2025-C-1

Revise the generic limits of *Accipiter*: (a) Accept recommended generic placements; (b) Accept recommended generic placements except for *Dinospizias*; (c) Accept new linear sequence of current and former Accipiter; (d) Accept new linear placement of *Circus*

YES (a) (c) (d). NO (b). I accept all recommendations except for (b) which should be retained for now in *Accipiter* pending additional data. The proposal lays out the rationale nicely for these generic-level changes, and this will bring NACC in line with other gobal taxonomic authorities.

YES (a) (b) (c) (d). I feel that A, C, and D are all straightforward. We cannot retain a monophyletic *Accipiter* as currently defined, and merging *Circus* makes little sense. For B, I lean slightly towards recognizing *Dinospizias* for *poliogaster* for a few reasons. Although the relationship is based on a single gene, it sits on a long branch. I don't necessarily trust the position of that branch, but I think the fact that it is an old branch is fairly well supported. That, plus the very distinct morphology, pushes me towards recognizing a monophyletic genus for this species, although the position of that genus may change with additional data.

YES (a) (c) (d). NO (b). *Accipiter* needs to be split based on non-monophyly, and the arguments for new placements are explained well in the proposal and the work of Catanach et al. (2024). I agree with the proposal that it is best to keep *poliogaster* in *Accipiter* for now, pending further data.

YES (a) (b) (c) (d). All of these except B are very clear-cut and seem essentially mandatory changes. On B, I can see the arguments for retaining *poliogaster* in *Accipiter* given that its position isn't as well-supported as we'd like; however, it is clearly an outlier in the newly circumscribed genus in multiple ways, and I think it is unlikely that further data would change the picture significantly. Even though morphology is massively misleading in Accipitridae, as we now know, that doesn't negate the fact that this taxon has multiple morphological characters that are hard to explain away as being uninformative, especially when the evidence also supports a very deep divergence. So I think that on balance recognition of *Dinospizias* is warranted.

YES (a) (c) (d). NO (b). I prefer to keep *poliogaster* in *Accipiter* for the time being, following the recommendation of Catanach et al. (2024), until additional data can help confirm its relationships. It's a borderline case for sure, but I think placing it in a monotypic genus before we can be certain of its relationships potentially creates more instability.

YES (a) (c) (d). NO (b). I agree with the proposal's justification for splitting *Accipiter* and agree that the best course of action is to retain *poliogaster* in *Accipiter* until we have more confidence on its phylogenetic position.

YES (a) (c) (d). NO (b). I agree with the proposal, with a combination of enough molecular data.

YES (a) (c) (d). NO (b). I can well appreciate that *Dinospiza* may not belong in *Accipiter* and would be in-line with other split-offs from this genus, but I'd like more data and am uneasy about erecting new genera unless the case is pretty solid. I could go either way on that.

2025-C-2
Treat *Larus smithsonianus*, *L. vegae*, and *L. mongolicus* as separate species from Herring Gull *L. argentatus*

Option A: 4-way split - *L. smithsonianus, L. vegae, L. argentatus, L. mongolicus*
Option B: 3-way split - *L. smithsonianus, L. vegae* (with subspecies *mongolicus*), *L. argentatus* (with subspecies *argenteus*),
Option C: 3-way split - *L. smithsonianus, L. vegae, L. argentatus* (with subspecies *argenteus); mongolicus* not addressed
Option D: 2-way split - *L. smithsonianus* (with subspecies *smithsonianus*, *vegae*, *mongolicus*), *L. argentatus* (with subspecies *argentatus, argenteus*)
Option E: No change - *L. argentatus* (with subspecies *smithsonianus*, *vegae*, *mongolicus*)

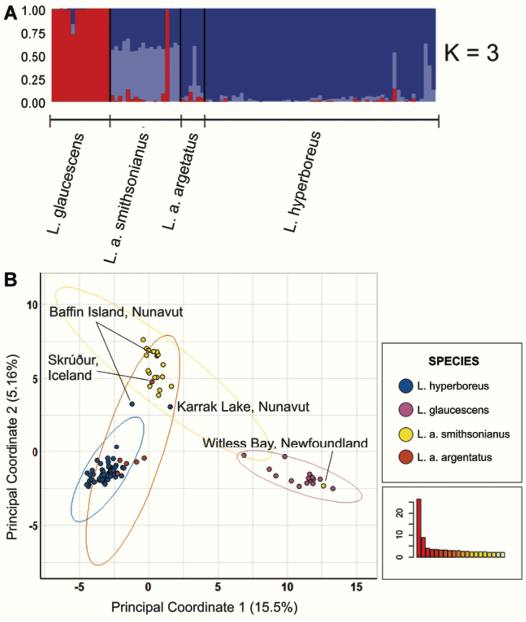
YES (Option A). It is clear from different lines of evidence that *smithsonianus* and *argentatus/argenteus* should be treated as separate species. Regarding *vegae* and *mongolicus*, my inclination is to follow the recommendation of the proposal which also puts NACC in line with other global taxonomic authorities.

YES (Option A). I was happy with the four-way split in the last version of the proposal, and the qualitative vocal data further support that treatment. I do have two minor concerns, though. One, it does seem that the breeding ranges of *vegae* and *mongolicus* approach one another, and data from this region seem critical. Second, the data in Cerny and Natale have very low support in this part of the tree, especially in the molecular-only tree (see previous versions of the shorebird genus revision proposals for the tree), so I do not trust their claim of non-monophy for the Herring group.

YES (Option A). Ecological, vocal, and phenotypic evidence support 4-way split; I was fine with a 4-way split after reading the addendum in last year's proposal.

YES (Option A). No other option accounts for the genetic, morphological, and vocal differentiation in this group, and I think certainly it is not feasible to keep *mongolicus* within *vegae*, given the vocal divergence. Also note that *mongolicus* vocalizations are too different from those of *cachinnans* for a lump of those two to be a reasonable alternative.

YES (Option A). Reasons are outlined in the proposal. All *Larus* species are contentious and messy, but the evidence for separating the herring gulls seems about as strong as any other large white-headed gull.



YES (Option E). If we're operating under a biological species concept, I'd argue that *Larus* is perhaps oversplit, given how much gene flow occurs among lineages with very shallow divergence. The vertical line in the time-calibrated phylogeny from Černý and Natale (2022) shown in the proposal corresponds to the Pleistocene / Pleiocene boundary ~2.6 Mya, so the crown age for the four *Larus* groups in question is maybe half of that (if I'm eyeballing it) or ~1.25 Mya? That's quite recent. Combine that with the mess of a mtDNA haplotype network in Figure 2, and it's clear that many species lack monophyly due to some combination of introgression and ILS. Also, the Linklater (2021) thesis was published later as Linklater et al. (2024), I've included their most relevant figure here. To me, *L. a. smithsonianus* and *L. a. argentatus* are not clearly distinct population assignments: all of the *L. a. smithsonianus* individuals sampled here have some ancestry (roughly r = 0.4?) attributed to the Eastern Hemisphere *L. a. argetatus* / *L. hyperboreus* cluster. One out of five of the *L. a. argetatus* individuals included in this study look very similar to the *L. a. smithonianus* barplots as well. More generally, I don't think that population-level clustering itself is strong evidence for reproductive isolation and species delimitation. Depending on the spatial scale and vagility of the system in question, we can use whole-genomes or similar 1000's of SNPs data sets to find population-level clustering in many groups that I think we'd all agree are a single species. I disagree with the assertion in the proposal that "Linklater (2021), who both used multilocus datasets that continued to show that *smithsonianus* and *argentatus/argenteus* were not particularly closely related". Contrastingly, much of their clustering algorithm output, like the Evanno method, favored these as the same cluster. I'm also not sure I follow the statement "Sonsthagen et al. (2016), who also included nuclear intron and microsatellite data, found that *vegae* instead grouped with Caspian Gull (*L. cachinnans*), whereas *smithsonianus* grouped with California Gull (*L. californicus*)." In looking at Sonsthagen et al. (2016), I see *smithsonianus* falls out in three different parts of the mtDNA phylogeny shown in Fig. 7 of that paper. One of those (USNM 641400) falls out with *californicus*, but the others cluster with other taxa in the *Larus sp*. complex. In general, these species of large white-headed gulls are operating much more as networks of populations than distinct evolutionary lineages. I would say all of these taxa are *very* closely related and exhibit recent, if not ongoing, hybridization and introgression. If we are arguing that genetic diagnosability equals species status, then I don't think we're operating under the BSC any more? This is probably a protest vote as much as anything, but I don't think that more fine-scale splitting of this complex approaches a more accurate species-level taxonomy under a biological species concept.

Regarding phenotypic differences, the authors of the proposal state: "Adult *smithsonianus* and *argentatus/argenteus* are extremely similar and in many cases seem impossible to separate, with differences being subtle and not diagnostic." There are some differences in juvenile plumages and I don't doubt the existence of cryptic species complexes in nature, but these are very similar looking and don't tip the scales on the genetic data we have.

This is a complex and confusing system for sure, but to me *smithosnianus* and *argentatus* don't seem like separate species unless we start invoking criteria from other species concepts. For the record, I'm fine doing that, we should just strive for consistency.

Lachance Linklater, E., S. A. Sonsthagen, G. J. Robertson, L. Colston-Nepali, F. Vigfúsdóttir, and V. L. Friesen (2024). Reduced representation sequencing reveals weak genetic differentiation between Canadian and European Larus hyperboreus (Glaucous Gull). Ornithological Applications 126:duae037.

YES (Option A). The evidence is enough to recognize the four species.

Yes (Option C). This is a well-crafted motion, but the subject is a mess. A few side comments from the proposal. "Taimyr Gull" makes me cringe as to what is a Taimyr Gull? It's a region where many taxa come together and we don't know well what they do! The subspecies *birulai*, I believe, is merged into *vegae* by some (many?). I noted this in comments before but the range of *mongolicus* extends well to the west of Lake Baikal, by perhaps roughly 750 miles to the Altai region of Russia and proximal (roughly 200 miles, maybe less) to northeast Kazakhstan where all breeders are said to be *cachinnans.* Shouldn't lakes with breeding gulls in northeast Kazakhstan and the southwest Altai be studied? I asked Lars Jonsson, a Laraphile for sure, especially on Herring Gulls. He's traveled widely in Russia and the "stans" in the former Soviet Union studying them. He was ambivalent about whether *cachinnans* and *mongolicus* should be treated as separate species. I agree that *mongolicus* should not be with *vegae* but I don't see why we even have to go beyond saying that *mongolicus* is not with *vegae* and we leave it to Old World authorities to sort out the taxonomic relationships between *mongolicus* and *cachinnans.* I thought another committee member opined that their calls were similar but apparently differences were heard. It calls for more studies needed.

One thing about *vegae* is that Brina Kessel in her Seward Peninsula book (I believe 1989) talks about habitat differences in nesting between *smithsonianus* and *vegae,* the latter nesting on cliffs, or at least that cliffs are included as nesting locations. I asked Paul Lehman where they nested on St. Lawrence Island and he didn't know, other than well away from Gambell. He mentioned a few locations where he thought they nested, one of which did not have cliffs.

Another committee member opines that *mongolicus* will likely occur in North America. It might, but who will recognize it, particularly the adults which are not identifiable based on our current understanding and only a few in Japan have the courage to identify first cycle birds? By the time one is identified, hopefully collected, we are likely to have more information regarding the relationship between *mongolicus* and *cachinnans.*

Beyond these four-year gull problems there is still the matter of Lesser Black-backed Gull to sort out, including *heuglini, taimyrensis* and *barabensis*. I hear plenty of complaints about the lumping of *L. thayeri.*

2025-C-3

Treat Warbling Vireo *Vireo gilvus* as two species

YES. Different lines of evidence from multiple independent studies support species-level status for Eastern and Western Warbling Vireos: genetics, morphology, song, molt, migration, ecology, response to brood parasitism, relatively low levels of hybridization and cytonuclear discordance across a large area, and occupancy of adjacent territories by the two taxa where they contact (at least in Alberta). Regarding English names, we should go with what's already in the literature and I think that the hyphenated version (Eastern Warbling-Vireo and Western Warbling-Vireo) fit our English name guidelines. However, I'm open to other suggestions and thoughts.

YES. Multiple lines of evidence from a variety of characters: genetics, molt, behavior, song, etc. supporting species level differences between the two forms. Studies of contact zone show steep cline indicating selection against hybrids.

YES. Great proposal, summarizing an amazing amount of published work that all points to the same conclusion. If these are not species, then neither are quite a few other taxa long or even always considered as such. (As an aside, in the mountains of BC last summer I didn't even recognize Warbling Vireo song, despite hearing it almost every day in willows in Michigan.) And I agree with the hyphenated versions of the English names: Eastern Warbling-Vireo and Western Warbling-Vireo. I doubt that better or more appealing names for these relatively featureless species are out there somewhere.

YES. This is a fascinating system, but it fits a pattern of many other eastern and western taxa that hybridize in either the Great Plains or along the Front Range of the Rockies. This particular hybrid zone seems rather narrow compared to other similar zones, with very strong evidence for either selection against hybrids or assortative mating. The patterns of molt migration provide a strong mechanism for selection. I'm especially surprised by how few hybrids were identified in Lovell et al. (2021). I have no strong preference for whether we use a hyphenated or un-hyphenated name for the species, but agree that just "Eastern" and "Western" modifiers on Warbling Vireo are likely the best approach here (however uninspired it is).

YES. The eastern and western lineages are similar phenotypically, but quantitative phenotypic data on morphology, song, habitat, and plumage reveal geographically cohesive differences. Hybrid individuals have been documented, but seem rare in the hybrid zones studied thus far. Divergence between the two parental lineages is pronounced. I would vote for the unhyphenated version of Western Warbling Vireo and Eastern Warbling Vireo since compound nouns involving gerunds are not typically hyphenated in the English language (i.e., washing machine).

YES. I agree with the proposal, enough evidence to recognize two species. Eastern Warbling Vireo for *V. gilvus* and Western Warbling Vireo for *V. swansoni*

YES. A suite of morphometric, vocal, and genetic characters all point to a narrow hybrid zone with selection against hybrids, likely with post-zygotic reproductive isolation. The vocal data are also a convincing pre-zygotic isolating mechanism, and even though the DFA from Lovell (2010) didn't perfectly classify all songs, the PCA does not appear to show any intermediate songs at the contact zone. I'm convinced by the mention of the two taxa having adjacent territories, which suggests that there are pure birds (or mostly so) even within the contact zone, which is better evidence of species rank than for many hybridizing species that we've been splitting recently.

Although it's a very low sample size and far from the contact zone, I have done some playback trials on western birds in New Mexico and those birds showed no response whatsoever to eastern song. However, I have also done a few playback trials on the eastern birds in Michigan and those do respond strongly to western song. Not sure how to interpret that for species limits.

As for English common names, I am in favor of the un-hyphenated version (Eastern Warbling Vireo and Western Warbling Vireo). Although we typically use hyphens to denote monophyly, there is no potential confusion with the first two words being associated (e.g., "Eastern-Warbling"), so the dash seems unnecessary.

YES. The Alberta BBA published in 1992 outlined the issues well. Edmonton is the main point of contact between the two groups. To my ear the songs of the two groups sound pretty similar. I doubt I would pick out an Eastern Warbling-Vireo by song in the West and visually the main difference is size, again problematic for an identification even though the size difference is considerable. Western birds are more like Philadelphia Vireos in size. Living in Ohio for eight years, yes indeed Eastern Warbling-Vireos molt and leave being mostly gone by late August. In California, Western Warbling-Vireo is a common migrant in many parts into the middle of October.

2025-C-4

Treat *Riparia diluta* as a separate species from Bank Swallow *R. riparia*

YES. This split is clearly overdue given the breeding information along with genetic and morphological differences. I agree with retaining Bank Swallow for *R. riparia* and adopting Pale Martin for *R. diluta* in keeping with eBird/Clements and IOC.

YES. Sympatric in mixed breeding colonies is about the clearest evidence we could ask for. Bank Swallow is extremely well-established for *riparia*, at least in the Americas, so there is no reason to change it. For, *diluta*, I am happy to go with what most regional/global authorities choose, which so far seems to be Pale Martin. Having these sister taxa be called “Martin” and “Swallow” is unfortunate, but Bank Swallow is the outlier in this genus, not Pale Martin.

YES. The two species occur in sympatry without interbreeding. Additional evidence from genetics and morphology support species status. Recognizing *R. diluta* would also align us with all global checklists.

YES. Long recognized elsewhere based on unambiguous evidence. The English names issue is a long-standing North American vs. everyone else problem without an easy solution. (Fortunately, eBird etc. allow people to use the name of their choice, e.g. Sand Martin in the Old World.) Keep the English name Bank Swallow for *R. riparia* and adopt the English name Pale Martin for *R. diluta.*

YES. Reasons are outlined in the proposal. Retaining Bank Swallow for *riparia* and adopting Pale Martin for *diluta* seems to be the best approach for English names.

YES. I agree with the proposal, there is no breeding between them and the differences in plumage and genetics support the split.

YES. Interesting system, the nesting site data was cool to see. These two overlap in sympatry with no indication of interbreeding, and they also differ in various phenotypic characters. Best treated as two separate species.

YES. An easy call given widespread breeding sympatric breeding with no hybridization. As for English names, Bank Swallow is well established in the Americas, and changing the name to martins would make folks think of the much larger *Progne.*

2025-C-5
Transfer Fan-tailed Warbler *Basileuterus lachrymosus* to *Euthlypis*

YES. I agree with transferring *Basileuterus lachrymosus* back to *Euthlypis* on the basis of strong support in the UCE tree along with other distinctive traits as noted in the proposal.

YES. The UCE data are clear that *lachrymosus* is not part of *Basileuterus*, and the monotypic genus *Euthlypis* is required. This change is backed up by its distinctive morphology.

YES. Change back to *Euthlypis* is required by its new position in the phylogeny based on better data. It is also supported by taxon uniqueness as well (behavior, morphology, foraging ecology).

YES. Reasons are summarized in the proposal; this seems essentially mandatory.

YES. Reasons are outlined in the proposal; this is a necessary change.

YES. I agree with the proposal.

YES. This makes sense in light of the new UCE phylogeny.

YES. I can’t remember how I voted on this previously, but I’ve not seen any warbler act quite like this one, so am pleased to see it back in its own monotypic genus.

2025-C-6
Treat Black-crested Titmouse *Baeolophus atricristatus* and Tufted Titmouse *B. bicolor* as a single species

YES. Reasons are in the proposal. These seem to freely hybridize where they meet with little to no selection against hybrids and good evidence based on robust genomic analysis of introgression, backcrossing, F2s and other advanced generation hybrids. If Northern Flicker and Yellow-rumped Warbler are treated as a single species under our taxonomy, I would argue these should be too. Otherwise, we should reevaluate the criteria we are using to make these decisions if consistency is a shared goal.

YES. Reasons are given in the proposal.

YES. Great summary of the issues. I am reminded of the situation in Yellow-rumped Warblers, which don't hybridize much but are nothing but hybrids in those narrow zones where they meet in northwest Canada. As such I have voted consistently not to re-split those two warblers. With these two titmice at least hybrids can be recognized, but without specimens and tissue there is no way that a hybrid Juniper x Oak Titmouse would be recognized. The material about the narrower hybrid zone in Oklahoma was fascinating. It does make me uneasy to go back and forth on this, so on a certain level I feel that the status quo is best until the case becomes perhaps more overwhelming. Or, in other words, if we knew what we know now, I doubt that we would have re-split the taxa.

NO. I have a few concerns here. The primary one is that this hybrid zone is still extremely narrow in the grand scheme of the distributions of these two taxa, and that hybrid zone is apparently fairly stable. I would like to know how this neutral diffusion dynamic compares with that of other major avian hybrid zones that have been studied recently, especially in our case, the main ones of the Great Plains like Baltimore/Bullock's Oriole, Black-headed/Rose-breasted Grosbeaks, and Indigo/Lazuli Buntings. My qualitative understanding is that those hybrid zones, all of which we consider species, are considerably wider and more diffuse than what we see here, thus indicating less selection against hybrids. More relevant are likely the various taxa that are in contact in Alberta, such as the vireos we are considering in this same batch, or Winter/Pacific Wrens, Townsend's/Black-throated Green Warblers, the sapsuckers, etc. Those are in contact at a major ecotone, like with these titmice. Certainly, in cases like the sapsuckers, the hybrids are far more prevalent than in these titmice, and the hybrid zone is much wider.

I especially want to see comparisons with the Juniper/Oak Titmouse hybrid zone. In my view, those are much more similar in plumage than in Black-crested/Tufted and are about equally divergent in song. If we consider Black-crested and Tufted as conspecific, then we should probably revisit Oak and Juniper. I do also worry that we would be reversing a fairly recent decision, so for the sake of not flip-flopping, I think whatever change we make with the newer data should be rock-solid. I do appreciate the comments by other committee members below, especially those regarding the estimates of dispersal distance. If those dispersal estimates are off, that completely changes the picture regarding neutral diffusion vs. selection against hybrids.

In short, I do agree that the available genetic data point toward these being one species, but I would like to see more comparisons with other well-studied hybrid zones and also revisit the data that was considered during the initial split.

NO. Great proposal, and great work underlying it. Yes, they hybridize extensively within the relatively narrow hybrid zone (at least compared to that of some other taxa), and there is no evidence for selection against hybrids. But the pure parental phenotypes exist over much larger areas, in which they are considered to differ vocally from each other as well. Of course, these differences could be interpreted, perhaps validly, as dialects, but it seems that further study is needed of that aspect. And, if these titmice are considered conspecific, then for consistency we should consider all other taxa with similar-width hybrid zones that show a similar lack of selection against hybrids as conspecific. This would entail a massive shift both in our region and globally, one that would meet a lot of resistance. Perhaps further study will cement the issue, so I vote to wait and see.

NO. This is a really tricky case and is definitely a borderline situation. However, right now, I am swayed by the still relatively narrow hybrid zone, which, despite showing evidence of neutral diffusion (more discussion of this later), has still stayed relatively stable over time (for the old transect). Hybrid zone widths for the titmouse hybrid zone are similar to calculated cline widths for the Baltimore x Bullock's Oriole hybrid zone (121 km), and either equivalent or wider than different transects of the Red-naped x Red-breasted Sapsucker hybrid zone (clines vary in width from 20 km wide to 138 km wide). I also am skeptical of the dispersal distance used (only 0.248 km), which seems especially small for a North American passerine; for example, another paper estimated the median dispersal distance for Tufted Titmouse as 75 km (Tittler et al. 2009). If even a modestly higher dispersal distance were used in place of 0.248, then our conclusions about this being a tension zone versus an area of neutral diffusion would be very different.

While I am a little concerned about the extent of hybridization within the zone, and the apparent "hybrid swarm," I think it is also important to consider that this hybrid zone occurs along an ecotone, and so in this case, hybrids may in fact have higher fitness within the narrow ecotone, resulting in extensive admixture, but outside of this ecotone, hybrids may be selected against, perhaps helping to explain the relative narrowness of the zone. Indeed, admixture is rather uniform at three sites in the center of the old transect, but these sites are also represented by relatively few individuals.

NO. This is a relatively narrow hybrid zone, in an ecotone, of two widespread taxa. Vocal differences are present. The comments on this one make a good point that we should think consistently about different hybridizing taxa; more discussion is probably warranted, or perhaps a comparative, simultaneous reassessment of multiple hybridizing taxa.

NO. I've gone back and forth on this one, and for now I'm inclined to continue recognizing these taxa as species for reasons given by others. The contact zone is narrow and in a sharp ecological transition, with clear vocal, phenotypic, and genetic differences between pure Black-crested and Tufted over a much broader area. I am curious about the density of individuals within the contact zone versus outside of it. In the Oak-Juniper titmouse contact zone, birds occur at a much lower density than outside of the zone - suggesting that the area of contact, which also occurs in a sharp ecological/bioclimatic transition, is less suitable. It is interesting that there are no pure parentals in the contact zone and no hybrids outside of the zone, which suggests (as noted by another committee member) that hybrids have higher fitness in the narrow transitional area but are selected against outside of the contact zone.

NO. The two species show differences in plumage, particularly in the color and size of the forehead and the crest, and song. There are relatively narrow contact zones with intermediate phenotypes that are restricted to hybrid zones. The hybrid zones are located in ecotones, therefore, environmental selection against hybrids is suggested. The two species are recently diverged (~250,000 years ago), so small differences between them are expected. Absence of parental and F1 hybrids in the contact zones. I would like to know more about the breeding behavior of the two species and the hybrids. Also, how does the width of the ecotone in the old hybrid zone relate to the width of the ecotone in the new hybrid zone? Does the ecotone match the width of the hybrid zones?

2025-C-7
Transfer Alpine Swift *Apus melba* to *Tachymarptis*

YES. The molecular and vocal data, along with differences in feather lice and nestling foot structure, support this change. This also puts NACC in line with other global taxonomic checklists for a species that is a rare vagrant to our data.

YES. This aligns us with global checklists for this largely extralimital group, despite this change being unnecessary. I would like to know what exactly is different about the foot morphology, as this is often used as a genus-level trait in swifts, but I'll trust that there are differences. I do not, though, think that the vocal differences are very great. Some of the smaller species of *Apus* that I'm familiar with, such as *nipalensis* and *affinis,* have trilled calls not very different structurally from those of *melba*. Also, in listening to some calls of *aequatorialis*, those seem fairly similar to those of some of the larger dark *Apus* (the *A. apus* clade). The genetic p-distances are also not that huge. Regardless, the huge size and the foot structure give us something to justify the change.

YES. This puts us in alignment with other global lists. However, I'm not completely convinced the change is necessary, as *Apus* + *Tachymarptis* is monophyletic. The support for relevant nodes justifying the split is ok, but not great.

YES. This is quite a deeply diverged clade, and in addition it does exhibit multiple distinctive phenotypic characteristics. I don't see a good rationale for retaining it within *Apus*.

YES. While I find this change completely unnecessary, I will vote in favor to ensure that we align with global checklists for a species that is only a vagrant to our region.

YES. I agree to align us with global checklists and there are some data supporting this change.

YES. I agree with others that this change seems somewhat superfluous given that these genera are already monophyletic, but I am inclined to follow other global authorities for this largely extralimital taxon.

YES. Reasons are presented in the proposal.

2025-C-8

Treat Red-crowned Ant-Tanager *Habia rubica* as six or seven species: (a) Separate *H. rubica* into more than one species; (b) If YES on part A, specify 6 spp., 7 spp., or some other number of species

POSTPONED

2025-C-9
Treat Gray-crowned Goldfinch *Carduelis caniceps* as a separate species from European Goldfinch *C. carduelis*

YES. Given that these taxa are mostly extralimital, I vote in favor of this split for conformance with the WGAC. This treatment appears to be supported by plumage and vocal differences as well as what appears to be a low incidence of hybridization and the presence of both groups during the breeding season close together in one region of Siberia. Regarding English names, I am fine with Gray-crowned Goldfinch and European Goldfinch.

YES. I vote in favor of following regional and global authorities. Hybridization appears to be less common than previously thought.

YES. My vote is mainly based on conforming with global lists for this extralimital taxa. The genetic data that are available are unconvincing. Evidence of vocal differences is helpful, as is the online search for hybrids which proved to be scarce.

YES. I support this based on the differing vocalizations and widely distributed pure phenotypes in contrast with a seemingly narrow (but understudied) hybrid zone.

YES. I vote in favor for reasons outlined in the proposal and to follow global authorities for a bird that does not occur in our region.

YES. Reasons are given in the proposal.

YES. Reasons are discussed in the proposal.

YES. The split aligns NACC with global checklists, considering these mostly extralimital taxa. English names: Gray-crowned Goldfinch and European Goldfinch.

YES. I vote in favor mainly for alignment with other global checklists and the helpful analysis of different songs and limited interbreeding. Yes to the proposed English names.

2025-C-10
Transfer Yellow-breasted Chat (*Icteria virens*) from Icteriidae to Icteridae

YES. I have been a proponent of including Yellow-breasted Chat as part of Icteridae for a while now. I'm not as concerned about the lack of inclusion of *Teretistris* in the Oliveros et al. (2019) tree, given the strong support of the placement of *Icteria* with the rest of Icteridae. This is also where my personal philosophy on bird families comes in again; I much prefer fewer larger families where possible, versus more monotypic families that don't tell us anything meaningful about relationships. While an odd addition to Icteridae, I think Yellow-breasted Chat still fits in there okay, as there is a reasonable diversity in that family already, plus the apparent Yellow-breasted Chat x oriole hybrid from California also lends further support for including it in Icteridae. Further, the feather mites found on Yellow-breasted Chat are more closely related to those of other Icteridae than to other groups (Matthews et al. 2018).

NO. I agree with the proposal that it's best to wait and see if additional data provide unequivocal support for moving *Icteria virens* into the Icteridae. The lack of sampling of *Teretistris* in the UCE tree is especially problematic. *Icteria virens* is behaviorally and phenotypically distinct, and is best kept in its monotypic family for now.

NO. This poor bird has been bounced around to so many different families that I prefer to wait until we have absolutely conclusive data on its phylogenetic relationships before making yet another change. Even then, I would not be surprised if a monotypic family is the best place for this bird, given its unique morphology.

NO. Interesting, and the putative hybrid is astounding! But we'd better await more solid phylogenetic evidence before making such a move.

NO. I prefer to wait until new data.

NO. I agree with the proposal that there is still extensive uncertainty in the phylogenetic relationships of the Yellow-breasted Chat. I would prefer we retain the current classification.

NO. I agree with the proposal - better to wait for more complete analyses before we move this bird yet again. Even if it does turn out to be sister to Icteridae, differences might still warrant continuing to place it in its own family.

NO. Certainly a species with unique characteristics and difficult to classify. I agree that until conclusive information is published, we should wait and keep it in its own family.

NO. I have come to believe that having this species in its own monotypic family is best until a solid case can be made for moving it. The case for hybridization was with a Bullock's Oriole in California, and a paper with color photos was published in Western Birds.

2025-C-11

Merge Nesospingidae and Spindalidae into an expanded Phaenicophilidae

YES. I have long felt that this radiation was over-split at the family level. Although it is a phenotypically heterogeneous group, I think the amount of variation fits within that of other nine-primaried oscine families. Also, if we apply a temporal banding approach, the crown age of the expanded Phaenicophilidae approximately matches that of other families like Passerellidae and Thraupidae, based on the Oliveros tree. As an alternative, I think a two-family treatment is also an option here, with the larger-bodied, more canopy-dwelling, short-tailed, and rounder Spindalidae and Nesospingidae in one family and the remaining longer-tailed, more slender species in Phaenicophilidae (i.e., the current Phaenicophilidae).

With the revised voting structure to include subfamilies, I lean strongly towards subfamily rank for each of the current families, including both Spindalidae and Nesospingidae. Yes, they are already in separate genera, but the subfamily rank would highlight that these are deeply diverged taxa. Their close relationship is already apparent, based on them now being in the same species-poor family. Also, Nesospingidae is currently treated as an island-endemic family, and under this revised classification, we wouldn't even be recognizing it at the subfamily level. It really is a unique bird, and demoting it by two ranks (down to "just" a genus-level endemic) would need to be well justified, which it is not.

YES. I vote in favor but this could reasonably go other ways too. I think that morphologically they can all be included comfortably in a single family (just look at the diversity within, for example, Icteridae!), and it makes biogeographic sense too. But the lineages are ancient, and two separate families also would be reasonable (my 2nd choice), while maintaining the three families currently recognized is also tenable but least preferable to me.

I agree with the comment endorsing two subfamilies, which sums up the rationale for two vs. three subfamilies best. Key for me is the sister taxon relationship between Nesospingus and Spindalis. But given the age of the divergence, either two or three subfamilies is reasonable.

YES. I am very happy to merge these Caribbean families together, as I agree they were oversplit to begin with. Given that these groups are an entirely Caribbean radiation, it makes merging them even easier in my mind. While they initially seem different, they really are no more different from each other than many other members of other long-recognized songbird families.

For subfamilies, I think I actually favor treating each of the former families as their own subfamily. I can see the merits of both, but given that until now we were treating these as separate families, I think it is appropriate to recognize each as a separate subfamily. But, I do not have very strong feelings on this, and would also be fine with recognizing only two subfamilies, with *Spindalis* and *Nesospingus* together.

YES. I don't have strong feelings on this and could go either way, but I'm inclined to follow the recommendation's proposal which recognizes this endemic Caribbean radiation as a single family. If we are to recognize subfamilies, then I slightly favor the two subfamily treatment option (one subfamily for *Nesospingus* and *Spindalis* and another for *Phaenicohilus*, *Xenoligea*, and *Microligea*).

YES. The data support placing the endemic Caribbean radiation into a single family. I vote for two subfamilies.

YES. I tend to lean more towards having families with multiple taxa to emphasize shared evolutionary histories than monotypic taxa to emphasize uniqueness. I agree with the proposal's recommendation to treat these as a single, Carribean-endemic family, Phaenicophilidae and vote for three subfamilies.

YES. I went back and forth on this one, but in the end I think recognizing them as a single family is a better option because it would illustrate monophyly and emphasize that this is a previously unappreciated Caribbean radiation. For subfamilies, I think these two subfamilies are the best option: Phaenicophilinae for *Phaenicohilus*, *Xenoligea*, and *Microligea* and a second subfamily for *Nesospingus* and *Spindalis*. To me, this is preferred to separate subfamilies for *Nesospingus* and *Spindalis* since each of those are already in separate genera and making a single subfamily for the two together emphasizes their sister taxon relationship.

YES. Endemic family of the Caribbean. I support recognizing two subfamilies, Nesospinginae/Spindalinae and Phaenicophilinae; as mentioned in the previous comment, having *Nesospingus* and *Spindalis* together in the same subfamily recognizes their close relationship.

NO. These are just too diverse for me in appearance, structure, behavior, etc. for me to feel comfortable accepting these in one family. I suppose subfamilies is better than not having them in subfamilies but it's kind of a fall back, better than subgenus and more accepted as a term. For some of these species, I just see nothing in common with others, but I suppose one could say the same about the family Parulidae.

2025-C-12

Treat *Turdus daguae* as a species separate from White-throated Thrush *T. assimilis*

YES. I am in favor for all the reasons in the proposal. I prefer Dagua Thrush over Choco for *daguae*, and support retaining White-throated for the widespread *assimilis*.

YES. I agree with the proposal that the combination of genetic, phenotypic, and vocal differences support splitting *daguae* as a separate species. This treatment also puts NACC in line with WGAC. I like Dagua Thrush and favor retaining White-throated Thrush for *assimilis* (assuming that SACC agrees with the split and these names).

YES. I voted a “reluctant yes” on this split when presented in proposal 2022-A-04. The additional discussion presented in this version of the proposal reinforces my decision. I favor Dagua Thrush over Choco Thrush.

YES. Excellent proposal! The evidence all seems to point to species status for *daguae*, and I'd think with such a different song it cannot be retained within *assimilis*. Dagua Thrush is a nice, appropriate name that is already quite familiar, and of course changing White-throated Thrush would be unnecessary and unwarranted.

YES. The reassessment of the genetic and vocal data is particularly compelling, and certainly suggests that *daguae* is not part of *Turdus assimilis*. I also agree with adopting Dagua Thrush for *daguae*, and retaining White-throated Thrush for *assimilis*.

YES. I agree with the proposal (elevate *daguae* to species rank and adopt the name Dagua Thrush.

YES. Phenotypic and genetic data sets together support recognizing the species status of *daguae*, and I agree with the proposed English names.

YES. Multiple lines of evidence (plumage coloration, morphometrics, genetics, vocalizations) support splitting *Turdus daguae* from *T. assimilis*. English names: Dagua Thrush for *T. daguae* and White-throated Thrush for *T. assimilis*.

YES. I supported the split before and do so now based mainly on vocal differences. Dagua Thrush is just fine for the English name, as is retaining White-throated Thrush.

2025-C-13

Revise the classification of the Columbidae: (a) Revise the linear sequence; (b) Recognize subfamilies

YES. An excellent proposal. The updated linear sequence appears to be correct based on my reading of the trees and species richness for each clade. Regarding (b), five subfamilies should be recognized, not four (Columbinae, Claravinae, Starnoenadinae, Raphinae, and Treroninae). If the former four are recognized, which I agree they should, then Treroninae should also be recognized as it is an older group than the combined Columbinae + Claravinae + Starnoenadinae. It is entirely extralimital, however (contra the proposal); *Geopelia striata* is part of Raphinae *sensu stricto*. I could see an argument, though, for maintaining *Starnoenas* within the Columbinae, as the overall morphology is clearly quail-dove-like, but the osteological differences highlighted by Olson and Wiley tip me towards recognizing it as a distinct subfamily.

YES. I vote in favor of the recommendations for reasons given in the proposal.

YES. The proposed change to linear sequence is required based on new analyses. I agree with recognizing these subfamilies as well as Treroninae as recommended by another committee member. However, I'm not sure if doing that would change the proposed linear sequence.

YES. I vote for all.

YES. I vote for recognizing five subfamilies, including Treroninae, as mentioned above by others.

YES. Reasons are outlined in the proposal.

YES. Reasons are mentioned in the proposal.

YES. I agree with the reasons in the proposal.

YES. I vote for revising the linear sequence and recognizing subfamilies.

2025-C-14

Treat *Piaya mexicana* and *P.* "*circe"* as separate species from Squirrel Cuckoo *P. cayana*: (a) treat *P. mexicana* as a separate species

YES. Reasons are given in the proposal. I agree to adopting the names Mexican Squirrel-Cuckoo for *mexicana* and Common Squirrel-Cuckoo for *cayana*.

YES. Multiple lines of evidence as given in the proposal supports treating *mexicana* as a separate species, and this change also puts NACC in line with WGAC. Adopt the names Mexican Squirrel-Cuckoo for *P. mexicana* and Common Squirrel-Cuckoo for *P. cayana*.

YES. I voted for this split in proposal 2024-A-9 and that decision is reinforced by the vocal analyses presented here. Together with other data (narrow contact zone, genetics, morphology), there is enough evidence for a split. I agree with the proposed English names.

YES. I think this change is clearly supported by multiple lines of evidence, not least the new vocal information. I agree to the proposed English names.

YES. I vote in favor, although not strongly. I agree with the proposed English names.

YES. I agree with the line of reasoning presented in the proposal. I am good with the proposed English names.

YES. Genetics, morphology, and vocalizations support treating *Piaya mexicana* as a separate species from *P. cayana*. I agree with the proposed English names: Mexican Squirrel-Cuckoo for *P. mexicana* and Common Squirrel-Cuckoo for *P. cayana*.

YES. This is supported by morphology and vocalizations. I am fine with the proposed English names.

YES. Glad we have better evidence on the vocalizations. I agree with the proposed English names, even though the two species are widespread in Mexico - East and West (includes south too).

Treat *Piaya mexicana* and *P.* "*circe"* as separate species from Squirrel Cuckoo *P. cayana*: (b) Treat *P.* "*circe"* as a separate species

NO. This is a primarily South American issue and should be adopted first by that committee, along with a first reviser action. I also want to see better data from the contact zone between *cayana* and the "*circe*" group.

NO. Wait to see what SACC does.

NO. It's probably best to defer to SACC at this point.

NO. I vote reluctantly against this, not because I don't think there are at least two species in South America but because it's more complicated. Any vocal differences from *thermophila* do not stand out to me (except, as a matter of degree, the cackle), as they do for *mexicana*. I agree that the first reviser issue could probably technically be dealt with in the Supplement, although I can't think of another such case in which the Supplement made such nomenclatural changes that haven't been published elsewhere and I'm not sure that establishing such a precedent is the best idea (but maybe it is!). Even without the first reviser issue, which perhaps need not stand in the way of a split, the overall situation in South America is too complex to comfortably deal with here. Hopefully SACC will take it on soon.

NO. I agree this issue should be addressed first by SACC, as there do seem to be a lot of complicating factors here that need to be addressed.

NO. Defer to SACC first.

NO. We should wait for SACC to assess this split.

NO. I recommend waiting for the SACC comments.

NO. Leave that to SACC.