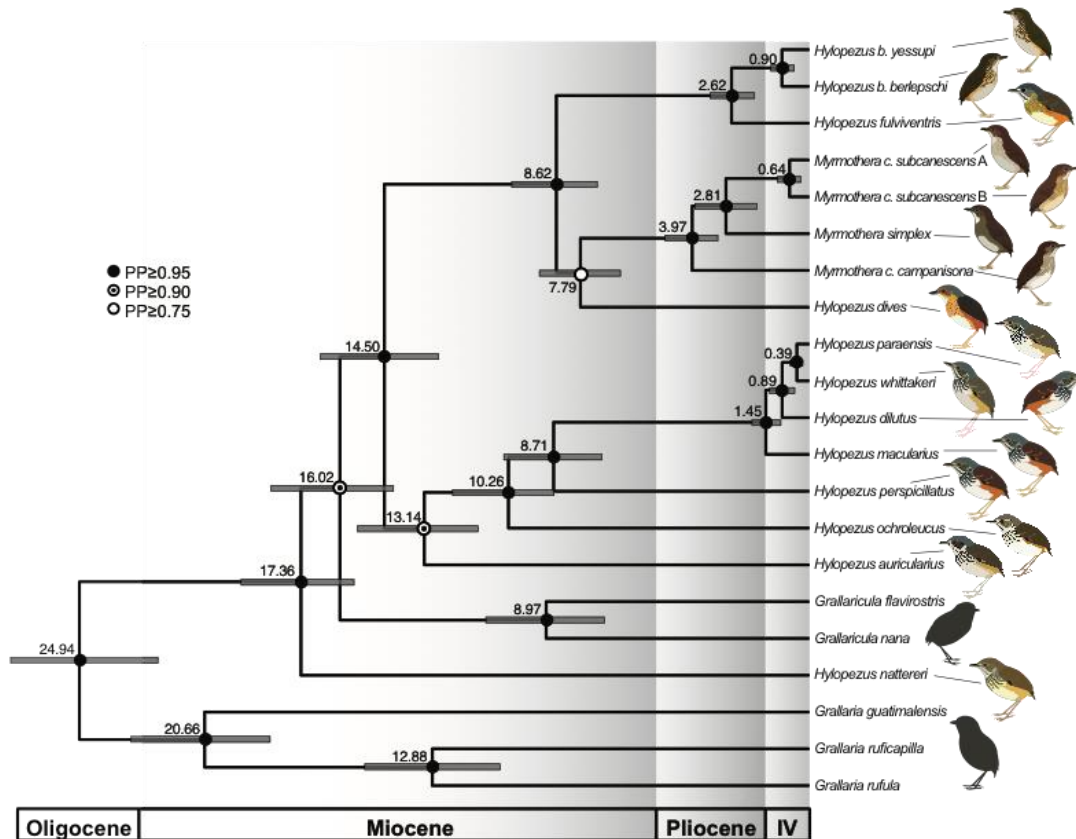
Figure 1. Reconstruction for antpittas estimated from multilocus dataset (species tree) using *BEAST. Bars indicate 95% highest posterior densities of divergence dates. The mean estimated dates are shown above nodes. Bayesian posterior probability (PP) support for nodes is indicated by coded circles according to the figure legend. IV = Quaternary. Images of antpittas species are adapted from Krabbe and Schulenberg (2003) and the Handbook of Birds of the World Alive. (Retrieved from Carneiro et al. 2019.)

The terminal taxa in this tree reflect the classification of these species prior to Carneiro et al. (2019), who recommended that *Hylopezus berlepschi*, *H. fulviventris*, and *H. dives* be transferred to *Myrmothera*, and that the extralimital species *H. nattereri* be placed in the new genus *Cryptopezus.*

The topology of the UCE phylogeny in Harvey et al. (2020) agrees with that in Carneiro et al. (2018):
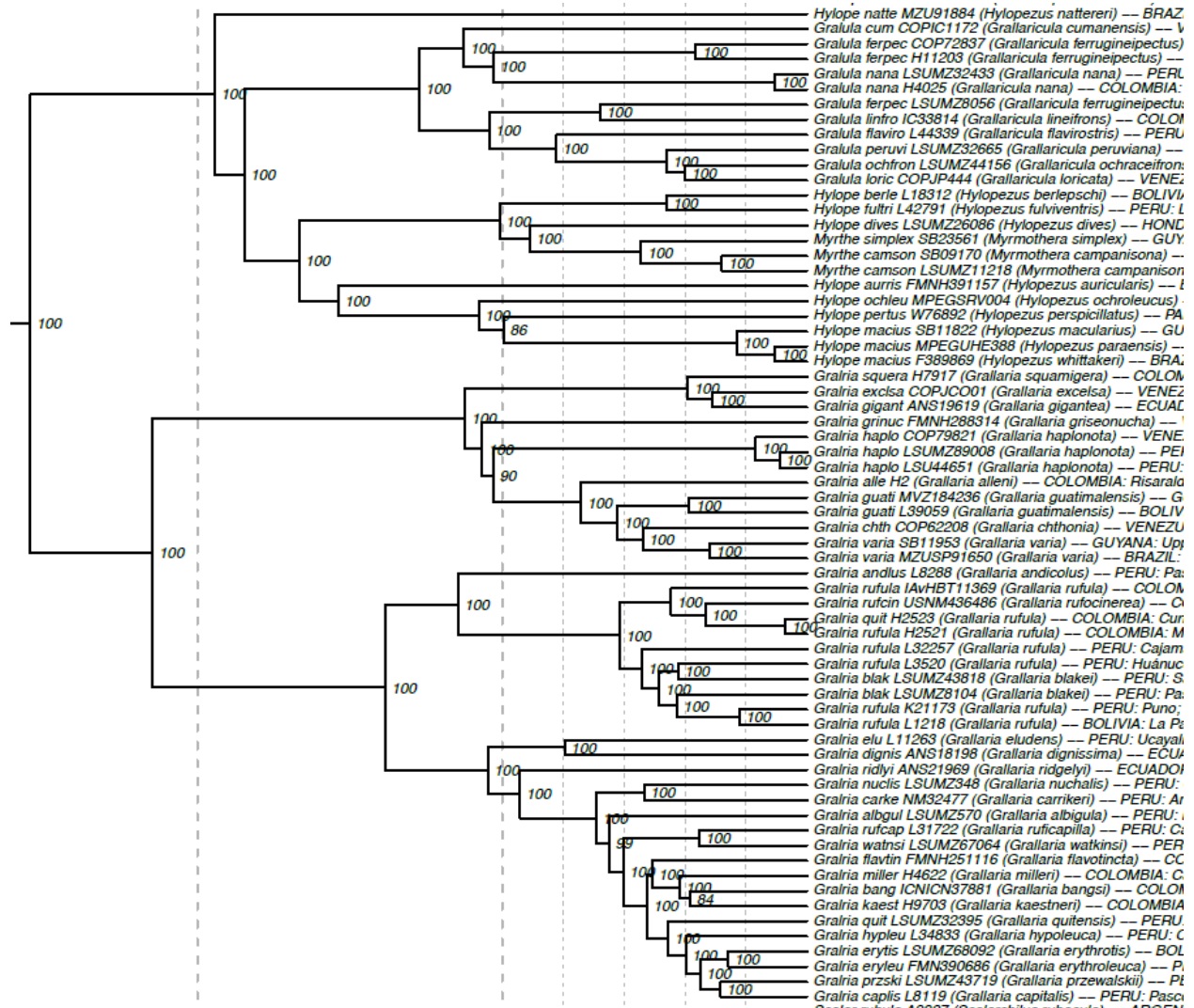
Our linear sequencing protocols mandate that sister groups be placed so that the group with fewer species precedes the group with more species. The number of species currently recognized in these genera is 45 for *Grallaria*, 1 for *Cryptopezus*, 10 for *Grallaricula*, 6 for *Hylopezus*, and 6 for *Myrmothera*. Thus, the number of species in *Grallaria* greatly exceeds that in its sister clade (i.e., the rest of the family), so *Grallaria* should be placed last in the linear sequence. Within its sister clade, the monotypic genus *Cryptopezus* should be placed first, and *Grallaricula* should be placed second due to having slightly fewer species than its sister clade *Hylopezus-Myrmothera*. *Hylopezus* and *Myrmothera* have the same number of species; in this case, our protocols indicate that the northwesternmost clade should be placed first and the

southeasternmost clade last. Distributions of these genera are remarkably similar: both extend north to eastern Honduras and both are primarily distributed in tropical South America. However, *Hylopezus ochroleucus* is the species with the southeasternmost distribution, extending to Minas Gerais, Brazil. Thus, *Hylopezus* should come last in the linear sequence.

These considerations result in the following linear sequence: *Cryptopezus* [extralimital], *Grallaricula*, *Myrmothera*, *Hylopezus, Grallaria*.

Recommendation:

I recommend that we adopt the following linear sequence:

Grallaricula
Myrmothera
Hylopezus
Grallaria

Literature Cited:

Carneiro, L., Bravo, G. A, Aristizbal, N., Aleixo, A. (2018) Molecular systematics and biogeography of lowland antpittas (Aves, Grallariidae): The role of vicariance and dispersal in thye diversification of a widespread Neotropical lineage. Molecular Phylogenetics and Evolution 120:375-389.

Carneiro, L., Bravo, G. A, Aleixo, A. (2019). Phenotypic similarity leads to taxonomic inconsistency: A revision of the lowland's antpittas. Zool Scr. 48:46–56. https://doi.org/10.1111/zsc.12324

Harvey, M. G., G. A. Bravo, S. Claramunt, A. M. Cuervo, G. E. Derryberry, J. Battilana, G. F. Seeholzer, J. S. McKay, B. C. O'Meara, B. C. Faircloth, et al. (2020). The evolution of a tropical biodiversity hotspot. Science 370:1343–1348.

Submitted by: Terry Chesser

Date of Proposal: 20 April 2023

Treat Cordilleran Flycatcher *Empidonax occidentalis* as conspecific with Pacific-slope Flycatcher *E. difficilis*

Note: some passages in this proposal are directly borrowed or modified from Hopping (2022).

Background:

Previously considered conspecific, Pacific-slope Flycatcher *Empidonax difficilis* (*sensu stricto*) and Cordilleran Flycatcher *E. occidentalis* were split from Western Flycatcher *E. difficilis* (*sensu lato*) by the American Ornithologists' Union (AOU 1989), based primarily on Ned K. Johnson's impressive 1980 monograph concerning the *Empidonax difficilis–flavescens* complex (Johnson 1980), as well as the conclusions drawn by Johnson & Marten (1988). The stated justification for the split was that the two forms "differ in vocalizations and allozyme frequencies and are sympatric in the Siskiyou region of northern California" (AOU 1989).

Despite the extensive dataset featured in his original monograph, Johnson (1980:110–115) concluded at the time that the only clear species break in the complex was between Western Flycatcher *E. difficilis* (*sensu lato*) and *E. flavescens* (Yellowish Flycatcher), and he recommended that interior (*E. d. hellmayri*) and coastal (*E. d. difficilis*) forms were best left tentatively as "megasubspecies" (Amadon & Short 1976). Following analysis of allozyme frequencies, reinterpretation of the earlier samples, and the collection of 17 new specimens (including three pairs from the Siskiyou of region of northern California, where the two forms were suspected to occur in sympatry) in the summer of 1981, Johnson revised this stance (Johnson & Marten 1988), leading to his successful push for the split (AOU 1989).
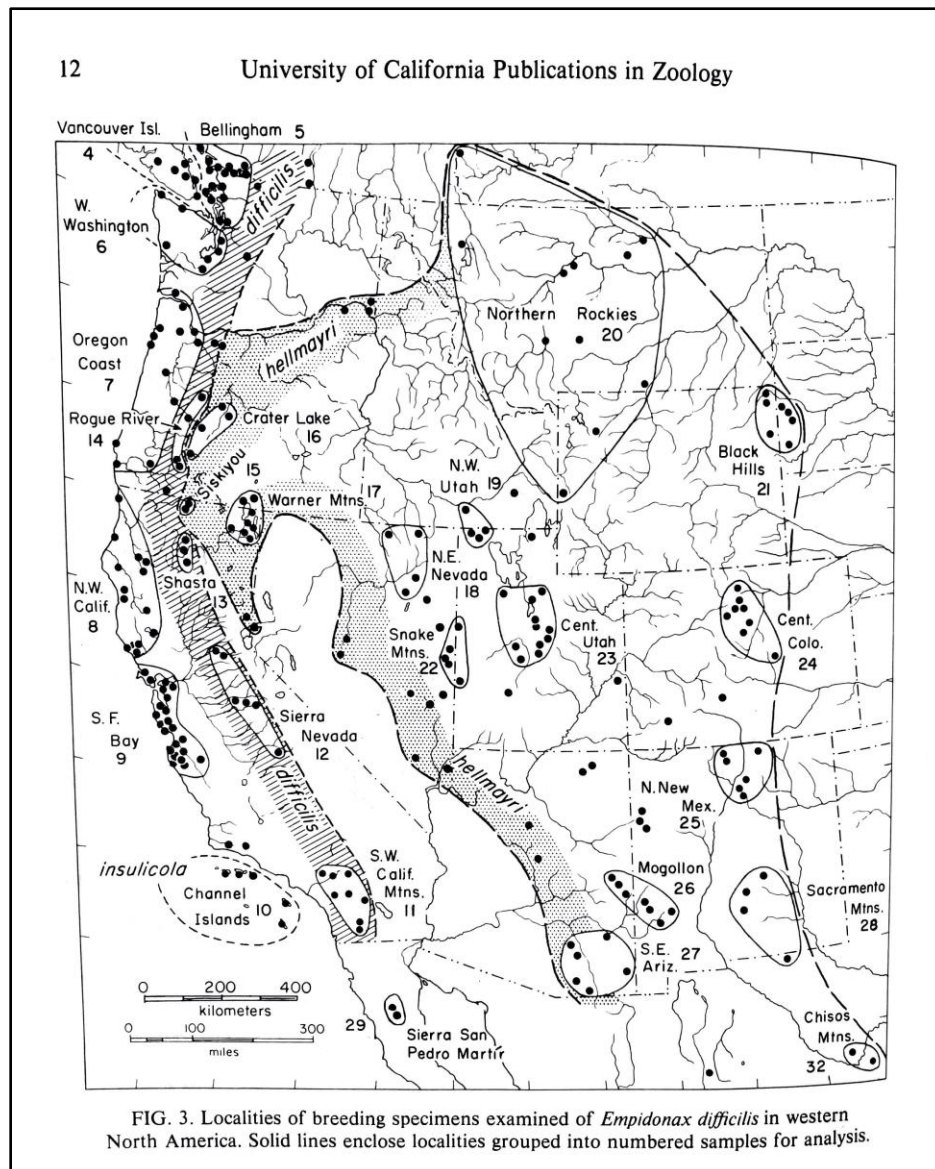
Johnson & Marten (1988) stated that interior and coastal populations of Western Flycatcher were "strongly differentiated" in morphology, vocalizations, and preferred habitat, in addition to their differing allozyme frequencies and apparent assortative mating in sympatry. At the time of the split, the established knowledge concerning these important factors was as follows:

Biogeography

In the 1989 split, the breeding distribution of Pacific-slope Flycatcher *E. difficilis* was described as extending from southeastern Alaska and northwestern British Columbia south to Baja California, generally occurring west of the Cascades and Sierra Nevada (AOU 1989). Cordilleran Flycatcher *E. occidentalis* was described as breeding from southeastern Washington, southwestern Alberta, and northern Idaho through Montana, Wyoming, and western South Dakota, generally occurring east of the Cascades and Sierra Nevada through northern California, Nevada, Colorado, and Arizona, south to the Mexican highlands of Oaxaca and west-central Veracruz. Johnson (1980:85) acknowledged that the distributional picture of Western Flycatcher in eastern Washington was more complex than indicated in the literature, with coastal-type birds occurring east of the Cascades. Regarding habitat preferences between the two forms, Johnson stated that the preferred habitats of [*E. occidentalis*] "shift dramatically from that described for the coastal forms," occurring in drier habitats and at higher elevations (4500–9000 ft.), while [*E. difficilis*] breeds in "shady forests from sea level to mid-elevations"

(Johnson 1980:15). No consistent differences in migration or breeding timing were documented between populations.

Although his extensive surveys covered much of the western U.S., Johnson (1980) made no mention of *E. difficilis/occidentalis* breeding in a large region of the northern Rockies henceforth referred to as the "greater Kootenays": primarily Ferry, Stevens, Pend Oreille, Spokane, and eastern Okanogan counties in Washington; Kootenai, Bonner, Boundary, and Shoshone counties in Idaho; Lincoln, Sanders, and Flathead counties in Montana; and the regional districts of Kootenay Boundary, Central Kootenay, and East Kootenay in British Columbia, plus adjacent Alberta. Despite containing suitable mid-elevation forest habitat and regional connectivity to areas where *E. difficilis*'s presence was recognized, this region was left blank in the range maps featured in both Johnson (1980) and Johnson & Marten (1988) (Fig. 1). As a result, the Siskiyou region of northern California and adjacent southern Oregon was believed to be "the only certain region where [contact between the two forms] occurs" (Johnson 1980:87).

FIG. 3. Localities of breeding specimens examined of *Empidonax difficilis* in western North America. Solid lines enclose localities grouped into numbered samples for analysis.
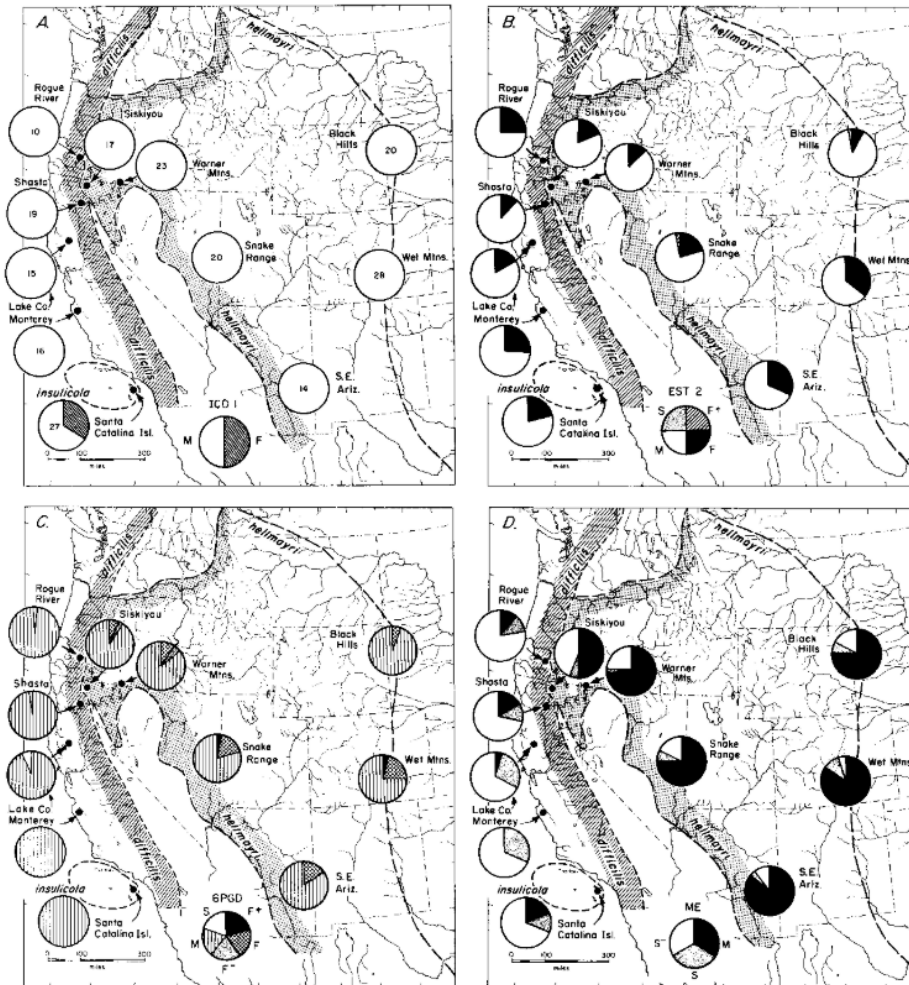
Fig. 1. Geographic occurrence and percentage frequency of alleles at four loci in the *Empidonax difficilis* complex. The 11 samples represent three taxa: *E. d. insulicola* (1 population), *E. d. difficilis* (4), and *E. d. hellmayri* (6). The key to alleles present is located in the lower center of the quadrant for each locus. Sample sizes are given within the symbol for each population in quadrant A.

Figure 1: The range maps of *E. difficilis/occidentalis* and featured breeding specimens from Johnson (1980) (his Fig. 3 on the previous page) and Johnson & Marten (1988) (their Fig. 1 above), which notably omit the primary overlap zone between the two forms.

Population Genetics and Phylogeography

Using gel electrophoresis, Johnson & Marten (1988) examined allozyme variation at 41 genetic loci from 208 individuals in 11 geographic populations of *E. d. difficilis* and *E. d. hellmayri.* Of these 41 loci, 21 were variable within or among populations, and 5 showed clear geographic variation in allele frequencies which were largely clinal and consistent with a model of isolation-by-distance. A single locus showed strongly divergent allele frequencies between coastal *E. d. difficilis* and interior *E. d. hellmayri,* with intermediate frequencies present in the population sample from the contact zone in California's Siskiyou region. Johnson and Marten calculated

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uncorrected genetic differences among populations, finding divergence between *E. d. difficilis* and *E. d. hellmayri* comparable to values reported for other "megasubspecies" in the literature. Calculating F_{ST} to assess differentiation across populations, they found evidence of population subdivision elevated in *E. d. hellmayri* compared to *E. d. difficilis.* Applying Slatkin's (1985) method for assessing gene flow among populations with private alleles (a.k.a. singletons), they found evidence of widespread gene flow throughout mainland populations of the complex. Application of the WPGMA clustering algorithm showed strong clustering by subspecies; a UPGMA approach lumped the closest populations to either side of the contact zone and excluded those in Arizona, Colorado, and Santa Catalina Island. A Wagner-network-based phylogeny reflected geography, with a monophyletic *E. d. difficilis* clade within a grade of *E. d. hellmayri* populations; applying a simple molecular clock to genetic distance between subspecies yielded an estimated divergence time of 248,700 years before the time of the analysis.

Based on these results, Johnson and Marten argued that "*E. d. difficilis* and *E. "d." hellmayri* [are] full species and formally recommend that they be so considered by the Committee on Classification and Nomenclature of the American Ornithologists' Union". In support of this statement, they further pointed to a discriminant analysis of phenotypes from samples in the Siskiyou region that suggested that the majority of samples have traits within the range of intraspecific variability of *E. d. hellmayri* and *E. d. difficilis* as measured in populations adjacent to the contact zone. By doing so, they implied that intermediate allele frequencies in this sample are not driven by hybridization but are instead consistent with pooling individuals from two distinct lineages that demonstrate assortative mating in sympatry.

Morphology and Vocalizations

Johnson identified five vocalization types: the advertising song, the male position note, the female position note, the alarm call, and the "*chrrip*" call (Johnson 1980:61). Johnson considered the alarm and "*chrrip*" calls very similar or identical between forms, and found "no obvious differences" between female position notes among birds in the Channel Islands, the California coast, the far interior Rocky Mountains, or the mountains of Mexico south to Oaxaca (Johnson 1980:70–71). Johnson reported differences in the syllables of advertising songs between interior and coastal populations, noting that they were especially pronounced when comparing widely separated birds, such as those from San Francisco and southern New Mexico; however, he noted that birds from northeastern California were somewhat intermediate (Johnson 1980:65–67). Male position notes made up the largest sample of any vocalization type, with 68 individual birds represented. Johnson described these notes as displaying broad regions of uniformity separated by narrow belts of abrupt character change. He noted that calls from New Mexico, Colorado, South Dakota, and Arizona—which are usually two-parted—are easily distinguishable from those of the west coast. Furthermore, he stated that although calls were highly variable in the Siskiyou region, the Warner Mountains of California, and east of the Cascades in Oregon, in these places birds produced a mix of interior and coastal-type calls (Johnson 1980:68–70). Although they do show clear geographic trends, these male position notes are so variable overall that Johnson was "unable to develop a repeatable method of measuring the diverse shapes and angles presented by these vocalizations to permit their quantitative appraisal," and therefore his assessment was done subjectively by visual comparison of spectrograms (Johnson 1980:8).

Johnson assessed morphological differences among populations using a highly complex multivariate analysis that featured 11 different size and color characteristics. He found that birds in interior populations averaged larger than coastal breeders, with longer primaries and tails, greater body mass, and brighter breast coloration. But as with vocalizations, he found that birds in the Siskiyou region were intermediate, and that these features were only consistently non-overlapping when birds were differentiated by age and sex (Johnson 1980:72–83, Johnson 1994). Visual identification of populations is considered impossible in the field, and Johnson even struggled to classify many individuals in the hand, stating that "these flycatchers are all so similar to begin with that one experiences difficulty in attempting to distinguish the range of normal variability in pure parents from that shown by either F_1 hybrids or various backcrosses and recombinants" (Johnson 1980:112).

Additionally, Johnson found evidence that morphological and vocal characteristics are not always paired. Johnson reported that birds from Rogue River (Jackson County, Oregon) were "perfectly typical of coastal *E. d. difficilis* in song while being intermediate between coastal and interior populations in size and color," and that birds from Siskiyou were "perfectly intermediate" between coastal and interior populations in terms of song syllables but exhibited "enormously expanded variability" in size and color. Johnson suggested these combinations of characteristics were likely indicative of either a hybrid swarm or a situation of complex secondary contact (Johnson 1980:92).

Evidence of Assortative Mating in Sympatry

The evidence of assortative mating in sympatry described by Johnson & Marten (1988) and used as a core argument for the split (AOU 1989) was based on a sample of 17 individual specimens and four mated pairs collected in the Siskiyou region. One pair was featured in Johnson (1980), and three more were collected in 1981. Of these samples, 9 individuals and three pairs were described as representing "definite or probable pure parental types" of *E. difficilis.* An additional 8 individuals and one pair were described as "certain or probable" *E. occidentalis*. Finally, two birds were suspected to be intergrades based on multivariate discriminant scores. One bird was scored as a "typical male *E. difficilis*" in the discriminant analysis but had "an 'interior' genotype at the 6-PGD locus," which was not known to occur in coastal birds, leading to suspicion of recent backcross origin (Johnson & Marten 1988:186–187).

New Information:

Biogeography

Despite the region's omission from the ranges described in Johnson (1980), Johnson & Marten (1988), and the original split (AOU 1989), *E. difficilis/occidentalis* is not merely present in the "greater Kootenays" but is fairly common there (Campbell *et al.* 1997, Hopping 2022). Indeed, this area represents the primary region of overlap between the two forms (Rush *et al.* 2009, Linck *et al.* 2019, Lowther *et al.* 2020, Hopping 2022). Although some sources describe *E. difficilis/occidentalis* as "scarce" in northern Idaho and western Montana (Lowther *et al.* 2020), it is one of the more common birds in—for example—the vicinity of Sandpoint, Idaho (Bonner

County), and it is present in other nearby towns such as Bonner's Ferry, Idaho (Boundary County), and Libby, Montana (Lincoln County) (Hopping 2022). Because it is more often found in human-impacted habitats and in areas that are difficult to access such as gullies, it is possible that it may have been missed on formal surveys that failed to sufficiently sample these habitat types (Hopping 2022). It's also possible that it may have only become common in the area in recent decades (Campbell *et al.* 1997). The presence of breeding by *E. difficilis/occidentalis* has also since been confirmed in much of eastern Washington (Lowther *et al.* 2020), including Yakima County and the Blue Mountains, where previous records of suspected breeding (Dice 1918, Jewett *et al.* 1953) were dismissed by Johnson (1980:85) as lacking sufficient evidence.

Although *E. difficilis/occidentalis* is present throughout the greater Kootenays, the complete or near-complete lack of consistent, diagnostic vocal and/or morphological field identification features in the region means that the precise range limits of the two forms are unknown. Local state and provincial records committees all default to the form expected in their largest human population center (e.g., Seattle, Washington; Vancouver, British Columbia; Boise, Idaho): the bird records committees of both Idaho (Idaho Bird Records Committee 2020) and Montana (Montana Bird Records Committee 2022) feature only *E. occidentalis* on their state lists, whereas adjacent British Columbia and Washington include only *E. difficilis* (British Columbia Bird Records Committee 2018, Washington Bird Records Committee 2021), and Alberta simply lists "Western Flycatcher" (Alberta Bird Records Committee 2022). Likewise, there are no known differences between the two populations with respect to habitat preference, migration timing, or behavior within the greater Kootenays region.

Population Genetics and Phylogeography

Two studies in the last 15 years have advanced our understanding of the evolutionary history and distribution of genetic variation in *E. difficilis/occidentalis.* In a 2009 paper in *The Journal of Avian Biology*, Rush and colleagues generated AFLP data (a method of sampling the nuclear genome; n=48) and sequenced the mitochondrial DNA locus ND2 (n=46) from *E. difficilis/occidentalis* individuals across the contact zone in southern British Columbia that was not included in Johnson & Marten (1988). Although all birds carried the mitochondrial haplotype of *E. difficilis,* AFLP data revealed widespread nuclear introgression across the region. The authors attributed these patterns to pervasive hybridization on secondary contact after a period of isolation, followed by stochastic loss of the *E. occidentalis* ND2 haplotype, possibly driven by small effective population sizes (a pattern exacerbated by uniparental/maternal inheritance of mtDNA). The authors interpreted these results as undermining evidence of reproductive isolation and assortative mating between the two forms.

Later, Linck *et al.* (2019) generated genome-wide sequence data (using ddRADseq and UCE library preparation approaches, as well as Sanger sequencing of ND2) to describe range-wide phylogeographic patterns and assess evidence of introgression at multiple contact zones within *E. difficilis/occidentalis.* Notably, the team sampled breeding *E. occidentalis* individuals throughout Mexico, including in the isolated Sierra Madre del Sur, a mountain range previously identified as a hotspot for lineage-level endemism. Their phylogenetic analyses revealed a monophyletic *E. difficilis* clade nested within *E. occidentalis* (i.e., *E. occidentalis* as currently described was paraphyletic with respect to *E. difficilis,* with a monophyletic clade of *E. occidentalis* individuals in the Sierra Madre del Sur sister to a clade containing all other *E.*

difficilis/occidentalis samples). Analysis of genetic structure suggested that a four-population model (K=4) was best supported, with geographically coherent clusters corresponding to *E. difficilis, E. occidentalis* north of the U.S.–Mexico border, *E. occidentalis* in Mexico excluding the Sierra Madre del Sur, and *E. occidentalis* within the Sierra Madre del Sur. Second, they found evidence of far-reaching admixture among lineages, with significant *E. difficilis* ancestry as far east as the Black Hills of South Dakota (Fig. 2). Although Siskiyou Mountain birds appeared to have predominantly *E. difficilis* ancestry, birds in the Warner Mountains of northeast California were highly admixed, with nearly equal proportions of *E. difficilis* and *E. occidentalis* ancestry when conditioning on K=4. Similarly mixed birds were identified in the inland Pacific Northwest/greater Kootenays (specifically, in regions of Washington, Idaho, and Montana immediately south of the hybrid zone identified by Rush *et al.* 2009) and in southern California (in both the Transverse Range and the southernmost portion of the Sierra Nevada).
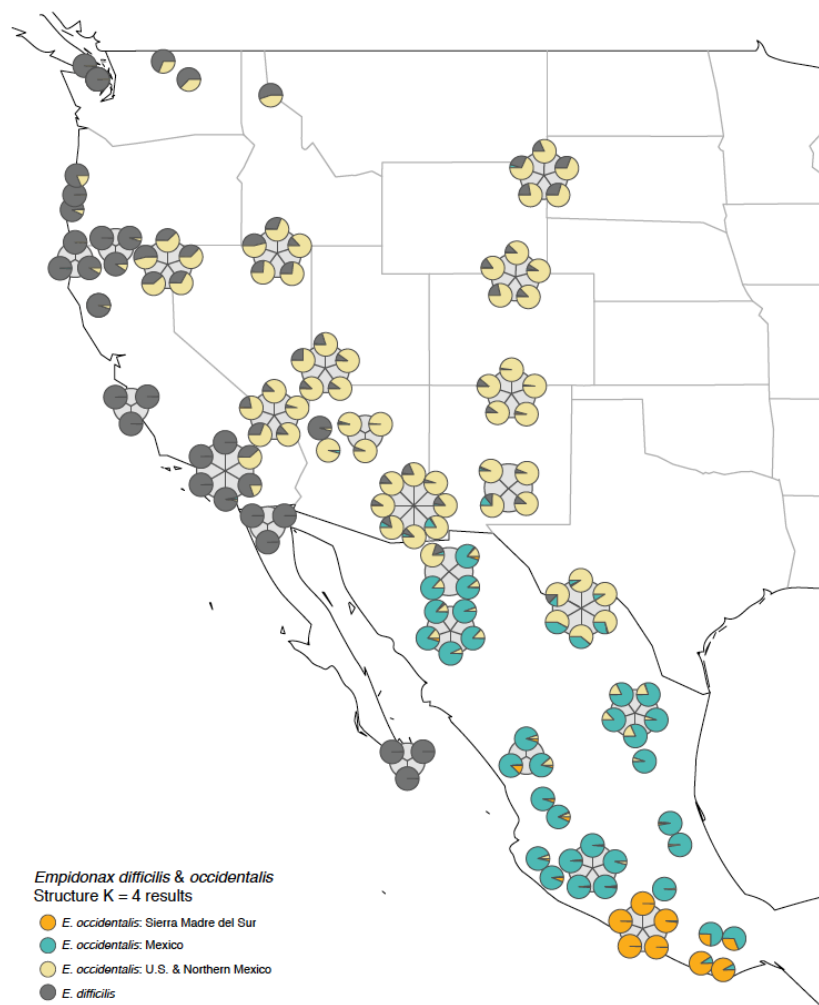

Figure 2 (from Linck *et al.* 2019): Genome-wide sequence dating captured widespread admixture between *E. occidentalis* and *E. difficilis*. Proportional ancestry at k=4 for *E. difficilis* and *E. occidentalis* individuals. Each circle represents an individual, and clusters of circles represent multiple individuals at a single sampling locality.

The authors refrained from making taxonomic recommendations but suggested that their data were consistent with one, two, or four species, depending on the species concept invoked. A phylogenetic species concept was most consistent with two species corresponding to a lineage restricted to the Sierra Madre del Sur, and a lineage distributed across the remainder of North America. A genotypic clustering species definition was most consistent with four species and aligned with the four-population model outlined in the previous paragraph.

<u>Morphology and Vocalizations</u>

Recent analyses of *E. difficilis/occidentalis* vocalizations in Washington, Idaho, and Montana have revealed that the distribution of intermediate vocalizations is far broader than the narrow zones of rapid character change described by Johnson (1980:68). Isacoff (2021) found that 28 of 29 available advertising song recordings from eastern Washington and the Idaho panhandle featured mixed characteristics, meaning that field identifiable *E. difficilis/occidentalis* forms in the overlap zone were "very rare, or perhaps non-existent," and that "even the seemingly reliable dawn song is likely not as reliable as was thought." Hopping (2022) performed a similar analysis of male position notes in Montana, including birds well east of the continental divide in Hill, Blaine, and Fergus counties, and found that only 3 of the 26 recordings uploaded to eBird in the state matched the two-parted shape that Johnson (1980:68) described as typical of *E. occidentalis*. Hopping (2022) also found that every available dawn song recording from Montana was consistent with those of the presumed intergrades featured in Isacoff (2021), rather than either "pure" form. Although phenotypes in Mexico await serious study, *E. occidentalis* individuals within the highly divergent Sierra Madre del Sur clade are "essentially indistinguishable from adjacent [populations outside this clade elsewhere in Mexico] with many standard morphometric measurements" (Linck *et al.* 2019).

Discussion:

<u>Biogeography</u>

The arguments made in Johnson & Marten (1988) rely heavily on the premise that Siskiyou is the only contact zone between *E. difficilis* and *E. occidentalis.* The ranges of *E. difficilis* and *E. occidentalis* described in Johnson (1980), however, are connected by virtually contiguous mid-elevation forest which extends from western Montana through northern Washington and British Columbia all the way to the Pacific Ocean. Indeed, *E. difficilis/occidentalis* is present in suitable habitat throughout this broad region. It is this area—not Siskiyou County—which represents the primary overlap zone between the two forms. Moreover, the Siskiyou region appears most likely be a recent, and relatively minor, point of re-contact, in a manner similar to what one would expect to see from an incipient ring species (Martins *et al.* 2013) (i.e., greater differentiation at disjunct ends of a cline of more continuous variation). As a result, the dynamics that Johnson (1980) and Johnson & Marten (1989) recorded in Siskiyou County are not necessarily representative of the complex at large.

Johnson (1980) acknowledged that the presence of *E. difficilis* east of the Cascades in Washington proved that the boreal habitats of the northern Cascades were not serving as a range limit, and he suggested that the birds in this region may have arrived from the Okanagan

Valley of British Columbia to the north; however, he did not discuss what, if anything, would prevent *E. difficilis* from expanding further eastward towards Montana if this were the case. Johnson stated that *E. difficilis* would not be expected to summer near the Alberta border, but his justification for this statement is unclear given that other characteristic breeding species of the Pacific Northwest (e.g., Varied Thrush *Ixoreus naevius*, Chestnut-backed Chickadee *Poecile rufescens*, Townsend's Warbler *Setophaga townsendi*, Pacific Wren *Troglodytes pacificus*) all breed in northwestern Montana (Marks *et al.* 2016).

Nor are the supposed habitat differences described by Johnson (1980:15) — that *E. occidentalis* occurs in drier habitats and at higher elevations (4500–9000 ft.), whereas *E. difficilis* occurs in "shady forests from sea level to mid-elevations" — informative characters for identification or species limits. At broad scales, these habitats are largely non-overlapping and segregate almost entirely between the known distributions of the two forms. In fact, the primary region where moist, maritime-influenced conifer forest interdigitates with the more arid Ponderosa-pine-dominated forests of the interior west is the Greater Kootenays region, which was not included in Johnson's original work and is now known to be a hotspot for gene flow between *E. difficilis* and *E. occidentalis,* as previously discussed. As a result, we argue that observed habitat differences are unlikely to reflect prezygotic isolation by habitat selection in areas of sympatry. We suggest that the complete lack of meaningful differences in behavior or migration timing between the two forms at these northern latitudes also contributes to the effect of apparently unimpeded gene flow and a broad, unstable intergrade zone.

Although there is some evidence that *E. difficilis/occidentalis* occurrence may have increased in the greater Kootenays in recent decades (Campbell *et al.* 1997), and that it was previously undetected as a result, the high frequency of admixture documented in the region by Rush *et al.* (2009) and Linck *et al.* (2019) suggests that this contact has occurred unimpeded for some time—most likely following the recession of Pleistocene glaciers. Even if the extent of secondary contact between forms in this region is a relatively recent phenomenon, the rampant gene flow now recorded between them is itself sufficient to undermine the original case for their split. We think it most likely that Johnson never reached the greater Kootenays region (Hopping 2022), as he makes no mention of personal fieldwork conducted there in any of his papers published on the topic (Johnson 1973, Johnson 1980, Johnson & Marten 1988, Johnson 1994), and it is unlikely that birds would have been overlooked with sufficient survey effort there.

Population Genetics and Phylogeography

At the time of the original split, the Siskiyou region of northern California was the only known area of sympatry between the two forms, and interbreeding had not yet been demonstrated (Johnson & Marten 1988, AOU 1989). Recent fieldwork and population genetic analyses, however, have revealed a broad area of intergradation where the two forms occur in sympatry in interior British Columbia and southwestern Alberta (Rush *et al.* 2009), and continental-scale sampling has uncovered evidence of genetic introgression from *E. difficilis* into *E. occidentalis* reaching as far east as the Black Hills of South Dakota (Linck *et al.* 2019). The high frequency of admixture and lack of isolated, discrete population genetic structure where U.S. and Canadian-breeding populations of *E. difficilis* and *E. occidentalis* come into contact undermine claims of assortative mating or other forms of prezygotic reproductive isolation between the two forms. Instead, the pattern is consistent with clinal variation in a single widespread lineage

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generated by isolation-by-distance, followed by one or more vicariance events (likely related to Pleistocene glacial cycles) that interrupted gene flow and promoted primarily neutral divergence in genotype and phenotype that corresponded to little build-up of reproductive isolation. Later, population expansion or the removal of biogeographic barriers (e.g., glaciers) allowed interior and coastal populations to experience secondary contact in regions of suitable habitat in at least three locations: the inland Pacific Northwest, the Siskiyou/Warner Mountains of Northern California, and the Transverse Range/southern Sierra Nevada).

We note that this hypothesis for the origin of *E. difficilis/occidentalis* populations is similar to the one described for canonical "ring species" (Martin *et al.* 2013). Indeed, the geography and climatic history of western North America appears to lend itself to generating interrupted clinal variation. Several other western species (e.g., Black-headed Grosbeak *Pheucticus melanocephalus* [Van Els *et al.* 2014] and Mountain Chickadee *Poecile gambeli* [Manthey *et al.* 2012]), have similar phylogeography, and ecological niche models applied to the latter species also identified Siskiyou County, California, as an overlap zone between lineages. Like Western Flycatcher, both of these species show stronger genetic structuring in the southern parts of their breeding ranges than in the north, most likely as a result of Pleistocene glaciation cycles (Manthey *et al.* 2012, Van Els *et al.* 2014, Linck *et al.* 2019), and we note that both are treated as single species with subspecific variation in the most recent edition of the AOS *Check-list of North American Birds* (1998). Lastly, we would be remiss not to mention that *E. occidentalis* in the Sierra Madre del Sur of Mexico shows greater genetic divergence from its nearest neighbors than any other two populations in the complex (Linck *et al.* 2019); this is consistent with other evidence showing the mountain range to be a hotspot of lineage-level endemism (Van Els *et al.* 2014). Yet to date, birds in the Sierra Madre del Sur are treated as conspecific with *E. occidentalis* elsewhere and, furthermore, subsumed under the subspecies *E. o. occidentalis.*

In light of this new evidence, additional scrutiny of the conclusions of Johnson & Marten (1988) is warranted. We suggest that their genetic data are consistent with the results of later studies in showing shallow population genetic structure generated by the interruption of an isolation-by-distance pattern, partly counteracted by genetic introgression. Geographic trends in the frequency of the small minority of allozyme frequencies in their study were clinal—not discretely clustered; the two alleles at the EST-2 locus were described as "widespread" and showed "weak clines in their geographic frequency", and the glutathione reductase (GR) locus showed a "clear clinal pattern of allelic frequencies". The "most striking pattern" of geographic trends in allozyme frequency, exhibited by the malic enzyme (ME) locus, also showed clinal variation, with neither fixation nor disappearance of the two most common alleles occurring in either the furthest interior or coastal populations. Notably, this consistent clinal variation was still visible in Johnson & Marten (1988) in spite of the absence of samples from Washington, British Columbia, Alberta, Idaho, and Montana—the primary contact zone for the two forms. Lastly, Johnson & Marten's analysis is consistent with the results of Linck *et al.* (2019) in showing *E. d. hellmayri* to be paraphyletic with respect to *E. d. difficilis.*

Morphology and Vocalizations

The complex multivariate analysis of morphological characteristics conducted by Johnson (1980) allowed for only statistical distinctions rather than biological ones (Phillips 1994, Pyle 2012). The complete lack of specimens from the primary overlap zone likely exaggerated the

morphological divergence between the two forms, as the relatively slight differences reported by Johnson (1980) among birds at widely separated locations could easily be the result of distance effects at the extremes of a broad cline. This is also true for the vocal differences documented by Johnson (1980), which are similarly consistent with a neutral isolation-by-distance process. Johnson himself found it impossible to quantify the differences between male position notes, owing to their extensive variation — a conclusion further supported by more recent analysis of these calls (Hopping 2022). Both supposedly diagnostic vocalization types (the dawn song and the male position note) blend together completely in the overlap zone (Isacoff 2021, Hopping 2022), the extent of which appears broad and unstable. Even at extremes, the two forms are not known to be identifiable visually.

Evidence of Assortative Mating

Johnson's direct evidence for assortative mating in the Siskiyou region is weak, as it featured only four mated pairs (Johnson 1988). Even if substantiated, the dynamics in this disjunct region of secondary contact are likely to have little bearing on their interactions in the primary overlap zone. Anecdotal evidence from the broader population points in the opposite direction: virtually all birds display intermediate vocal and genetic characteristics in a broad and unrestricted region from central Washington to at least central Montana (Rush *et al.* 2009, Linck *et al.* 2019, Isacoff 2021, Hopping 2022).

To our knowledge, playback experiments or field studies focused on the pairing and mating behavior of these taxa — which usually accompany recommendations for taxonomic changes — have not been conducted in the primary overlap zone. In this case, however, we believe that such studies are unlikely to be informative or even viable, owing to the complete lack of stable, diagnosable characteristics between forms in this region. This is true not only in the field, but also in hand or with tissue samples, as existing analyses of vocalizations and population genetics suggest that all or virtually all of the birds in this region are intermediate. Even if assortative mating between "pure" forms were documented in the primary overlap zone, we note that recent work has cast doubt on the ability of assortative mating to drive speciation in the absence of postzygotic isolation (Irwin 2020). This is particularly true when intergradation is frequent, mixed genotypes are widespread, and the fitness of intermediates is high: patterns that Rush *et al.* (2009) and Linck *et al.* (2019) appear to document in the Western Flycatcher complex. We hold that there exists no evidence that the two forms behave as separate species where they overlap in the primary contact zone in the greater Kootenays.

Recommendation:

Pacific-slope Flycatcher *Empidonax difficilis* and Cordilleran Flycatcher *E. occidentalis* exhibit no evidence of fixed phenotypic differences in morphology or vocalizations and are not known to be identifiable in the field across a broad and apparently unstable contact zone. They exhibit little to no evidence of barriers to gene flow, either prezygotic (no documented differences in behavior, migration timing, habitat usage, or significant biogeographic barriers between their breeding ranges) or postzygotic (the broad, unrestricted distribution and high frequency of intermediate genotypes and phenotypes suggests that birds of mixed ancestry are not at a fitness disadvantage). Additionally, there is evidence that the original split was premature and based on geographically extreme samples: the documented differences in morphology,

vocalizations, and DNA between these widely separated populations are consistent with what should be expected under neutral isolation-by-distance or vicariance processes, without the need to invoke speciation. The original analysis of their interactions in sympatry was conducted entirely in a small, disjunct region of secondary contact, rather than the primary contact zone between the two forms, which was overlooked at the time. Johnson's assertion of assortative mating in sympatry (1988; AOU 1989) was based on an extremely small sample (*n*=4 pairs) in a geographically peripheral region of contact; indirect evidence from more recent research does not support the case for assortative mating in the primary contact zone.

AFLP data from Rush *et al.* (2009) and genome-wide sequence data from Linck *et al.* (2019) provide no evidence of discrete population genetic structure that maps onto modern taxonomic categories. Instead, these studies show genetic patterns consistent with clinal variation generated by an isolation-by-distance process which was likely interrupted by vicariance events related to Pleistocene glacial cycles that did not result in the build-up of measurable barriers to gene flow. There is likewise no evidence that the two forms behave as different species in mating preference or habitat selection, or that they are reproductively isolated in any other way where they overlap. Indeed, the two forms appear to be substantially less differentiated than adjacent Mexican populations of *E. occidentalis*, which have to date been exclusively treated as conspecific. As a result, we suggest that the burden of proof should now fall on demonstrating reproductive isolation between and species status for *E. difficilis sensu stricto* and *E. occidentalis.*

In conclusion, we see no supporting evidence for species-level differences between *E. difficilis* (*sensu stricto*) and *E. occidentalis* as they currently stand, and we recommend that they be lumped under Western Flycatcher *E. difficilis (sensu lato)*, reverting to their treatment prior to the 1989 split. At most, a subspecific relationship can be claimed. Although we cannot rule out that some, or all, of the following populations are linked by constant gene flow resulting in clinal variation, for the sake of completeness we recommend the recognition of subspecific status for six forms (though we acknowledge that these are not officially within the scope of the NACC), as follows:

Three subspecies currently recognized under *E. difficilis*:

- *E. d. difficilis* Baird 1858 (Pacific-slope).
    - Type locality: Ft. Tejon, Kern County, California, USA.
    - Distribution: Breeds along the Pacific Slope from southeastern Alaska south to the Sierra San Pedro Mártir of Baja California, Mexico. Intergrades with *E. d. hellmayri* occur at least from northeastern California (e.g., Siskiyou County) north to southeastern Alberta and east to central Montana (e.g., Hill County), perhaps as far as the Black Hills of South Dakota. Birds throughout the Great Basin, interior Pacific Northwest, and northern Rocky Mountains may pertain to intergrades with *E. d. hellmayri*. Winters in western Mexico in Baja California Sur and from Sinaloa south to Michoacán, with small numbers irregularly occurring south to Oaxaca and north to Arizona (south of the Colorado Plateau) and coastal California.
    - Includes: *E. bairdi perplexus* Nelson 1900.

- *E. d. insulicola* Oberholser 1897 (Channel Islands).
  - Type locality: Santa Rosa Island, Santa Barbara County, California, USA.
  - Distribution: Breeds on the Channel Islands of southern California; overwintering distribution unknown.

- *E. d. cineritius* Brewster 1888 (Baja California Sur).
  - Type locality: Sierra de la Laguna, Baja California Sur, Mexico.
  - Distribution: Year-round resident in mountains of southern Baja California Sur, Mexico.

One subspecies currently recognized under *E. occidentalis:*

- *E. d. hellmayri* Brodkorb 1935 (Interior West).
  - Type locality: Boot Spring, Brewster County, Texas, USA.
  - Distribution: Breeds inland from west Texas (e.g., Brewster County) and northwestern Mexico (e.g., northern Sonora) north to northeastern California, southern Idaho, south-central Montana (e.g., Lewis and Clark County), and east to South Dakota. Intergrades with *E. d. difficilis* occur at least from northeastern California (e.g., Siskiyou County) north to southeastern Alberta and east to central Montana (e.g., Hill County), perhaps as far as the Black Hills of South Dakota. Birds throughout the Great Basin, interior Pacific Northwest, and northern Rocky Mountains may pertain to intergrades. Intergrades with *E. d. bateli* occur in northern Mexico (e.g., in Chihuahua and Coahuila). Winters in Mexico from southern Sonora and Coahuila south to Oaxaca; exact range limits uncertain.

Two subspecies currently included together under *E. o. occidentalis,* but which we recommend recognizing as separate subspecies:

- *E. d. bateli* Moore 1940 (Mexican).
  - Type locality: Rancho Batel, 6 miles north of Santa Lucía, Sinaloa, Mexico.
  - Distribution: Breeds in mountains of Mexico west of the Isthmus of Tehuantepec, excluding the Sierra Madre del Sur, north to Sinaloa, Chihuahua, and Coahuila, where it intergrades with *E. d. hellmayri*. Intergrades with *E. d. occidentalis* may be present in central Oaxaca.
  - Includes: *E. d. immemoratus* Moore 1940; *E. d. culiacani* Moore 1940; *E. d. infelix* Phillips 1966.

- *E. d. occidentalis* Nelson 1897 (Sierra Madre del Sur).
  - Type locality: Pluma Hidalgo, Oaxaca, Mexico.
  - Distribution: Year-round resident in the Sierra Madre del Sur of Guerrero and southern Oaxaca, Mexico. Possible intergrades with *E. d. bateli* occur in central Oaxaca.
  - Includes: *E. d. annectens* Phillips 1966.

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Submitted by: W. Alexander Hopping & Ethan Linck

Date of proposal: 10 March 2023

Establish English names for various newly split species

English names have not been resolved for most species splits recently passed by this committee. A small number of these are complex enough to require individual proposals, but seven others are straightforward (or nearly so) and are treated together here in a single proposal:

(a) Separation of *Antrostomus ekmani* from Greater Antillean Nightjar *A. cubanensis* (proposal 2023-A-2). These species were treated as groups in AOU (1998) under the English names Hispaniolan Nightjar for *ekmani* and Cuban Nightjar for *cubanensis*. *Antrostomus ekmani* is endemic to Hispaniola and *A. cubanensis* is endemic to Cuba, with a separate subspecies on the Isla de la Juventud and Cayo Coco. The AOU group names are used for subspecies groups by Clements, and are also in use for species by the IOC list and HBW-Birdlife.

Recommendation: Adopt Hispaniolan Nightjar for *A. ekmani* and Cuban Nightjar for *A. cubanensis.*

(b) Separation of *Accipiter atricapillus* from Northern Goshawk *A. gentilis* (2023-B-11). These species were treated as groups in AOU (1998) under the English names Eurasian Goshawk for *gentilis* and American Goshawk for *atricapillus*. Sangster (2022) also recommended using these names, and Clements uses them for their subspecies groups.

Recommendation: Adopt Eurasian Goshawk for *A. gentilis* and American Goshawk for *A. atricapillus.*

(c) Separation of *Lepidothrix velutina* from Blue-crowned Manakin *L. coronata* (2023-C-1). AOU (1998) recognized three groups within *L. coronata*: Velvety Manakin *velutina*, Blue-crowned Manakin *coronata*, and Exquisite Manakin *exquisita*. Our split of *L. coronata* into two species follows SACC's treatment of these taxa. SACC adopted the English names Velvety Manakin for *L. velutina* and Blue-capped Manakin for *L. coronata* (incl. *exquisita*). The latter English name distinguishes the newly split *L. coronata s.s.* from the English name (Blue-crowned Manakin) of the parent species *L. coronata*.

Recommendation: Adopt Velvety Manakin for *L. velutina* and Blue-capped Manakin for *L. coronata*.

(d) Separation of *Sclerurus obscurior* from Tawny-throated Leaftosser *S. mexicanus* (2023-C-6). AOU (1998) did not recognize groups within *S. mexicanus*. SACC split *S. mexicanus* using the English names South American Leaftosser for *S. obscurior* and Middle American Leaftosser for *S. mexicanus.* These were acknowledged to be unexciting names but were adopted in anticipation of further splits in this complex, which would render these new names obsolete. Clements also used these names. The original SACC and NACC proposals by Cooper and Cuervo recommended Dusky Leaftosser for *S. obscurior* and Central American Leaftosser for *S. mexicanus*, and the IOC list adopted Dusky Leaftosser for *S. obscurior* and retained Tawny-throated Leaftosser for *S. mexicanus*. Central American Leaftosser is less

appropriate for *mexicanus* than is Middle American because the distribution includes Mexico, and Dusky Leaftosser was previously used for subspecies *pullus*, now part of *S. mexicanus*, so these names are not recommended.

An alternative approach would be to retain Tawny-throated Leaftosser for *S. mexicanus*, because *S. obscurior* is sister to *S. rufigularis* rather than to *S. mexicanus*, meaning that treating *mexicanus* and *obscurior* as conspecific was based on an incorrect assessment of their relationships. Under these circumstances, our guidelines state that the parental English name may be retained for *S. mexicanus*.

Recommendation: Adopt South American Leaftosser for *S. obscurior*, following SACC for the South American species, but retain Tawny-throated Leaftosser for *S. mexicanus*.

(e) Separation of *Corvus minutus* as a separate species from Palm Crow *C. palmarum* (2023-B-8). AOU (1998) did not recognize groups within *C. palmarum*, but *C. minutus* is endemic to Cuba and *C. palmarum* is endemic to Hispaniola. Accordingly, the names Cuban Palm Crow and Hispaniolan Palm Crow have been adopted by the IOC for *C. minutus* and *C. palmarum*, respectively, and they are used by Clements for the subspecies. Our policy on hyphens dictates that "Palm-Crow" be hyphenated to indicate a sister relationship between these new species, which are the only species worldwide that include "palm crow" in their names. (The English name Cuban Crow is already in use for *C. nasicus*.)

Recommendation: Adopt Cuban Palm-Crow for *C. minutus* and Hispaniolan Palm-Crow for *C. palmarum*.

(f) Separation of *Chlorophonia sclateri* and *C. flavifrons* from Antillean Euphonia *C. musica* (2023-B-7). AOU (1998) did not recognize groups with *C. musica*, but *C. sclateri* is endemic to Puerto Rico, *C. flavifrons* is endemic to and widespread in the Lesser Antilles (according to Greeney 2021, it has been recorded from the Netherland Antilles [Saba], St Kitts and St Barts, Antigua, Monserrat, Guadeloupe, La Désirade, Dominica, Martinique, St Lucia, St Vincent, and Grenada, and *C. musica s.s.* is endemic to Hispaniola and Gonâve Island. Accordingly, the names Puerto Rican Euphonia, Lesser Antillean Euphonia, and Hispaniolan Euphonia are in use by HBW-Birdlife for *C. sclateri*, *C. flavifrons*, and *C. musica*, respectively. These English names are also used by Clements for the subspecies, although an apparent error has rendered "Lesser Antillean Euphonia" as "Lesser Euphonia" (*flavifrons* is the smallest of the three taxa, so this is unlikely to have been intentional).

Recommendation: Adopt Puerto Rican Euphonia for *C. sclateri*, Lesser Antillean Euphonia for *C. flavifrons*, and Hispaniolan Euphonia for *C. musica*.

(g) Separation of *Amaurospiza aequatorialis* from Blue Seedeater *A. concolor* (2023-C-7). AOU (1998) did not recognize groups within *A. concolor*. The distribution of *A. concolor s.s.* extends from Mexico south to Panama, whereas *A. aequatorialis* is found mainly in western and central Ecuador (also in extreme southwestern Colombia and northwestern Peru). The range disparity indicates that retention of the English name Blue Seedeater for *A. concolor* would be in keeping with our guidelines for English names. Equatorial Seedeater, presumably following the scientific name, has been used previously for *A. aequatorialis* (e.g., by the IOC and for the

subspecies by Clements), but the proposal recommended Ecuadorian Seedeater (as in Areta et al. 2023), both because this name reflects the vast majority of its distribution but also because "equatorial" might suggest a lowland distribution rather than the montane range that the species occupies.

Recommendation Adopt Ecuadorian Seedeater for *A. aequatorialis* and retain Blue Seedeater for *A. concolor*.

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Submitted by: Terry Chesser

Date of Proposal: 15 March 2023

Change hummingbird subfamily name from Topazinae to Florisuginae

McGuire et al. (2009) incorrectly introduced the group-name Topazini for the genera *Topaza* Gray, 1840, and *Florisuga* Bonaparte, 1850. We did not realize that the oldest group name was Florisuginae Bonaparte, 1853. This was corrected by Dickinson & Remsen (2013), who changed the group-name to Florisuginae. This was subsequently fully explained by Dickinson & Gregory (2020). In the 53rd Supplement, Chesser et al. (2012) had used Topazinae, not Florisuginae, and this needs to be corrected.

This is a mandatory and straightforward application of Article 23 of the Code, which establishes that the oldest group-name has priority, regardless of which genus name in the group is the oldest.

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Submitted by: Van Remsen

Date of Proposal: 15 March 2023

Treat *Gygis microrhyncha* as a separate species from White Tern *G. alba*

Background:

The taxonomy of *Gygis alba*, White Tern, has been complex, with some authors considering the taxon *microrhyncha* a separate species (e.g., Pratt et al. 1987, Sibley and Monroe 1991), largely based on the work of Holyoak and Thibault (1976). The taxon *microrhyncha* was described as a separate species, *Gygis microrhyncha* Saunders, 1876, on the basis of its smaller size, differently shaped bill, more rounded tail feathers, and pale-colored shafts to the primaries (Saunders 1876). As currently recognized by the AOS and most global authorities, White Tern is a single species, generally considered to consist of four subspecies, including nominate *alba* of the southern Atlantic Ocean, *candida* and *leucopes* of the tropical Pacific Ocean and Indian Ocean (Thibault and Cibois [2017] treat *leucopes* as a synonym of *candida*), and *microrhyncha*, which is restricted to the Marquesas Islands, Phoenix Islands, and Line Islands in the Pacific Ocean (Dickinson and Remsen 2013, Clements et al. 2022, Gill et al. 2023). The inclusion of *microrhyncha* as a subspecies of *Gygis alba* follows Peters (1934), who was the first to classify it as a subspecies. Del Hoyo and Collar (2014) more recently treated *microrhyncha* as a distinct species, employing the scoring criteria of Tobias et al. (2010), highlighting its smaller size, shallower tail notch, whitish versus dark shafts of the primaries, and narrow and entirely black bill:

> Apparently interbreeds with *G. alba* in Kiribati, and possibly E to Marquesas (Baker 1951, Holyoak & Thibault 1976); recent study proposes conspecific treatment, on basis of genetics and morphometrics alone (Yeung, Carlon & Conant 2009). Recognized as a species here on basis of previously published evidence (Pratt, Bruner & Berrett 1987), supported by other authors (Olson 2005): smaller size, i.e. 23 vs 31 cm in length (based on a small sample of NHMUK measurements, effect size -5.03; ns); shallower tail notch (tail-length effect size -11.78; score 4); more black around eye (at least 1); whitish vs dark shafts of primaries (2); bill black, with no blue or only trace at base (subscore 1) and markedly narrower (subscore 2) (3).

Under this classification, *G. microrhyncha* is a monotypic species and *G. alba* consists of the three subspecies *alba*, *candida*, and *leucopes*.

New Information:

Yeung et al. (2009) used mitochondrial DNA sequence data and morphometric data to study the validity of the taxa of White Tern. No differences were found among the named taxa, with a mean estimated sequence divergence of 0.25% between *microrhyncha* and *candida*; the two largely shared mitochondrial haplotypes, and no significant structure was found across the species (Fig. 1). However, morphometric analyses did find that *microrhyncha* differed significantly from all other taxa in bill depth and length of the longest rectrix. In their discussion, Yeung et al. (2009) concluded that their data did not support recognizing *microrhyncha* as a distinct group, because all subspecies shared at least two mtDNA haplotypes, arguing that their

data did not even support recognition of distinct subspecies, although *microrhyncha* did show significant morphological divergence. They also suggested that the morphological differences could reflect adaptations to different feeding niches that reduce competition, and that *microrhyncha* should be considered a separate management unit from other Pacific populations. Thibault and Cibois (2017) analyzed additional morphological data, which included wing length, bill length from skull, bill length from nostril, bill depth, and tail length; in a PCA, the first axis explained 80% of variation, and included all variables, which largely separated *microrhyncha* from the other taxa. Birds from the Line Islands were also distinct morphologically and were only slightly larger than *microrhyncha* from the Marquesas, which could be evidence these birds represent intermediates between *microrhyncha* and *candida*. Based on the lack of genetic differences between taxa, which Thibault and Cibois (2017) hypothesized could be due to introgression or recent divergence, they argued that *microrhyncha* should be recognized as a subspecies.
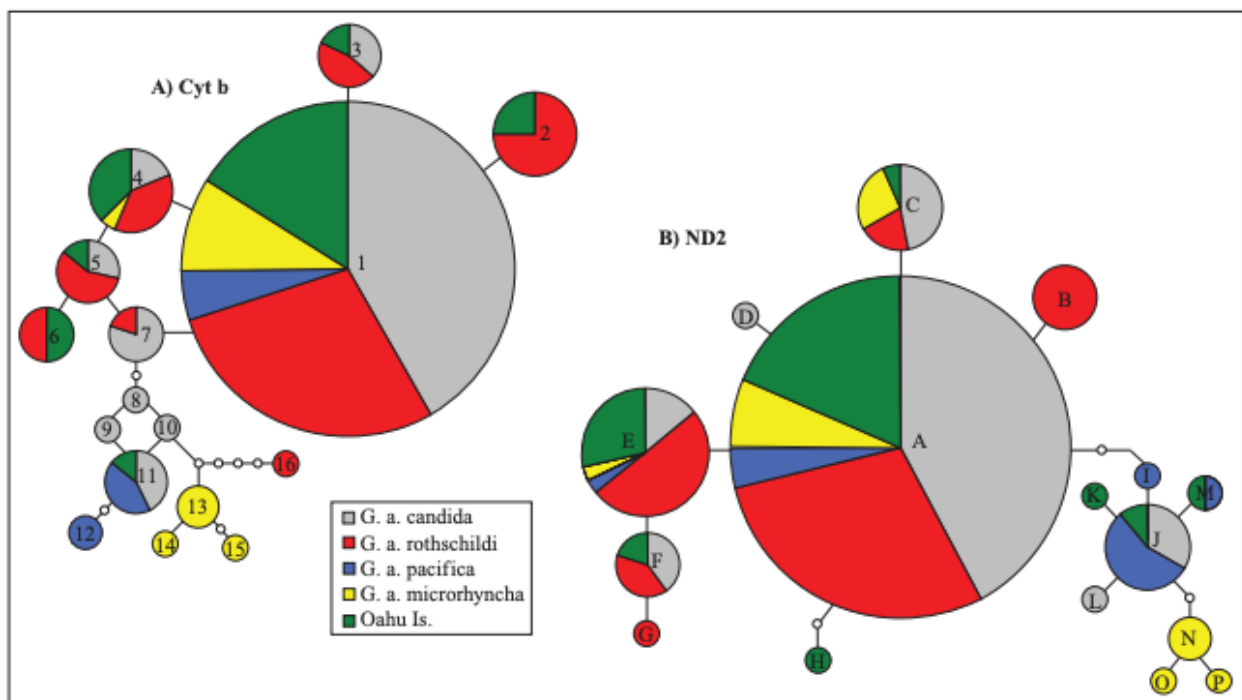

Figure 1. From Yeung et al. (2009), showing the haplotype diversity of *Gygis alba* samples across four proposed taxa, including *microrhyncha*. Note that *microrhyncha* shares a lot of haplotype diversity with the other taxa, but does have three unique haplotypes for both Cyt-b and ND2.

Although analyses by Yeung et al. (2009) and Thibault and Cibois (2017) suggested that White Tern is best treated as a single, broad species, Olson (2005) and Pratt (2020) have argued that *microrhyncha* deserves species status. Olson (2005) found consistent differences in the morphometrics between *microrhyncha* and *candida*, and based on fossil records, the two were widely sympatric and maintained these morphometric differences over a broad distribution historically. More recently, however, it appears that *candida* has displaced and swamped *microrhyncha* through hybridization, evidenced by the presence of intermediate birds (Olson 2005, Thibault and Cibois 2017, Pratt 2020), such that *microrhyncha* appears now to be mostly restricted to the Marquesas. In his paper discussing species limits in *Gygis*, Pratt (2020) argued

that the morphological differences, as well as vocal differences, which he described in the paper (reproduced below), warrant recognition at the species level, and went further arguing that the Atlantic subspecies, *alba*, should also be split, resulting in three *Gygis* species. Pratt (2020) also provided representative photographs and illustrations of *candida* and *microrhyncha* that demonstrate the striking bill shape and tail shape differences between the two taxa (see paper [here](#)).

Additional photographs from Macaulay Library showing differences can be viewed here:

microrhyncha (https://macaulaylibrary.org/asset/226463021) – shows the very rounded tail and clay-colored shafts to the first three primaries

candida/leucopes (https://macaulaylibrary.org/asset/205120461) – shows the forked tail and blackish shafts to the first three primaries

In his discussion of vocal differences, Pratt (2020) wrote that more information and study were needed, but did find one apparently distinctive vocalization ([ML203895301](#)) in a recording of *microrhyncha*, which he described as a "series of five two-syllable raspy notes, *shi-dick, shi-dick, shi-dick*,… quite unlike anything I have heard or find in archives for *G. [a.] candida*…" Typical *candida* calls were described as "a series of identical short raspy notes, *yik-yik-yik*…" ([ML32673](#)).

Recommendation:

The taxonomy of the *Gygis* terns is complex, and recent studies have only added to the complexity. Olson (2005) and Steadman (2006) showed that the two Pacific taxa, *candida* and *microrhyncha*, were historically largely sympatric with no evidence of intermediates in the fossil and archaeological record. However, more recently, it appears that the range of *candida* is rapidly expanding, and it is replacing *microrhyncha*; for example, on the Line and Phoenix Islands, only *candida* appears to occur now, but specimens from the 1920s and 1930s show intermediate characters (Pratt 2020). Now, *microrhyncha* is apparently restricted to the Marquesas Islands, where intergrades with *candida* have also been found. Pratt (2020) argued that *microrhyncha* may be driven to extinction through hybridization and genetic swamping with *candida*, which seems to be replacing it across its entire range.

Although it seems that *candida* and *microrhyncha* were reproductively isolated historically, it appears as though that isolation has broken down, and *candida* has replaced *microrhyncha* across nearly its entire distribution. Given this apparent breakdown of reproductive isolation, very little genetic divergence (possibly due to *microrhyncha* ancestry being left behind in the wake of the expanding *candida*, as suggested by Pratt [2020]), I would recommend a NO vote to split these two taxa.

If the two are split, I recommend the English name Little White Tern for *microrhyncha* and Common White Tern for nominate *alba*, which were used by del Hoyo and Collar (2014).

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

Date of Proposal: 16 March 2023

Establish English names for the newly split *Chlorothraupis carmioli* and *C. frenata*

Now that the proposal on *Chlorothraupis* species limits has passed, we have to decide what to do about English names for the taxa formerly grouped under Carmiol's Tanager, e.g., *Chlorothraupis carmioli* and extralimital *C. frenata*.

In my opinion, the decision for the new North American species, *C. carmioli sensu stricto*, is straightforward and covered under NACC guidelines for English names: retain Carmiol's Tanager. When splits are simple parent-daughter splits, our guidelines call for new names for the daughter taxa in most cases. But as the genetic data show, this is not an elevation of sister taxa to species rank but instead the removal of South American *frenata* from *C. carmioli*, which is not its sister species. This has the benefit of retaining the current and venerable name Carmiol's Tanager for the species in the NACC area, and promoting stability, which is our primary mission on English names. Carmiol's Tanager is also the name currently used for *C. carmioli s.s.* by IOC and HBW-BLI, and by Clements/eBird for the *carmioli* subspecies group. *Chlorothraupis frenata* occurs only in the SACC area, and so SACC should determine the name for that species. In the meantime, I recommend using Yellow-lored Tanager, which derives from the group name used by Sibley & Monroe (1990) and AOU (1998) for *frenata*, because that is the name currently used in most global classifications, although IOC uses Olive Tanager for *frenata* (see below for more on this name). (As long as we have the opportunity to do it, I might recommend to SACC that we change to the minor modification of "Yellowish-lored" because the lores aren't particularly yellow and are not the yellowest part of the frontal view of the bird, and in some view the lores actually appear whitish in contrast to the yellower breast. By the way, *frenata* means "bridled", so that's another possibility, although the bird doesn't look particularly "bridled" to me, in the sense of Bridled Titmouse.)

In case you're wondering, Carmiol's Tanager dates from at least Ridgway (1902). Hellmayr (1936) restricted Carmiol's to the nominate subspecies, as "Carmiol's Olive Tanager", with each subspecies being a Something Olive Tanager, including *frenata* as "Peruvian Olive Tanager"; evidently, he was impervious to problem of confusion with *C. olivacea*, which he called Yellow-browed Tanager (following Ridgway). That's why some classifications have unfortunately used "Olive Tanager" for the *carmioli* group.

By the way, on Carmiol from [Jobling]: "Francisco Carmiol (born Ferdinand Otto Ludwig Franz Carnigohl) (1844-1875) German immigrant, son of Julián Carmiol, resident and collector in Costa Rica (Rafael Carmiol Murillo, *in litt.*)" The ambiguity of that statement, i.e., whether Francisco was also a collector, was clarified in a lengthy series of [posts on Bird Forum]. Francisco was also a collector and sent birds to the Smithsonian. Evidently, father and son worked together to collect not only birds but all sorts of other plants and animals. The son died from a snake bite, likely on one of their expeditions. All indications are that they were thoroughly Costa Rican, including changing their first names to Spanish names.

Recommendation:

Retain Carmiol's Tanager for *C. carmioli* and provisionally adopt Yellow-lored Tanager for *C. frenata*.

For voting purposes:

(a) A YES vote endorses continuing use of Carmiol's Tanager for *C. carmioli*. A NO vote is for some other name, TBD.
(b) A YES vote endorses use of Yellow-lored Tanager for *C. frenata*, at least for now, as in the Supplement and Notes.

Submitted by: Van Remsen

Date of Proposal: 17 March 2023