2024-A-1
Reconsider the generic placements of *Haplospiza rustica* and *Acanthidops bairdi*

NO (Option 4). For all the cogent reasons outlined in detail in the proposal, leave everything as is until we have additional genetic data to confirm the topology of the tree. These are the kind of things best mentioned in footnotes until additional data require a change that might cause major instability in nomenclature. I think that combining all these genera in a single genus is the way to go given their genetic and morphological similarities (other than bill shape), but this has to be done in a publication that proposes a replacement name for *Phrygilus unicolor*.

NO (Option 4). Given the uncertainty in the nodes supporting relationships among the taxa in question, I agree with the proposal that it is best to leave the taxonomy as is until we have more information.

NO (Option 4). Maintain *rustica* in *Haplospiza* and *bairdi* in *Acanthidops* until phylogenetic relationships are fully resolved for the clade that includes the genera *Geospizopsis*, *Haplospiza*, and *Acanthidops*.

NO (Option 4). I agree with the proposal, I suggest that we wait for more or different data and a clearer analysis about the relationship between *Haplo*spiza *rustica* and *Acanthidops bairdi*, and among the three genera *Geospizopsis*, *Haplospiza*, and *Acant*hidops.

NO (Option 4). Although this arrangement will likely be incorrect at some point in the future, I would rather wait with the imperfect status quo than to change it now, only to have to change it again soon thereafter. The low support values for parts of the tree, inconsistent results with different analyses, and promise of better results with more genetic data all should make us wait. Three monotypic genera is inconceivable with such closely related taxa.

NO (Option 4). The proposal lays out the arguments for different options and why it makes sense to wait for additional data before changing these generic treatments.

NO (Option 4). As the proposal lays out a very strong argument, this seems to be the least disruptive option for the time being, until the relationships among these 5 species can be clarified. I would strongly prefer to avoid any move that would create additional monotypic genera, especially for species that all seem quite similar. While bill shape is indeed distinct, as the proposal notes, this is something that is very plastic in Thraupidae, and there are several genera in the family that have quite a range of bill shapes and sizes (notably *Geospiza*).

NO (Option 4). I have little familiarity with these species, other than *Acanthidops bairdi*, but I prefer stability until the genetic evidence is more convincing and uniform in agreement as to how to rearrange these similar appearing species.

NO (Option 4). What an interesting puzzle. The discord between limited genetic data (dominated by mtDNA) and morphology causes what seems to be best treated as a yet-unresolved phylogeny with respect to generic limits. I agree that each of the first three options are undesirable and that the best course is to hold the status quo until a more trustworthy understanding of relationships is reconstructed.

NO (Option 4). This seems like the only viable option given the published phylogenetic data. If the unpublished UCE topology holds up, I would favor option 1 with an expanded 3-species *Haplospiza*. *H. unicolor, rustica*, and *bairdi* seem a phenotypically cohesive group, with similar plumage, vocalizations, and bamboo specialization. The different bill morphologies don’t bother me, given the plasticity in this trait within the Thraupidae.

NO (Option 4). Option 3 or 4, probably a preference for 4. My thoughts on the various options:

Option 1: Given the existing data, there isn't justification for this option at this time, since the support for this relationship is so low. The proposal is correct in its dissection of individual gene support for the relationships, given the data in Burns et al. 2014 - there is little published support for the clade containing *unicolor*, *rustica*, and *bairdi*. However, there is an unpublished UCE tree that supports the topology of the Burns et al. 2014 tree (*G. plebejus*, *G. unicolor*)(*H. unicolor* (*A. bairdi*, *S. rusticus*)). But this tree is too preliminary to base a decision on, so I'm not yet going to recommend option 1. But hopefully, we can eventually go with option 1 - three species *Haplospiza*.

Finally, I would never recommend the alternative where there would be the required name change of *unicolor* species - what a nightmare. At the end of the day, I'm more persuaded by stability than making the genera make "sense".

Option 2: I can't remember if we considered putting *rustica* into *Acanthidops* (option 2), but this is not as preferable as option 3 since option 3 has already been proposed and used.

Option 3: This is what is recommended in the Zootaxa paper (Burns et al. 2016) where the generic classification was revised. That paper reverted to *Spodiornis* for consistency with the "rule" of having no genera that didn't have strong support for monophyly, so something had to be done with *Haplospiza*. Looks like Clements/eBird is following this with *Spodiornis* used for Slaty Finch (*rusticus*). This option is fine with me.

Option 4: This option seems the least disruptive, especially given that there will likely be an opportunity to have all three in *Haplospiza* in the future.

2024-A-2

Make changes to our classification of the herons (Ardeidae): (a) Modify the linear sequence and existing taxonomic structure within the family

YES. 1 with no comment.

YES. This looks like the correct linear sequence based on the available phylogenetic data.

YES. This classification is based on topologies that showed up repeatedly.

YES. The revised classification appears to be well-supported by different data sets.

YES. Adopt the new linear sequence and subfamily classification based on Hruska et al. (2023).

YES. A tentative vote in favor.

YES. The Hruska et al. (2023) study is a great advance in our knowledge of relationships in this group.
YES. Yes to the sequence and to the subfamilies, but with some reluctance. In my opinion, until we have a time-calibrated tree of the Ardeidae, maintaining the subfamily

category in the family is based mainly on tradition (as opposed to other families with deep internal divisions for which no subfamilies are designated. We need to have at least a somewhat objective reason for maintaining that category in some families and not others, e.g. rough criteria based on divergence times.

YES. Reasons are stated in the proposal.

YES. Makes sense based on the UCE species tree.

Make changes to our classification of the herons (Ardeidae): (b) Revise the genus-level taxonomy of the bitterns (*Ixobrychus*, *Botaurus*)

YES (Option B). I checked the seven listed synonyms for *Ixobrychus* and none of the type species listed on zoonomen are *exilis* or *involucris*, so it seems like there's no available genus name for *exilis* (if we wanted to transfer it to a monotypic genus). Of the alternatives, I prefer expanding *Botaurus* to include all of *Ixobrychus* for a few reasons: 1) the crown age of an expanded *Botaurus* is roughly comparable to that of other heron genera when accounting for the branch length inflation mentioned by the Hruska study, and 2) it negates the issue of not having sampled the type of *Ixobrychus* in the UCE sampling. Also, for some of the same reasons as I'm voting to merge *Bubulcus* into *Ardea*, I think one of the really cool things that the phylogenetic data from the Hruska study shows is that body size is extremely labile in herons. So, even though an expanded *Botaurus* is highly variable in size, they all essentially do the same thing (marsh skulkers) and the various Old World *Ixobrychus* span the range in size between our large and small New World taxa. I understand the issues with transferring some largely Old World taxa to *Botaurus* when it's not really within our purview, but I am absolutely opposed to the idea of *exilis* being in a different genus than the extremely morphologically similar *sinensis* and *minutus*. I would prefer to leave *exilis* where it is if that is our other option. The mitochondrial data at least does place *minutus* with the rest of the *Ixobrychus*, so we do have some evidence that *minutus* and *exilis* are not sisters. If that were to hold up with genomic data (which I would imagine is not forthcoming), I really can't see any option other than transferring <u>all</u> of *Ixobrychus* to *Botaurus*. If we need to wait until a global checklist such as WGAC votes on this and then re-vote ourselves, that's fine by me.

YES (Option B). I vote for revising the genus-level taxonomy of *Ixobrychus* and *Botaurus*, with a preference for the option of subsuming *Ixobrychus* into a broader *Botaurus*. I originally voted yes to transferring *Ixobrychus exilis* to *Botarus* based on the UCE data, but other committee member arguments swayed me to prefer an expanded *Botaurus*.

YES (Option A). According to the most recent multilocus phylogeny, *Ixobrychus exilis* should be transferred to *Botaurus*. As recommended in the proposal, I think that transferring the species endemic to the Americas is the best option, in addition to being more consistent with the depth of nodes. I agree to re-vote if a global body such as WGAC endorses a different treatment.

Update on 2024-A-2b: Now that WGAC has endorsed merging all *Ixobrychus* into a broader *Botaurus*, I change my vote and support the decision made by global authorities.

YES (Option B). When I look at *Ixobrychus exilis* in specimen trays alongside five other *Ixobrychus* species, it would be a challenge to tell them apart if the labels were covered (i.e., Hruska et al. fig. 3 is no surprise). If *Botaurus* really does encompass this degree of phenotypic variation, it makes more sense to have a broad *Botaurus* that contains it all rather than ignore phenotype and split *exilis* out of *Ixobrychus*. (Unless there are some other traits clearly shared between *exilis* and *Botaurus* that are not present in the rest of *Ixobrychus*.) The node uncertainties here in their fig. 4 also suggest a single-genus treatment for now.

YES (Option B). This one is exasperating because the authors of the paper (including 5 friends) and the reviewers did not even mention the obvious alternative hypothesis, i.e. subsuming *Ixobrychus* in *Botaurus*. In disbelief, I just re-read relevant sections of Hruska et al., an otherwise excellent paper, to confirm that there is no mention of this obvious alternative.

First and foremost, any changes based on this paper should be DOA because the type species of *Ixobrychus* is *minutus* (*Ardea minuta* Linnaeus 1766). But *minutus* was not sampled by Hruska et al. The only mention of *minutus* in the text (as revealed by the *Find* function) is its initial mention as a member of traditional *Ixobrychus* and its inclusion in *Ixobrychus* sensu lato in the classification table. Huang et al. (2016) sampled *minutus* but not *exilis*. Päckert et al. sampled *minutus*, *sinensis*, and *exilis*, but not *dubius*. So, the only data relevant to the relationship between *exilis* and the type species of *Ixobrychus* is Päckert et al.'s mtDNA barcode tree, which indeed found *exilis* as sister to *Botaurus*, not *minutus*. But that same tree placed *cinnamomea* and *eurhythmus* as sister to everything else, including *minutus* and *flavicollis*, the latter sometimes placed in the monotypic genus *Zupetor*.

This absence in the analysis of the type species for the genus should be sufficient grounds for voting NO on the proposal. Proper taxonomic procedure requires assessment of the type species of the genera involved. **How can we revise the limits of *Ixobrychus* without its type species being included in the analysis**? How can we put *exilis* and *minutus* in separate genera based on this paper when one of them was not sampled? Step 1 of any valid taxonomic revision is analysis of the type taxa.

But let's just pretend that *exilis* and *minutus* are not closely related, as suggested by the barcode papers. Then, there would be no question that a change needs to be made in classification given these data. Here's the problem. The four *Ixobrychus* species *exilis*, *minutus*, *dubius*, and *sinensis* are so similar that they have always been considered part of a species complex. Mayr & Short (1970) officially designated them as a superspecies (parapatric replacements of monophyletic lineage). This was followed subsequently by basically all authorities to one degree or another. This is not to say that Mayr & Short didn't make mistakes in their superspecies designations, but they usually got it right (because recently diverged species typically remain morphologically similar and parapatric or allopatric), and in this case no one that I know of familiar with the group would fault them for having made this designation based on their parapatric replacement pattern and similar plumage and morphology, despite Hruska et al.'s possible falsification of it being a monophyletic group.

Note the extreme similarity between our *I. exilis* and the Australian taxon *dubius* (treated as a subspecies of *minutus* or as its own species depending on classification). They are so similar that I suspect without doing some advance studying, all of us would misidentify *dubius* in the field as our familiar *exilis* (and on a just a quick view would likely pass off male *minutus* as *exilis* also). See other comments on the similarities among these taxa from direct field experience and on covering up specimen labels. Note that Hruska et al.'s three sentence discussion of the issue includes no mention of this extreme phenotypic similarity, yet they want to put these remarkably similar taxa in different genera.

I can think of no analogous case in birds. Of course DNA has revealed some big surprises that have violated our world view of the value of plumage as a phylogenetic character. But this is different. *Exilis*, *minutus*, *dubius*, and to some degree *sinensis* are among the most ornamented of herons, with a suite of shared plumage pattern characters not found elsewhere in the group or even the family. If they were a cluster of pattern-less dull birds, then that they weren't each other's closest relatives might just have been hidden by an absence of characters – no big deal. But this is the opposite, at least within heron phenotypes. Add to this their parapatric replacement pattern and perhaps even vocal similarities (see other comments), and placement in separate genera, when a reasonable phylogenetic alternative that maintains them as congeners is available, will likely draw eyerolls, head shakes, and snickers from many ornithologists. I can think of a recent case in which we expanded one genus to include another despite morphological discontinuity: *Catoptrophorus* into *Tringa*. The Willet really differs phenotypically from typical *Tringa*, which are fairly homogeneous, but when faced with the genetic results, we had no problem expanding *Tringa* to include morphologically disparate *Catoptrophorus*.

Why not just expand *Botaurus* to include *Ixobrychus*? At least Terry's proposal brought up this possibility, but he argued that broad *Botaurus* would be too heterogeneous phenotypically. Here's my counter-argument. Structurally, one could make a case that *Botaurus* look superficially like giant juvenal-plumaged *Ixobrychus*. (This is the opposite of the *Bubulcus*-*Ardea* case, which many of you are in favor as treating as congeners.). Check out Jutglar's plate. One could also make a case that *involucris* is intermediate between *Ixobrychus* and *Botaurus* in plumage (and thus no surprise that it is on the branch *Botaurus sensu stricto*, as the recent genetic data suggest). From the illustrations, female *cinnamomeus* looks like a miniature *Botaurus*, as does female *eurhythmus* … in my opinion. The oddball *flavicollis* closes the size gap to some extent between big *Botaurus* and small *Ixobrychus*; body weights in HBW (1992, v. 1) show overlap between *flavicollis* and the low end of our American Bittern. My point is that once you look at the diversity of bitterns, beyond just our familiar Least and American, a single genus is palatable in my opinion, certainly much more so than placing phenotypically similar allotaxa in different genera.

I would change my mind (as long as *minutus* is also included in the analysis) if a time-calibrated tree indicated that the split between Hruska et al.'s broad *Botaurus* and constricted *Ixobrychus* was ancient, e.g. early Miocene as in many groups labeled as genera in birds.

YES (Option B). I agree to transfer *Ixobrychus exilis* to *Botaurus*, the evidence from UCE is clear.

YES (Option B). I think expanding *Botaurus* to include the Eurasian, African, and Australian taxa is the better solution. While there is a clear divide genetically, morphologically between the two main clades of bittern, all of the small bitterns are very similar, and it would make more sense if *Botaurus* just included all the bitterns, with the genus just being polymorphic.

YES (Option B). This is pretty subjective, but I prefer a larger *Botaurus* and for the bitterns that includes the Eastern Hemisphere taxa.

NO. Even though the topologies seem rather solid, the exclusion of the type species in the analyses is a critical lapse and makes it difficult to do any restructuring at this time.

NO. I've thought about this for weeks and just can't wrap my head around transferring *I. exilis* and presumably *I. involucris* (SACC decision) to *Botarus*, yet leave the rest of the Old World *Ixobrychus* as is. When I first went to Europe in the spring of 1977 and saw and studied a number of *I. minutus* everything about them (morphology and behavior) suggested Least Bittern (*I. exilis*) to me, so much so that I initially thought that they were the same species until I checked the scientific names. Recently I went to Xeno-Canto and checked vocalizations of Little Bittern and the single note of the song is certainly different from the *coo-cu-cu-cu* song of Least Bittern, but then I found an entry for call notes on Little Bittern and the chatter series of harsh *kek* notes (see the entry on Xeno-Canto recorded on 15 August 2019 at Campo de Moro Verde, Spain) sounds to my ear identical to the comparable call of Least Bittern. This call of Least Bittern was not well known, but once learned, you realize how common this species can be in appropriate habitat. In looking at the rest of the Old World *Ixobrychus* I see Cinnamon Bittern (*I. cinnamomeus*) fairly regularly in Southeast Asia and have once seen the much scarcer Schrenk's Bittern (*I. eurhythmus*). By far the commonest species in eastern Asia is Yellow Bittern (*I. sinensis*) and I've watched many over four decades of visits. They certainly resemble Least Bitterns on structure and somewhat on morphology, but again behaviorally they seem very similar and collectively quite different from the three species of *Botaurus* I've seen. The calls of Yellow Bitterns I've perused on Xeno-Canto seem similar enough in type to Least and Yellow Bitterns, but didn't find the harsh and rapid series of notes. I guess overall, I would prefer to do nothing on this for now and await further genetic studies than do something that seems pretty radical to me which will later need to be changed. I am also left despairing that just because there is no available name for a combined genus of *I. exillis* and *I. involucris* doesn't necessitate getting them thrown into *Botarus* as the only solution.

Update on 4 June 2024: Now that this has passed and we have an enlarged and expanded *Botarus,* we now have a linear sequence that is *B. exilis, B. lentiginosus*, *B. pinnatus, B. minutus, and B. sinensis.* We are asked to believe that *exilis* is closer to *lentiginosus* (and *pinnatus*). This is despite the very close phenotypic similarity between *exilis* and *minutus* and to a slightly lesser extent *sinensis.* This is also despite the year-round contact call (a quick series of harsh squawking notes) is to my ear identical between *exilis* and *minutus.* Really? I invite anyone to listen to the available recordings on Xeno-Canto and do their own evaluation.

I remember not too long ago we were asked to believe that Lazuli Bunting (*Passerina amoena*) was closer to Blue Grosbeak (now *P. caerulea*) than to Indigo Bunting (*P. cyanea*). This was based on two independent (I think) mtDNA studies. Given the concerns the linear sequence was slightly modified to *P. caerulea, P. amoena*, and *P. cyanea*. After this finesse and after the Supplement was published along came another paper based on nuclear DNA that showed that in fact *P. amoena* and *P. cyanea* were sisters, as expected, given their very similar songs, including all call notes which sound identical to one another, and somewhat frequent interbreeding. So here why not start with the large species of *Botarus*, then go to the small species, thus, *B. lentiginosus* (or *B. pinnatus*), then *B. exilis, B. minutus* and *B. sinensis*? Further genetic studies with an evaluation of all species (per Van's comments) would be the most desirable outcome for now at least we still have the small *Botarus* together and still next to the large ones rather than *exilis* isolated at the beginning of the linear sequence. Convergent evolution despite, very close phenotypic appearance, is one thing, but when you combine that with identical or nearly identical contact calls, I feel it more likely that something here is amiss.

Make changes to our classification of the herons (Ardeidae): (c) Revise the genus-level taxonomy of *Bubulcus ibis* (Cattle Egret) and related species

YES (Option A). 2 with no comment.

YES (Option A). According to the most recent multilocus phylogeny, *Bubulcus ibis* should be transferred to *Ardea*. I agree to re-vote if a global body such as WGAC endorses a different treatment.

YES (Option A). I'm opposed to placing *Bubulcus* into *Ardea* for the reasons others have raised, namely morphology, but especially behavior. When one watches the foraging gait of a flock of Cattle Egrets moving through a grassy field, one is not reminded particularly of any species of *Ardea*. Yes, Intermediate Egret (*A. intermedia*) does cause some confusion visually in the field with Cattle Egret, particularly with the eastern subspecies of Cattle (*coromandus*), perhaps best treated as a separate species. Also, Cattle Egrets have a distinct alternate plumage which involves much of the plumage while in *Ardea* and for that matter *Egretta* the alternate plumage mainly involves head and neck (and elsewhere) plumes and the change of soft part colors. I'm intrigued by the preference in another comment for transferring some species to *Casmerodias*, although I'm always struck by how similar the calls of *Ardea alba* and *A. herodias* (and presumably *A. cinerea*) are.

YES (Option A). I think we have to go with the UCE data, i.e. *Bubulcus* is embedded in broad *Ardea*. So, the decision is arbitrary. Sink *Bubulcus* or resurrect *Casmerodius*? I see good points for both treatments. However, the biggest difference between Cattle Egret and the others is size – if Cattle Egret were the size of a typical *Ardea*, I suspect we wouldn't balk at the decision. Size alone is not a criterion for a separate genus (think of *Chloroceryle* as just one of many examples). Also, I think two Old World taxa, with which we are less familiar, *intermedius* and *purpurea*, close the size gap somewhat. Cattle Egret is obviously a highly specialized feeder that has "broken out" of the standard *Ardea* morphology, and the smaller size likely is a benefit to its agile pursuit of flushed arthropods and small vertebrates. I will point out that Cattle Egret holds its own with the big *Ardea* in terms of voraciousness: for entertainment for anyone who read this far, here's my video of one swallowing a snake that is longer than the bird: https://www.youtube.com/watch?v=fMqjKbuDDUY&t=29s. Also, we've all seen Great Egret and Great Blue Heron regularly feeding facultatively in terrestrial situations. One final point: how would one diagnose resurrected *Casmerodius* other than by tree typology? Distinguishing Great White Heron from Great Egret takes a little practice, for example: https://www.youtube.com/watch?v=p0B4fOUDQWI.

YES (Option A). Transferring *Bubulcus ibis* to *Ardea* would involve the least change. In these cases, I also generally prefer to avoid successively splitting genera when it is not explicitly necessary; to me, fewer larger genera are more informative to relationships than a bunch of small and monotypic genera.

YES (Option A). For *Ardea*, I think that we need to make a change of some kind based on the phylogenetic data. I'm more confident in the UCE topology than the other phylogenetic data, and transferring *ibis* to *Ardea* is less disruptive than resurrecting *Casmerodius*. Also, as with the bitterns, we now know that body size is very labile in herons. Despite its unique behavior, I don't think it's too much of a stretch to include *ibis* in *Ardea*, as the various (former) *A. intermedia* species look quite similar to *ibis* and fill in the size gap between *ibis* and the larger *Ardea*.

YES (Option B). The Cattle Egret is so behaviorally and morphologically separate from other species in *Ardea*, that it does not make sense to place it in that genus. I much prefer to split off *alba*, *intermedia* (and *pacifica*) into *Casmerodius*.

YES (Option B). I see arguments for both options, and am slightly in favor of transferring *alba, intermedia,* and *pacifica* to *Casmerodius* rather than transferring *Bubuculus ibis* to *Ardea* for the reasons given by others. However, I could go either way on this issue.

YES (Option B). Similarly here, I tend to like decisions regarding genus limits that incorporate phenotypic traits and not just genetic ones. Huruska et al. (2023) focus only on the latter. The gene tree uncertainties in Hruska et al. (2023: fig. 4) make placement of *Bubulcus* uncertain with respect to its *Ardea* relatives. They are correct to note that "its behavioral and morphological distinctiveness have prevented a generic name change in the major bird checklists…" Those traits are so distinctive that I think recognition of a monotypic genus is warranted. Rather than lump it into *Ardea*, I support we splitting that clade into *Ardea*, *Bubulcus*, and *Casmerodius* (fig. 4), which would fit their fig. 3 as well.

Make changes to our classification of the herons (Ardeidae): (d) Remove the hyphen from the group name Night-Heron

YES. 1 without comment.

YES. The phylogenetic data show that the Night Herons are not monophyletic.

YES. Sequence looks good, unless either part of A2-b does not pass.

YES. Non-monophyly of the night herons based on UCE data mandate this change.

YES. Remove hyphen from Night-Heron group name. Phylogenetic analysis in Hruska et al. (2023) does not support monophyly for species currently considered "Night-Heron".

YES. Remove hyphen based on established policy.

YES. Changing Night-Heron to Night Heron is warranted given their findings.

YES. The UCE data do not support the monophyly for the species.

YES. Mandatory change required by our policy.

YES. Remove the hyphen from "night-heron" based on the naming guidelines.

2024-A-3
Revise the sub-family and genus-level classification of the Charadriidae

YES. I agree with all the recommendations in this excellent proposal (Yes to A,,D,E,F,G; No on B,C,H). I think this proposed classification balances changes where needed (some *Charadrius* to *Anarhynchus*) with stability to where change is less sure (species level sequence in larger genera)

YES. I agree with the proposal, it is valuable to review the classification of Charadriidae taking into account the published phylogenies. (a) YES. Several phylogenies consistently place *morinellus* on a long branch closely related to *Charadrius sensu* *stricto*, time since divergence supports genus-level divergence. (b) NO. Keep *dubius* within *Charadrius* until further research (with more species/samples and molecular markers) clarify the relationships. Consider recommendations from global authorities since it is a mainly extralimital species. (c) NO and (d) YES. Since support is low for many internal nodes in that clade, it will be best to leave all members of the group as part of the same genus. (e) YES. Adopt the new linear sequence. (f) YES. *Pluvialis* is consistently a separate group in available phylogenies. (g) YES and (h) NO. *Vanellus* is embedded within Charadriinae in phylogenies; keep *Anarhynchus* within Charadriinae.

YES. (a) YES. The data consistently place *morinellus* on a long branch that suggests generic-level divergence; thus, placement in the genus *Eudromias* makes sense. (b) NO. I agree with the proposal's recommendation not to transfer *Charadrius dubius* to *Thinornis*, given that this species is largely extralimital to the NACC area and global authorities have not yet adopted this treatment. (c) NO. Agree with the proposal's recommendation. (d) YES. (e) YES. (f) YES. *Pluvialis* is clearly on a long branch, thus placement in a separate subfamily makes sense. (g) YES. (h) NO. It seems preferable to merge Vanellinae into Charadriinae rather than recognize three subfamilies dominated by a single genus.

YES. Excellent proposal. (a) YES. I agree and when one spends time with *morinellus* they behaviorally are pretty different, starting with that you can often approach to within seemingly ten feet or so to them. (b) NO, but it would not surprise me if additional studies confirm that *Charadrius dubius* is pretty different and a change will be necessary. Their soft and plaintive vocalizations strike me as really quite different from other *Charadrius* along with the lack of a white wing stripe. (c) NO, as outlined in the proposal. (d) YES, (e) YES (f) YES. This one seems long overdue. (g) a reluctant YES. I'm on the fence on this, but am left with the feeling that the species in the dominant genus, *Vanellus*, are strikingly so similar collectively and so different from other groups that maintaining a separate designation is hard to resist. (h) YES.

YES. (a) NO. I'd rather wait for more data on this one. Long branches on a tree reconstructed with ~69% missing data are of questionable utility, so I'd rather be conservative for now and retain *morinellus* in *Charadrius*. While this might leave a paraphyletic *Charadrius*, filling in those large gaps in the data matrix could change that relationship quite a bit. And for example, we could even now simply broaden *Charadrius* to include *Thinornis* and *morinellus* and it would be roughly equivalent to the genus *Vanellus* in the same red-arrowed figure (I am ignoring morphology here, though *Thinornis* has a history of being considered a somewhat sketchy genus). (b) NO, for reasons outlined. Again, the *Thinornis*/*Charadrius* (sensu stricto) relationship could use some additional data to provide more confidence on this relationship.When I cursorily look at specimens, *Eudromias* looks more like a genus-level split than *Thinornis*, but our holdings of *Thinornis* and *Charadrius* are a bit spotty. (c) NO. D is a much better option. (d) YES. I agree this is not core *Charadrius* and this seems like a good taxonomic solution. (e-g) YES. All seem appropriate. On G, I do recognize that this makes for a more heterogeneous Charadriinae and that given more data and a clearer understanding of relationships we might break this into three subfamilies. (h) NO.

YES. I agree with the excellent proposal. (a) YES. (b) NO. (c) NO. (d) YES. The data are quite clear. (e) YES. (f) YES. (g) YES. (h) NO

YES. Yes to (a)(d)(e)(f)(g). NO (b), (c) (h). Reasons are given in the proposal.

YES. Kudos for extracting the reliable signal out of all that messy data, and all the proposal recommendations are cautious and wise in my opinion. That the banded plovers fall in two different genera is another example of plumage characters not necessarily providing reliable phylogenetic signal. However, that *morinellus* is on a long branch that argues for restoration of *Eudromias* is subjectively pleasing to those of us who never understood its inclusion in *Charadrius*. Another committee member made a good point on what we can/can't make of a long branch when there are so many missing data, but I think the new data shifted the balance in what is an arbitrary decision in terms of strict typology.

Mini-rant: That the gene-based tree was not published as a figure in the Černý-Natale paper is yet another of dozens of examples in the last decade that make me wonder sometimes if *MPE* is actually a peer-reviewed journal. Evidently, the message is not widely appreciated that phenotypic data have a difficult time eliminating convergence or strong divergence, as "proven" by the Livezey-Zusi monograph that produced a couple dozen conspicuous and indisputable examples of this (e.g., loons and grebes maintained as sisters, and diving-petrels and phalaropes restored to family rank). That was way back in 2007 with the world's largest-ever matrix of phenotypic data (2K+ characters).

YES. (a) YES to transfer *morinellus* to *Eudromias* for the reasons outlined in the proposal. (b) NO to transfer *dubius* to *Thinornis*, as I agree that the support is not strong and in this case it makes more sense to maintain it and the other species in this clade in *Charadrius sensu stricto.* (c) NO on recognizing the genus *Ochthodromus*, and instead (d) YES on moving these taxa to the genus *Anarhynchus.* It is very clear that these taxa are not part of *Charadrius*, and are supported as a well-supported clade in multiple studies, but subdivision within this clade does not have strong support, and I agree with the proposal that all of these taxa together should be transferred to *Anarhynchus* and not divided between *Anarhynchus* and *Ochthodromus*. (e) YES on adopting the new linear sequence for the plovers, for the reasons stated in the proposal. I also agree with the decision not to alter the sequence within each main clade for the time being, since the node support within clades is low. (f) YES on recognizing Pluvialinae given the long-branch length involved here; I do not support treating this as a separate family, given the many shared similarities between *Pluvialis* and the other plovers, they fit much better within Charadriidae. (g) YES on transferring *Vanellus* into Charadriinae, given the paraphyly of *Charadrius sensu lato* by the *Vanellus* lapwings, I think it is appropriate to include them in Charadriinae, rather than further recognize another smaller plover subfamily that is for all intents and purposes identical to the other, and all almost comprised entirely of a single genus. Single genera subfamilies describe nothing different from the subfamily itself, and are not useful for classification purposes if they can be avoided. (h) NO.

YES. Nice job on the proposal. I agree with all of their recommendations: YES on (a)(d)(e)(f)(g). NO on (b)(c)(h).

YES. Appreciate the work on this proposal to distill the strongly supported information from the trees. I agree with all the recommendations.

2024-A-4

Recognize extralimital *Puffinus bailloni*, *P. bannermani*, and *P. persicus* as species distinct from Audubon's Shearwater *P. lherminieri*

YES. This seems long overdue. Clearly there is a lot more work that needs to be done in this group but really this seems more like housekeeping given that everyone else has long treated these as specifically distinct, and the only ramification to our list is the range statement.

YES. This splits off three non-Atlantic subspecies from *lherminieri*, which makes biogeographic sense. This group has a subtle but confusing amount of variation in morphology and plumage, but restricting the long-tailed, but short-winged *lherminieri* to Atlantic populations makes lots of sense.

FYI: our current classification is:
Puffinus subalaris Galapagos Shearwater.
Puffinus puffinus Manx Shearwater.
Puffinus auricularis Townsend's Shearwater.
Puffinus newelli Newell's Shearwater
Puffinus bryani Bryan's Shearwater. (H, A)
Puffinus opisthomelas Black-vented Shearwater.
Puffinus lherminieri Audubon's Shearwater.
Puffinus baroli Barolo Shearwater. (A)

YES. Although heavily reliant on mitochondrial DNA, the genetic data do indicate that *bailloni*, *bannermani*, and *persicus* are unrelated to *lherminieri*. Based on the data of Austin et al. (2004) I'm less convinced that *persicus* should be considered separate from *bailloni*, but given that these are well outside our area I think we should follow global authorities that recognize the two as species. The node support for the sister relationship of *bannermani* and the *newelli* complex is rather weak, but at the very least *bannermani* seems to be unrelated to *lherminieri*.

Given the many different taxonomic treatments applied to the name "Audubon's Shearwater", ranging from a pantropical, to a North Atlantic, or western Atlantic species, I am in favor of abandoning the name Audubon's for *lherminieri*. Especially if proposal

2024-A-5 passes, the breeding range would be largely restricted to the Caribbean, so I would be in favor of the name Caribbean Shearwater for *lherminieri*, which is also the common name given by McAtee for nominate *lherminieri*. However, I was a bit confused as to why "Audubon's" was applied to *lherminieri* given that he was neither the collector nor the describer, and turned up a paper by Palmer (1931) who gave the reasons for the name. Palmer (1931) says that Audubon was in fact the first to collect the species, in 1826, but called the specimens *P. obscurus* Gmelin, a name now generally disregarded due to uncertainty about which taxon it applies to (Murphy 1927), but at the time applied to small black-and-white shearwaters from the Pacific and Indian oceans (= *P. bailloni*?). The confusion is understandable, given that we're still sorting out the identification and taxonomy of these birds! Lesson's name *lherminieri* from 1839 was overlooked by some authors, or at least his diagnosis was unavailable. Finsch, in 1872, named *P. auduboni* based on a specimen from Florida, which gives us the source for the common name, although *auduboni* is now a synonym of *lherminieri*. So, the common name "Audubon's" was originally applied to the Caribbean taxon, despite Audubon not realizing that he had collected a new species. The expansion of the name "Audubon's Shearwater" to a globally-distributed species was perhaps a poor choice, and could be a good reason for not changing the name of *lherminieri* now, as we are basically reverting to the original common name for *lherminieri*. A name change may also not be required, given that this is not a parent-daughter split. However, given the many subsequent taxonomic circumscriptions of the name "Audubon's Shearwater" I think it would be better to adopt a new name for the modern treatment of *lherminieri*.

Murphy, R.C. 1927. On certain forms of *Puffinus assimilis* and its allies. American Museum Novitates 276: 1-15.
Palmer, T.S. 1931. Audubon's Shearwater in the United States. The Auk 48(2): 198-206. https://www.jstor.org/stable/4076787

YES. It would be nice to see this corroborated with non-mtDNA data, but these changes make sense given the combination of genetics and biogeography. It also puts the NACC list in line with global lists.

YES. The UCE-ddRAD phylogeny from Ferrer Obiol et al. (2021) and previous mtDNA phylogenies support that *P. bailloni* and *P. lherminieri* are separate taxa, they do not even represent sister species, therefore recognizing the split of *P. bailloni* from *P. lherminieri* is long overdue. Recognizing *P. bannermani* and *P. persicus* as separate species from *P. lherminieri* is supported by mtDNA phylogenies and biogeography.

YES. I vote in favor for all of the reasons given, but particularly given the trend for splitting these island-breeding or island-group isolates as separate species makes it untenable that the Caribbean breeding taxon with distinct structural differences be maintained with other taxa found thousands of miles away.

I agree fully that we should consider changing the English name of Audubon's Shearwater to Caribbean Shearwater which well describes the range of the species acknowledging that they range into the western Atlantic. I note too (Howell and Zufelt (2019) that there is a small population of this taxon in Espirito Santo, Brazil. Given the drastic overhaul of these small shearwaters, English name changes can be justified. Retaining the English name of Audubon's Shearwater would be decidedly unhelpful.

Howell, S.N.G. and K. Zufelt. 2019. Oceanic Birds of the World, a Photo Guide. Princeton University Press.

YES. While I am reluctant to rely so much on mtDNA for species limits, it is clear that there are multiple species here and these are extralimital for us so going with the prevailing other authorities seems warranted.

YES. I agree with the proposal, based on the morphology, biogeography and genetic differences that supported the split of the three extralimital species.

NO. This is basically a protest vote. I think the proposal makes the best of a bad situation, but one could also state that genetics, biogeography, and morphology also support treatment of all of these taxa as subspecies. In some ways I see the advantages of following other world classifications, but I can also see a disadvantage: the conformity implies that data convincingly support that classification, and thus no further work is needed, when in fact this is far from the case. I think it is actually beneficial when the data can be interpreted in more than one way: if world classifications differ, then the problem is emphasized, not pushed under the rug. The section in Ferrer Obiol et al. "*Considerations of shearwater taxonomic classification*" is worth reading for its catalog of what data are missing and what data are need to produce a well-supported classification, with the following quote near the end:

> "As a final consideration, our analyses based on genomic data and the ongoing taxonomic debate suggest that the species status of these taxa should be re-evaluated. Future studies should use species delimitation approaches under an integrative taxonomic framework, combining genomic data with a thorough morphological re-evaluation including a detailed evaluation of vocalisations."

I'm in favor of waiting for those data and a "do no harm" approach until then.

YES. I vote in favor for the reasons outlined in the proposal, and to bring us in alignment with other global checklist authorities .

YES. While not a slam dunk due to heavy reliance on mtDNA, this seems the best course of action given the data and circumstances at hand.

YES. Although more data are needed, I think there is enough here to make this split and bring us into conformance with other lists. But I agree that this push to have one global world list will obscure taxonomic problems that need more work.

2024-A-5
Treat extralimital *Puffinus boydi* as a separate species from Audubon's Shearwater *P. lherminieri*

YES. I vote in favor, but with reservations. *Puffinus boydi* seems as distinct from *lherminieri* in morphometrics and genetics as is *baroli*, but there is limited divergence between *boydi* and *lherminieri* in plumage or vocalizations. I'm swayed by the nuclear DNA data showing that *boydi*+*baroli* is very divergent from *lherminieri*, with the ~1 Ma divergence time estimate. The Flood and van der Vliet 2019 paper mentioned in the proposal does an excellent job of sorting out the morphological differences between *boydi* and *baroli*, but does not analyze *lherminieri*. However, what strikes me from the paper is the extensive overlap in plumage between *boydi* and *baroli*, with shared morphometrics (just a slightly longer tail in *boydi*), in contrast to the larger and longer-tailed *lherminieri*, which mirrors the closer relationship between *boydi* and *baroli* shown in the genetic data.

The D-statistic introgression data are interesting, but tell us about ancient, not ongoing gene flow, which is not especially relevant to current species limits under a biological species concept. The proposal does note that this introgression between *boydi* and *lherminieri* was estimated to occur in the Pleistocene, but it seems that the paper authors did not do any demographic modeling to estimate recent gene flow.

What gives me pause is the vocalizations. As is mentioned in the proposal, there are few vocalizations available for any of these taxa, but it appears that at least some biologists are working at the breeding colonies of both *boydi* and *baroli*, but most recordings are not on the public repositories. The Sound Approach website has some interesting information on vocalizations (https://soundapproach.co.uk/species/boyds-shearwater/) as does this post documenting a *boydi* in a *barolo* breeding colony (https://subalpinebirding.com/blog/a-boyds-shearwater-in-a-barolo-colony). What strikes me is the very different (higher pitched / more notes) calls of *barolo* in comparison to *boydi*. However, the few recordings of *lherminieri* on ML (especially https://macaulaylibrary.org/asset/42998 and https://macaulaylibrary.org/asset/151481441) sound extremely similar to those of *boydi*. A formal analysis of these vocal differences, if any, would be very informative.

Although *boydi* is extralimital based on current knowledge, the movement data from Ramos et al. (2020) suggest that individuals could show up near the coast of northern South America, or even in the Lesser Antilles, where they would be near colonies of *lherminieri* in the Lesser Antilles and Fernando de Noronha.

YES. Recent phylogenetic analysis considering genomic data support that *P. baroli* and *P. boydi* represent sister taxa, and both are sister to *P. lherminieri*. Maintaining *boydi* as part of *P. lherminieri* results in a classification with paraphyletic groups. Several lines of evidence (vocalizations, morphology, and lack of evidence of hybridization) support *P. baroli* as a separate species from *boydi*, so lumping *boydi* with *P. baroli* is not an option (and it would be outside of the NACC jurisdiction). I agree with the proposed recommendation to consider the extralimital *boydi* as a separate species from *P. lherminieri*.

YES. I vote in favor, but I'm uneasy after reading other comments. There are 2-3 subspecies within the newly configured *P. lherminieri.* Perhaps *boydi* is another? For now, I think it is best to adopt European taxonomy for *boydi* which I believe pretty uniformly recognize it as a separate species.

YES. I agree with the proposal. *Puffinus boydi* and *P. ihermineri* have differences in genetics, distributional area, morphology, size, and foot color. And in most of the phylogenetic trees *P. boydi* is closely related to *P. baroli*, and not to *P. lherminieri*.

YES. Reasons are outlined in the proposal.

YES. I generally defer to global taxonomies on extralimital taxa and it seems there are multiple lines of evidence to support the split—although it does seem a very recent one.

YES. I vote in favor, but with reservations. I have gone back and forth on this one. Multiple independent studies show that *Puffinus boydi* is separate from *P. ihermineri* and more closely related to *P. baroli*; thus, it makes sense to separate *boydi* from *ihermineri* which is the basis of the proposal. The proposal specifically does not include an option to recognize *boydi* as a subspecies of *baroli*, so we can't vote on that. Factors that are swaying me in favor of elevating *boydi* to species include: (1) a combination of genetic, phenotypic, and at least subtle vocal differences; (2) my inclination to defer to global lists for extralimital taxa. However, my reservations are two-fold: (1) lack of a formal study of vocal differences; (2) uncertainty about current gene flow and what is maintaining reproductive isolation between *baroli* and *boydi*, given that there is movement between colonies (the proposal mentions "lack of evidence of hybridization despite occurrences at each other's colonies" but does not provide details).

YES. I vote in favor based on monophyly and phylogenetic position to other relevant taxa. Also agrees with biogeography and to some extent morphology, and makes it concordant with decisions on other taxa outside our purview.

NO. *P. baroli* and *boydi* are clearly closely related, and the evidence seems more commensurate with subspecies-level divergence. With divergence being just ~120 Kyr (Ferrer Obiol et al. 2023), a D-value indicating gene flow of unknown timing and extent (I am unclear on "lack of evidence of hybridization"), the Ferrer Obiol et al. (2022) observation of subspecies-level genetic divergence mentioned, and phenotypic differences being "subtle," the elevation to full species seems unwarranted.

NO. Although I would rather not buck the more global list, given that this taxon is outside the NACC area, I just do not see any evidence that *boydi* is reproductively isolated from *baroli*. Yes, it is quite divergent genetically, but what are the morphological, phenological, or vocal differences that could maintain reproductive isolation?

2024-A-6
Treat Cory's Shearwater as two species, *Calonectris diomedea* and *C. borealis*

YES. These two taxa breed sympatrically and differ in several traits (morphology, voice including differential response to playbacks, genetics, chemical profiles of uropygial secretions), with limited evidence of hybridization where they breed sympatrically. Thus, they appear to be reproductively isolated. Very interesting proposal that will put the NACC list in line with other global checklists.

YES. Both *diomedea* and *borealis* breed in sympatry with limited gene flow. They show genetic and phenotypic (vocalizations, uropygial secretions) differences. I agree with retaining the English names already in general use for these Old World species, even more so given that they are found in the NACC area as non-breeders.

YES. All the evidence supports these as biological species. The birds are clearly recognizing each other as different, even if we struggle to identify them based on plumage. To my ear, the vocalizations do sound quite distinct, and consistently different between the two taxa. This will certainly make east coast pelagic trips more interesting. Although it goes against our common name guidelines, I think it’s better to follow the global checklists and use the English names suggested in the proposal.

YES. I looked at the recent edition of Birds of Europe, 3rd edition (2023) which I just purchased. Here, the two taxa are still treated as subspecies. Svensson’s text in part: “Frequently more difficult to separate from Cory’s than many imagine: the two are often inseparable due to individual or age-related variation, or to field conditions (light, distance)....” Under voice, “calls [of Scopoli’s] very similar to those of Cory’s Shearwater but said to differ in being slightly less coarse and guttural.”

Svensson, L., K. Mullaney and D. Zetterstrom (2023). Birds of Europe (3rd edition). Princeton University Press.

YES. It's a good proposal. The almost allopatric distribution of *borealis* and *diomedea*, there isn´t any hybridization between them. I agree with the English name: Cory´s Shearwater for *C. borealis* and Scopoli´s Shearwater for *C. diomedea*.

YES. I vote in favor for the reasons outlined in the proposal. All of the published evidence strongly advocates for species status of these two taxa.

YES. Although I have previously argued that the preponderance of intermediate phenotypes casts doubts on whether *diomedea* (ss) and *borealis* are reproductively isolated, I think I have been using the wrong characters for assigning the taxa. Separating *diomedea* (ss) and *borealis* has long been primarily determined by the extent of white on the underside of the primaries, with size, especially of the bill, being secondary. A few other characters are rather subjective and variable (amount of dark on the outer primary coverts, darkness of cap). In contrast, Zidat et al assigned subspecies by seven mensural characters, five bill measurements, wing length, and tarsus length, and did not use extent of white on the underside of the primaries.They found strong evidence that, based on these characters, the individuals assigned to *diomedea* were reproductively isolated from *borealis* on the Chafarinas Islands, where they breed in sympatry. Despite ample evidence that the extent of white on the underside of the primaries shows a great deal of intermediates (my unpublished data; also see other comments), this character continues to be used in the field as the main criterion to identify these taxa. Although using the extent of white on the underside of the primaries to identify will be problematic for birders, the birds on the Chafarinas Islands are likely not using this character to identify mates.

YES. Reasons are stated in the proposal.

YES. I voted yes to this proposal in 2018: "based on the published information (genetics, vocalizations, morphology, and chemical differences)" and continue to support the split. I agree with the proposal that it's best to act on the evidence we have on hand instead of continuing to wait for (potentially) conflicting data.

NO. We know of unpublished evidence for intermediates, perhaps substantial numbers of them, and while there is "almost no evidence of hybridization on islands where both occur," you'll see below that I don't think that's an accurate summary. We have an unresolved issue of just how much gene flow is occurring. I'm not convinced that following the fashion of other lists is compelling enough to make this split. Finally, I go back to my 2018 vote and comments:

"No. The Zidat et al. (2017) study shows what appear to me to be rates of introgression that are too high for these to be full biological species (1 of 14 pairs mixed; other evidence of hybridization). They are differentiated to a small degree, but they have not achieved sufficient levels of reproductive isolation (disassortative mating still too high). This, with Andy's comments, leads me to consider that these are good subspecies."

Note that that is a 7% hybridization rate. The presence of assortative mating is not an effective species-limits criterion, because its effectiveness needs to be very high to push hybridization and gene flow to the low levels required for the "essentially reproductively isolated" criterion of the BSC. It is possible that there are additional postmating isolating mechanisms, although the unpublished evidence of substantial numbers of intergrades suggests that those are not highly effective either.

2024-A-7
Treat Jamaican Petrel *Pterodroma caribbaea* as a separate species from Black-capped Petrel *P. hasitata*

YES. The plumage differences, combined with differences in morphology and feather lice, lend support to recognizing the putatively extinct Jamaican Petrel as a separate species. It would be interesting to sequence the old museum skins for comparison with Black-capped Petrel.

YES. Most (all?) other *Pterodroma* that show dark and light morphs also show a wide range of intermediates (e.g. *neglecta, arminjoniana,* and *heraldica*), while extreme dark morphs are typically separate species (e.g. *atrata*). Given the lack of intermediate morphs, I would be surprised if *hasitata* and *caribbaea* were a case of intraspecific plumage variation. The feather lice differences also point to species status, as does the possibility of *hasitata* breeding on Jamaica, at least in modern times (Simons et al. 2013, p. 19). It would certainly be nice to have ancient DNA data to support this, but I think the weight of the evidence points towards species status for *caribbaea*.

Simons, T.R., D.S. Lee, and J.C. Haney. 2013. Diablotin *Pterodroma hasitata*: A biography of the endangered Black-capped Petrel. Marine Ornithology 41(Special issue): S3–S43.

YES. The variation that exists between *Pterodroma caribbaea* and *P. hasitata* does not correspond to intraspecific polymorphisms as evidenced by other species of petrels that present polymorphisms. Feather lice diversity also supports the differentiation between *caribbaea* and *hasitata*. I agree with the English names Black-capped Petrel (*P. hasitata*) and Jamaican Petrel (*P. caribbaea*).

YES. Reasons are outlined in the proposal. Surely, *P. caribbaea* is extinct?

YES. The morphometrics are a good indicator but the feather lice tip it for me.

YES. There is sufficient morphological (plumage) evidence for the separation of *Pterodroma caribbaea* from *P. hasitata*. I agree with the proposal about English names.

YES. Reasons are outlined in the proposal.

YES. Reasons are outlined in the proposal.

YES. Reasons are stated in the proposal.

YES. Plumage differences and lice differences are convincing. Let’s hope a population still survives**.**

2024-A-8
Treat *Coccyzus bahamensis* as a separate species from Great Lizard-Cuckoo *C. merlini*

NO. I agree with the proposal's recommendation that the current evidence for splitting these taxa is weak. As noted in the proposal, more data are needed on genetic and vocal variation along with a formal analysis of morphological and color differences.

NO. We need more genetic, vocal, morphological and color data, as well as analyses of these data to clarify the relationships between these species.

NO. The evidence currently available does not support the split. As mentioned in the recommendation of the proposal, analyses of vocalizations, plumage coloration, and morphometry are needed, in addition to analysis of intraspecific genetic variation and phylogenetic relationships of the different subspecies.

NO. These are subspecies-level characteristics, and as we know from the large-scale review of Hudson & Price (2014, Journal of Heredity, 105:821–833) island birds are already oversplit.

NO. Not on the basis of presently available data. Of course a genetic study might upend this but thus far this seems a weak case for a split.

NO. Comprehensive analyses would be desirable, but these seem like subspecies-level differences. With its rich brown plumage, nominate *merlini* seems to me the most phenotypically distinctive of the group, rather than *bahamensis.* A quick search of photos of *bahamensis* available online seems to show some variation in the amount of rufous on the outer vane of the primaries, with some individuals showing quite a bit of rufous at least at the proximal end of the primaries. However, none of the plumage differences among taxa in this group seem to approach those of other Lizard-Cuckoos currently recognized as species. Given the many other shared species between Cuba and the Bahamas, it does not seem surprising that these would be a single species.

The long call of *bahamensis* does sound slightly higher pitched to my ear (but the sample size is very small), but this is only in comparison to *merlini*, as it doesn't appear that any recordings are available for *decolor* or *santamariae*.

NO. The only data supporting separation are plumage characters, and these seem slight and not well supported. I am intrigued, however, by the large geographic distance in the range of these two taxa. Would be interesting to see genetic data.

NO. The current evidence for splitting seems very weak. The plumage/morphological differences seem well within the range of variation for subspecies. Given there do not appear to be any vocal differences, until there is more evidence in this case, these groups definitely seem best treated as subspecies of a single species.

NO. I agree with the proposal that the limited phenotypic differences alone are not sufficient to recognize *bahamensis* as a separate species from *merlini*. We need a more comprehensive data set.

NO. The rather subtle differences have not been put in the context of reproductive isolation, which is paramount in discussing whether they should be split.

NO. Reasons are given in the proposal. Without data on vocalizations, this split is DOA. This BLI split is an indictment of their methodology. Can someone point out an example of two species that differ only in extent of rufous in wing and in tail tip color?

NO. The island subspecies isolates off Cuba, *decolor* (Isla de Juventud) and *santamariae* (a dozen plus cays off the north coast) would seem to bridge some of the plumage differences between nominate *merlini* and *bahamensis*. And, these island isolates are largely unstudied. I think too that there isn't an appreciation as to how the Bahamas and Cuba are so similar in terms of a shared fauna. Within landbirds most of the shared species are either treated as subspecies or in the case of the Olive-capped Warbler (*Setophaga pityophyla*), the species is treated as monotypic with separate populations in west and east Cuba and the northern Bahamas (Grand Bahama and Little and Great Abaco). Only with the former Greater Antillean Oriole was there a decision to treat Cuban (*I. melanopsis*) and Bahaman (*I. northropi)* as separate species. These two showed (in adults) distinct morphological differences, largely black in the former, black-and-yellow in the latter, but were genetically closely related. I recall a split vote on whether to treat them as separate species. This for me heightens the importance of seeing firm evidence as to why the Bahamas and the three Cuba subspecies should be treated as separate species, and at the moment there is very little evidence to persuade me why the status quo (by almost all authorities) should not continue. I'll only add that I have rather extensive experience with nominate *merlini* and have seen and heard *bahamensis a* number of times on Andros and twice on New Providence; the latter population is now extirpated. I have seen *santamariae* a few times on Cayo Coco. I have not been to Isla de Juventud off the south coast of Cuba. At no time did I notice anything vocally different between the two "groups" and I have heard no discussion from anyone suggesting the two should be regarded as separate species. I'm perfectly willing to be persuaded otherwise once additional studies are undertaken.

2024-A-9

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

YES (a and b). Of course there is a lot more that needs to be done to sort out the details, as is normally the case with widespread complexes like this. But it seems to me there is sufficient evidence that *mexicana* is reproductively isolated despite essentially being parapatric, indicating it is better treated as a separate species, so I think we should adopt this improved understanding of species limits. There is also good evidence in the form of orbital skin turnover zones, supplemented by a deep mtDNA break found by both studies, that there are two separate species in South America. Again, there are plenty of issues to be worked out, including nomenclatural ones, but I don't think it is an improvement to do nothing when we have pretty convincing evidence.

YES (a and b). Reasons are given in the proposal. My primary concern is the nomenclatural issue with *circe*/*mehleri*. Perhaps it would be better to wait to adopt this split until a publication sorts this out with a first reviser action.

YES (a and b). I agree with the proposal. The problem is the nomenclatural issue.

YES (a and b). As noted in the proposal and others, this is indeed a very borderline case, and more information would be ideal, but the available information does suggest that the different taxa in question are either sympatric or parapatric with limited to no introgression on a scale that is similar to what we see in other classic hybrid zones where we consider the hybridizing taxa to be separate species. While detailed, population-level genetic analyses that includes more nuclear loci would be ideal for both the contact zone between *mexicana* and *thermophila* and between "*circe*" and *cayana*, the available evidence, particularly the abrupt turnover in orbital skin color, as well as the relatively deep mtDNA divergence, seems pretty strong that introgression is very limited.

YES (a), NO (b). Borderline cases, but at this point, there is more evidence arguing to split *P. mexicana* than to not split (narrow contact zone, genetics, morphology). I'm less convinced by the case for *P. "circe"*. It's probably best to defer to SACC anyway.

YES (a), NO (b). From evidence presented in this and the 2022 proposal, it seems highly likely that *mexicana* and *thermophila* approach one another with little or no gene flow. The eyeskin, plumage, and morphometric differences are quite dramatic and would likely serve as reproductively isolating. The rudimentary genetic data are indicative of little gene flow. Yes, it would be nice to have better data, but I think we have already reached the point where conclusions from the present data lean very heavily to separate species status. Even though the case to split *circe* and *cayana* is just as strong,I think we should defer to the SACC, or at least wait until they have voted.

NO (a and b). As noted in this thorough and complex proposal, this is a borderline case and the data are intriguing, but it still seems like more study is needed - in particular, formal analysis of vocal and plumage variation within and between populations/subspecies as well as a comprehensive study of what is happening in contact zones.

NO (a and b). Highly conflicted on this one. Borderline indeed. If the data assembled in the proposal were in the form of a peer-reviewed publication, I would vote YES because I think it more closely approximates species limits than does the current broadly defined, Peters-based single species. A thorough study that sampled all taxa might reveal some conflicts with a three-species taxonomy, and it is always easy to require more data before making splits in a complex like this one. But a “do no harm” conservative approach might be the wisest thing to do in a case like this given the data gaps. We already know that basing taxonomy on mtDNA gene trees is unwise, so I don’t trust the basics of the tree typology. And the contact zones outside of the *mexicana*-*thermophila* one are poorly characterized. And then there’s the *circe*-*mehleri* nomenclature problem. Given the absence of any sign of free gene flow between *mexicana* and *thermophila*, I personally would consider that sufficient evidence for a species split. Given the orbital ring color differences outlined in the proposal, I think it also might be safe to extrapolate from the *mexicana*-*thermophila* situation to the South American situation. If all this were summarized in a publication rather than NACC + WGAC proposals, I would be strongly in favor of a YES vote, especially because that would also provide the first revisor opportunity. If the proposal passes, then I highly recommend a separate one on English names rather than rush names through at this point.

NO (a and b). (a) Definitely a borderline case. Clear differences in the undertail color between *mexicana* and *thermophila*, in addition to differences in tail length. To date, there is only one study that has analyzed DNA and that has included *mexicana* representation (Sánchez-González et al. 2023). This study analyzed mitochondrial DNA and did not detect the presence of gene flow between *mexicana* and *thermophila*. However, the presence of individuals with an intermediate phenotype has been reported in a narrow contact zone between both forms, which is located in the state of Oaxaca (Binford 1989; photographs in proposal 2022-B-11). Mitochondrial DNA provides a partial history of the organisms under study and, furthermore, selection of mitochondrial DNA may impede detection of gene flow. Nuclear DNA needs to be analyzed to demonstrate the presence/absence of gene flow, quantify gene flow if present, and determine whether individuals with an intermediate phenotype represent (or not) hybrids. Although there appear to be differences in songs, quantitative vocal analysis and playback experiments are recommended. I notice that the geographic ranges of *mexicana* and *thermophila* seem to abut over a longer extent than the narrow hybrid zone mentioned (involving the states of Puebla and Veracruz, as shown on Figure 1 of Sánchez-González et al. 2023). It would be valuable to report how the two lineages behave there. (b) Detailed studies needed in the potential contact zones. It is an interesting idea to propose the orbital color as an indicator trait of two separate groups, an idea that should be explored in more detail (e.g., how does orbital color change through life?).

NO (a and b). Good proposal. I am going to be conservative on this one. These are both potentially good biological species, but at present the evidence is not compelling enough to show they are not subspecies, as they are currently treated. We’ve seen too many cases where mtDNA is not a reliable indicator of species limits, and "diagnosable differences across a small contact zone" is also not a reliable indicator, especially when intermediates are present. Earlier considerations of *mexicanus* and *cayana* as separate species (e.g., Ridgway 1916) used a different species concept than the BSC. Hybridization appears to be present, and it would be good to know what those levels are and whether only a few loci are involved in the phenotypic differences. There are even more unanswered questions between "*circe*" and *mexicana*, and mtDNA is notoriously unreliable as a species limits (and species tree) indicator.

NO (a and b). There is compelling evidence here to believe that there very well may be multiple species within the complex. However, I prefer to wait for more data, specifically a more thorough analysis of both contact zones. The PCA differences in morphometrics between *mexicana* and *thermophila* are slight and overlapping—I don't think these are strong evidence of reproductive isolation. In contrast, the lack of shared mtDNA haplotypes is compelling evidence for separate species, but I would like to see this bolstered with more sampling and nuDNA as well. We know very little about the contact zone between the *circe* and *cayana* groups. They are about a similar level of divergence based on mtDNA, so a three way split in the future seems a likely outcome. However, acting conservatively, I'd prefer to wait until we have a more complete analysis of putative hybrid zones.

NO (a and b). A weak NO to (a) and a stronger NO to (b). I'm sort of thinking after reading the proposal that this might be the 'cart before the horse' syndrome, or at least the majority of the issues fortunately lie outside of our area. Regarding part B, that matter should be left for the SACC to deal with, although the information is helpful for context. Regarding (a), I agree with others that *mexicana* is likely best treated as a separate species from *cayana* given the apparent parapatry in Oaxaca in the Isthmus of Tehuantepec, but I would prefer additional vocal studies and hopefully additional field work in the overlap zone. That said, the proposal is well-crafted and pretty convincing. I agree that the orbital ring colors are potentially significant. I'm left feeling there isn't that much new information since the last time we reviewed this proposal. I agree that a published peer-reviewed paper outlining the issues would be ideal.

2024-A-10
Treat *Stelgidopteryx ridgwayi* as a separate species from Northern Rough-winged Swallow *S. serripennis*

NO. A more thorough population-level study of known breeding birds with better sampling for genetic and vocal data are needed, especially to better understand areas of potential contact or sympatry.

NO. We voted this one down a few decades ago for all the reasons indicated in the proposal, and nothing meaningful has been produced since. The newer genetic data are essentially useless because of the absence of samples of breeding birds from anywhere near contact. As for nest-site differences, hole-nesters in general are notoriously flexible, so I don't put much stock in that. The proposal correctly outlines all the additional data that are needed to make an informed decision on this one, one way or another. Additional data may indeed show that *ridgwayi* is a valid BSC species, but I think it is prudent to wait for actual data rather than a compilation of anecdotes.

NO. I agree with the proposal that there are potential species-level differences here, but, again, the evidence is not sufficiently compelling to show they are not just subspecies, as we currently treat them.

NO. A better understanding of the distribution areas of the different subspecies and their potential overlap in the Yucatan Peninsula is needed. Evidence is also needed to demonstrate that nesting sites are different between *serripennis* and *ridgwayi*. Genetic studies with geographical representation of the contact zones are necessary to rule out the presence of extensive gene flow. Given the annual migratory cycle that some populations of these swallows present, all analysis must explicitly consider the time of year.

NO. The proposal makes abundantly clear that no line of evidence is really bulletproof in terms of establishing species status for *ridgwayi*. I won't be surprised if they turn out to be better treated as separate species, but for now there is way too much uncertainty in all respects.

NO. More data are needed that specifically links to localities near potential contact zone. Genetic and vocalization data would be particularly helpful. However, I am intrigued by the UCE data and the depth of the split between *ridgwayi* samples and northern/southern clade samples.

NO. These do seem like species but there are too many unanswered questions. It's not even clear to me which taxa would go with *ridgwayi* if it were split. The distribution statements in the proposal seem to indicate that both *burleighi* and *stuarti* occur in Belize, but the type locality of the former is in northern Belize and the latter is in central Guatemala. So, it seems more likely that *burleighi*, rather than *stuarti*, would be the taxon breeding in most of that country and therefore be part of the split species (i.e. *S. ridgwayi* with *burleighi* as a subspecies). Even photos and sound recordings from breeding colonies would go a long way towards sorting out the questions about distribution, breeding site characteristics, and potential sympatry. The genetic data are intriguing, but needs a focused study that incorporates all taxa and vouchered samples from known breeding sites, or at least from times when migratory taxa are absent.

NO. I agree with the proposal. We need a study that includes a broad sampling and includes molecular and vocalization data.

NO. This seems like a particularly messy system which needs much more work to figure out what's going on. The current available evidence seems contradictory in whether *ridgwayi* is a valid species, so it is clear that a more thorough analysis of genetics, vocalizations, and breeding behavior is needed to understand the species limits of these swallows.

NO. I agree with the proposal that there is a strong chance of multiple species within this complex, but we need more data before we can decide one way or another.

NO. I agree with the recommendation in the proposal that key information to make this call is lacking in several areas. Most importantly, are lack of samples in areas of close contact. It seems unclear how the subspecies would be divided up if split.

NO. I have heard *ridgwayi* a few times in the Yucatan, and maybe an allied subspecies (*stuarti*) in Belize too. I thought about the issue in view of the Howell and Webb (1995) split. I thought the calls sounded rather different, thus the split interested me. But as noted by all, much more research is needed. Looking at the ranges of *ridgwayi* and allied subspecies there may be a rather extensive area of sympatry or parapatry where studies could be done and maybe we could get some more detail on the calls of *ridgwayi* other than "harder than Northern Rough-winged Swallow" (Howell and Webb 1995). I note that in their description of the juvenal plumage, the wingbars and tertials are edged with cinnamon. This is shared with Northern Rough-winged and I find those characters the best way to age the latter species.

2024-A-11
Treat *Larus smithsonianus* and *L. vegae* as separate species from Herring Gull *L. argentatus*

YES (Option A). Great proposal! It seems clear that *smithsonianus* and *argentatus* are simply superficially similar, and their different-looking juveniles provide additional evidence of this. As mentioned in the proposal, the treatment of *vegae*+*mongolicus* could go either way but separate species status seems marginally like a better-supported option.

YES (Option A). Genetic evidence suggests that the species *Larus argentatus*, as currently considered by AOS, represents multiple taxa. Although the phylogeny from Sonthagen et al. (2016) is not fully resolved, with polytomies and low node support, and included only one sample from *argentatus smithsonianus*, in conjunction with other genetic studies (Sternkopf et al. 2010, Linklater et al. 2021) there is agreement that *smithsonianus* is a separate group from *argentatus*/*argenteus*. Although not of reproductive individuals, plumage differentiation of juveniles supports the split of *smithsonianus* from *argentatus*/*argenteus*. Additional information is needed to better understand *vegae* and *mongolicus*, but current evidence does not support them as part of *smithsonianus* or *argentatus*/*argenteus*.

YES (Option A). As noted in the proposal, there appears to be fairly good evidence to recognize *smithsonianus* as a separate species based on genetics, differences in juvenal plumage, and lack of response to at least feeding calls. Regarding *vegae*, I'm slightly swayed to also splitting that taxon (including *mongolicus*) based on the Sonthagen et al. (2016) study that included nuclear data in addition to mtDNA (versus Liebers et al. 2004). Note that there is currently a large genomic study of white-headed gulls underway, so hopefully that will help to further clarify relationships in the future once those data are published.

YES (Option A). A somewhat reluctant YES to Option A. I am more supportive of splitting *smithsonianus* apart from nominate *argentatus* and *argenteus* than I am for splitting off *vegae.* The one thing missing though is any analysis of the long display calls of the two groups, something that has helped sort out species status with other large white-headed gulls. Given the abundance and close proximity to urban areas of breeders, this would seemingly be fairly easy to do. As for *vegae* (more western *birulai* now not recognized by most as a valid subspecies), I'm even more uneasy, particularly with the inclusion of more poorly known *mongolicus* with this species. The subspecies *vegae* differs in adult plumage more from *smithsonianus* than either *argentatus* or *argenteus* does, mainly by its darker mantle. Juveniles differ from *smithsonianus* in the same way that *argentatus/argenteus* do (tail patterns and overall lighter and more speckled plumage though perhaps closer to *smithsonianus* and much individual variation). Subspecies *vegae* does nest on St. Lawrence Island, Alaska, where it is termed a fairly common and widespread breeder and is perhaps increasing (Lehman 2019). As with *smithsonianus* and *argentatus/argenteus* there is no 'long call' analysis. I note that Dickinson and Remsen (2013) treat American Herring Gull (*L. smithsonianus*) as consisting of three subspecies: *smithsonianus, vegae,* and *mongolicus.* That English name seems about as appropriate as American Pipit, although if *japonicus* is split as its own species, it would be more appropriate for the pipit.

As for English names, I'm fine with American Herring, European Herring and Vega gulls. I do wonder why everything has to be American this and American that. Most *smithsonianus* breed in Canada. East Siberian Gull rather than Vega Gull is a non-starter. It is cumbersome and while they do breed in the eastern portion of Siberia, the great majority breed in the Russian Far East with some breeding on St. Lawrence Island, Alaska. Mongolian Gull is fine, but again I oppose *us* making this split at this time.

YES (Option A). I've been going back and forth on this a lot. I think another committee member is spot-on in saying this is as close as we have to a syngameon in birds, which of course makes taxonomic decisions terribly difficult, in what is arguably one of the most problematic groups in avian taxonomy. The data we're dealing with is incomplete, and it sure would be nice to wait until the whole genome data are published.

I think the data in the Linklater thesis are problematic. There is clearly extensive gene flow here, but all of the *argentatus* samples are from Iceland, a place where *argentatus* arrived just ~100 years ago, and where based on phenotypic data we know that hybridation is rampant (as high as 55% of birds in some colonies; Ingolfsson 1970). So, are those *argentatus* samples in Linklater actually representative of the genetic patterns in that taxon? I don't think so. There is also some nuclear AFLP data in the Sternkopf et al. (2010) paper, which shows a very different pattern, and which I suspect is closer to the true evolutionary history. Using 43 highly differentiated loci (their Figure 7), they found *smithsonianus* was closer to *hyperboreus*, while *argentatus* was closer to *fuscus* (compare colors in K 5-7), and did not recover the polyphyletic patterns shown in the mitochondrial data.

There are also some odd things going on in the Linklater (2021) structure plots. The pale blue and dark blue colors are reversed in Figure 3a versus 3b/3c, so the proportions of ancestry in 3a vs 3b are actually essentially identical, which tells me that the species prior actually adds little or no information to population assignments. 3c is simply a population assignment based on allele frequencies (which population does an individual most closely resemble), so we shouldn't read too much into it in terms of gene flow. I was intrigued, though, by the one *argentatus/argenteus* and the three *hyperboreus* samples that genetically cluster with *smithsonianus*. Looking at Figure 3.4a and their sampling table, it looks like the three *hyperboreus* samples are from Nunavut, and given their clustering with *smithsonianus* I would hazard a guess that all three are *smithsonianus* x *hyperboreus* hybrids or misidentified *smithsonianus*. The one *argentatus/argenteus* that is genetically *smithsonianus* is from Iceland, and I wonder about the possibility of a *smithsonianus* showing up at a breeding colony there. *Smithsonianus* is known to occur in Iceland, although most detected there are juveniles in the non-breeding season. I don't think there's enough to be certain that these are hybrids, and to infer rates of hybridization from the structure plot. The BayesAss migration rate data seem to suggest minimal ongoing hybridization, which I find surprising given the known hybridization between many of these taxa based on phenotypes. However, I went and read Linklater (2021) and she notes that BayesAss did not converge for any runs involving *argentatus*, so those estimates are unreliable.

We also know that hybridization is rampant (or at least occurs) between basically every possible pairwise combination of Herring x another large *Larus*, and is often common in cases where the two parental species look nothing alike, even with drastically different back color or wing tip color. This is reflected in the rampant allele sharing in Figure 7 of Sternkopf et al. (2010). *Marinus* x *smithsonianus* is common in the northeast. *Hyperboreus* hybridizes extensively with *smithsonianus, argenteus/argentatus,* and at least some with *vegae*. *Smithsonianus* x *glaucescens* hybrids are common in southern Alaska. So, I'm not sure what the presence or absence of hybridization among *smithsonianus*, *vegae*, and *argentatus* would really tell us about species limits, even in a BSC framework. And I don't think anyone is suggesting we lump all the large *Larus*. That multiple species show up in multiple parts of the tree (*hyperboreus*, *californicus*, and of course *argentatus* sensu lato) also suggests that hybridization has been going on for quite a long time.

The nuclear data, especially, seem to indicate that *smithsonianus* and *argentatus* are not especially closely related within the large *Larus*, which tips the scales towards splitting for me. Yes, they are extremely similar phenotypically, but there are some differences in wingtip pattern of adults that differentiates most individuals. The juveniles are quite different, too, as others have noted.

Although it would be good to see more genetic data on *vegae*/*mongolicus*, the phylogeny in Sonthagen et al. (2016) seems to suggest that *vegae* at least is closer to *cachinnans* than to *smithsonianus*, again suggesting that the phenotype is misleading. Having seen a fair number of *vegae*, including as vagrants among *smithsonianus*, it strikes me as the most phenotypically distinct of the group, often quite strikingly so. The combination of the darker mantle, red orbital ring, fine head streaking (in basic plumage), dark eye, "string of pearls" in the primaries, and slimmer structure, all suggest to me that it is a different species than *smithsonianus*. Smaller individuals can look closer to *californicus* and some can look quite dark-backed.

The playback data from Fring is intriguing, but I would want to experiments with the long call, rather than just the feeding calls. Although the proposal suggests that nothing has been published, I was interested in whether recordings of the long call available online might indicate differences among the taxa. Surprisingly, long calls of all taxa are available on Macaulay. In listening to recordings, it sounds to me like *smithsonianus* has harsher introductory notes, while *vegae* gives a slower series. The differences are not as drastic as in comparison to *cachinnans* or *fuscus*, though.

smithsonianus:
https://macaulaylibrary.org/asset/355718271
https://macaulaylibrary.org/asset/224708
mongolicus:
https://macaulaylibrary.org/asset/591678611
vegae:
https://macaulaylibrary.org/asset/64404891
https://macaulaylibrary.org/asset/64404891
argentatus:
https://macaulaylibrary.org/asset/203898201
https://macaulaylibrary.org/asset/203905841
argenteus:
https://macaulaylibrary.org/asset/167776321
https://macaulaylibrary.org/asset/167774571

Olsen (2018) also has descriptions of the long calls that suggest some differences between the taxa. He lists *vegae* being drier / higher pitched than *argentatus* and hoarser than *smithsonianus*, and *smithsonianus* being "similar to *argentatus*, but somewhat dryer and deeper with quicker series: *ci-auww*, often combined with deep, cackling *gag-ag-ag-ag*."

Ingolfsson, A. (1970). Hybridization of Glaucous Gulls *Larus hyperboreus* and Herring Gulls *L. argentatus* in Iceland. Ibis, 112: 340-362.

Olsen, K. M. (2018). Gulls of the World: A Photographic Guide. Princeton University Press.

YES (Option A). As one would expect from any *Larus* gulls, the Herring Gull taxonomy and classification complex is very complicated, and there are no perfect choices available for us. More information would definitely be preferable, but the available evidence argues fairly strongly for species status, especially for North American and European populations. The split of these two populations is at least as strong as any other recognized gull species. The situation with *vegae* and *mongolicus* is definitely much different, but based on available evidence, I think it is best to treat them as a separate species together, although the placement of *mongolicus* may prove different with additional research (however, this should not prevent us from acting now on other splits in the complex that we feel are warranted).

YES (Option A). Good genetic and phylogenetic evidence for *smithsonianus* and *argentatus* to be considered separate species. The other taxa are more uncertain, but to me there is more evidence to not treat them as part of *smithsonianus*. More data of course are needed, but if we always wait for more data, nothing will ever change. To me, there is better evidence at this point to go ahead and treat as 3 species.

NO (Option C). Status quo: No change. This is a good proposal on a difficult group. But I think subspecies rank best fits our current understanding of these birds. Genetic distinctiveness and cladistic preferences for monophyly and sister relationships are of less utility in groups where gene flow is common. Phenotypic distinctiveness is also an attribute of subspecies and in this group I think that is a far better taxonomic fit. We have unpublished UCE data from our group that show extensive gene flow between *smithsonianus* and *vegae*, so under the BSC that part of the proposal does not fit the Beringian situation.

Most evidence suggests incomplete reproductive isolation and substantial levels of gene flow in members in contact; so sister relationships I don't think are particularly important – historic refugia are just that. The formerly isolated populations are out of refugia now and mixing quite a bit to create the ongoing confusion that their taxonomy has been. Northern hemisphere white-headed gulls are perhaps the best example of a syngameon in birds. We'd have to adopt a botanist-like species concept to recognize them as species, and that is unlikely (compare Barraclough 2019:6, *The Evolutionary Biology of Species*, Oxford, with the working BSC in ornithology).

Linklater's (2021) results look to me like substantial levels of gene flow (3a) enable more distinctive groups to emerge only when priors like phenotypic-based ID (i.e., taxon) are added to the model. If the results had been clean without priors, I'd be more inclined to see that these genetic differences might reflect species-level taxa. (Even with the priors, it looks like there is substantial gene flow.) Rather than split off *smithsonianus*, these results could be viewed to provide stronger support for lumping *hyperboreus* and *argentatus* (see also the PCA figures) or providing some confirmation that *hyperboreus* could be a species distinct from "*smithsonianus*" (though see fig. 3.3c and its three likely hybrids). Overinterpretation of STRUCTURE results is common, and the software is designed for population genetics, not species limits. In reading Linklater (2021), it looks like the results were not examined critically in terms of biological species limits, but rather interpreted wholly in the framework of the IOC (i.e., split) taxonomic framework. A problem with using Linklater to inform us about species limits between *argentatus* and *smithsonianus* is very limited sampling. All of her 6 samples of the former are from Iceland and, given the genomic results, likely have a lot of admixture from *hyperboreus*. However, and this is informative, 1/6 of the *argentatus* looks like a hybrid with *smithsonianus* (figs. 3.4 and 3.5; text results p.30). **That's a 17% hybridization rate in this small sample.** In fact, her fig. 3.5 PCA indicates substantial hybridization among all 4 of the "species" in the study. Finally, her analyses of migration rates are likely wrong, being far lower than both STRUCTURE and PCA analyses show.

I think we'll eventually find levels of ongoing gene flow that would require lumping these all under the BSC. There is some genomic work in progress that should shed additional light, but for now I don't see that the isolating mechanisms that are present are particularly effective among our current concept of *Larus argentatus* sensu lato.

NO (Option C). I feel that using the genetics results presented in the proposal are a poor means to understand reproductive isolation in this group. With current range expansions, LWH gulls have been shown to hybridize with little regard to genetics, or even plumage. There is no reason to think that such hybridization also did not occur in the past, as environments changed throughout the Pleistocene. In my view, current genetic similarities are as likely to be related to geography as they are to ancestry. In such situations it is imperative to use traditional means of assessing actual or potential reproductive isolation. Adult *smithsonianus* and *argenteus/argentatus* show negligible differences in plumage, soft parts, and morphometrics. Immature plumages have no bearing on reproductive isolation. Long call displays have not been studied in any sort of detail. I do not see any means by which *smithsonianus* and *argenteus/argentatus* wuld be reproductively isolated if they were in contact, especially since LWH gulls are especially prone to hybridize.

NO (Option C). A very difficult case, and I appreciate the quality of the proposal and the work done on the group thus far. Hybridization rates still seem quite high to me for separate species under the BSC, so I'm going to opt for the status quo in this instance and retain these as subspecies.

NO (Option C). It is a very complicated taxonomic group, the information in the proposal provides some information about the species limits between *smithsonianus*, *vegae* and *mongolicus*, but the results are weak and contradictory. Although there is a little light on the group, I think we should wait to have more information to make a change.

NO (Option C). As noted, the extent of gene flow among all these taxa suggests that the dichotomous branching pattern we're used to thinking of does not apply, Therefore, which taxa are each other's closest relatives may not be the appropriate conceptual framework and may obscured by gene flow, particularly the mtDNA that dominate current analyses. So, *smithsonianus* and *argentatus* may not appear to be each other's closest relatives in the analyses based on currently sampled variable loci only because they do not share an active contact zone. That said, I have no solution to this problem other than making the usual lame appeals for more data, particularly genomic data, as well as some solid data on whether eye ring color, bill spot color, long calls, or other things are involved in mate selection. I thank the proposal author for taking on this tough case and synthesizing the data for us – excellent proposal.

2024-A-12

Transfer *Coccothraustes abeillei* and *C. vespertinus* to *Hesperiphona*

YES. This seems to me the better option than maintaining what appears to be non-monophyly or to lumping all these disparate taxa into one genus. And, the *Hesperiphona* species differ obviously from *Coccothraustes*, and there was apparently never any published rationale for the lump.

YES. The species *vespertina* and *abeillei* were transferred from *Hesperiphona* to *Coccothraustes* without rationale. The phylogenetic relationships of grosbeaks in the genera *Hesperiphona*, *Coccothraustes*, *Eophona*, and *Mycerobas* are not resolved, a phylogeny including representatives of all the species in that grosbeak clade does not exist; therefore it is not clear whether *vespertina* and *abeillei* (*Hesperiphona*) are more closely related to *Coccothraustes* or to *Eophona* or *Mycerobas*. The phylogeny in Zuccon et al. (2012) provides some evidence that *Hesperiphona* and *Coccothraustes* might not represent sister groups. Moreover, Sushkin (1925), based on his anatomical research (mainly osteological), mentioned that *Perissospiza* [currently within *Mycerobas*] is extremely similar to *Hesperiphona* in the shape of the bill, and concluded that *Perissospiza* is the nearest relative to *Hesperiphona*. I think that transferring back *vespertina* and *abeillei* to *Hesperiphona* is the best approach until the phylogenetic relationships of the four genera of grosbeaks are better understood.

YES. I vote in favor, mainly because there was no published rationale for the lump. The relationships of these finches were uncertain when *Hesperiphona* was merged into *Coccothraustes.* Little clarification has emerged since. Viscerally, I have wondered about Evening Grosbeak, the species of *Hesperiphona* I know best, being with Hawfinch, a species I know fairly well in Asia (Japan) and also from multiple birds in western Alaska. The waddling gait of Hawfinches strikes me as pretty different from the foraging gait of Evening Grosbeaks, and their calls (contra Oscar) sound pretty different. Hawfinches calls on Xeno-Canto sound like the calls of a number of species of *Emberiza* buntings, or even like Northern Cardinals, not the loud and shrill Evening Grosbeak calls. I can easily hear the latter, less so the former, particularly when high overhead. Despite their similar shape, Hawfinches look larger headed and they are much less strongly sexually dimorphic. I believe that Hawfinches have a much more strongly undulating flight. I guess this is a philosophical matter, but I'm unhappy about maintaining a *fiat* decision for decades when there was no initial rationale, particularly when I think it may have been the wrong decision. For what it is worth, I see that Svensson *et al.* (2023) continue to recognize *Hesperiphona.*

Svensson, L., K. Mullarney, and D. Zetterstrom. 2023. Birds of Europe (3rd edition). Princeton University Press.

YES. I vote in favor, but without strong conviction. I wish we had some definitive evidence for these relationships. This solution prolongs our oversplitting of oscines at the genus level.

YES. Reasons are stated in the proposal.

NO. I could be swayed to change my vote, but the available molecular data do not provide strong resolution to phylogenetic relationships and *Coccothraustes abeillei* was not sampled. Although the original AOU decision to lump *vespertina* and *abeillei* into *Coccothraustes* was made without comment, I'd prefer to see stronger evidence for moving them back into *Hesperiphona.*

NO. The genetic data are inconclusive and do not require a change in genus limits. I would like to see more loci and taxa sampled before making a change, especially to be certain that *abeillei* and *vespertinus* are actually sister taxa. Vocally, *abeillei* and *vespertinus* are fairly similar, but *abeillei* bears more than passing plumage resemblance to some species of *Mycerobas*. If *abeillei* + *vespertinus* do turn out to be sister to *Coccothraustes* (thus not requiring a change), I would actually be inclined to resurrect *Hesperiphona* based solely on plumage dissimilarity, but I would prefer to be certain that *abeillei* and *vespertinus* form a clade. For now, I think we need more data and would prefer to stick with the status quo before making a change.

NO. Not for now, the molecular data presented are contradictory. I prefer to wait for more data and a robust and clear analysis.

NO. I definitely follow a philosophy of more inclusive genera as being more informative about the taxonomy and relationships of species rather than many smaller ones. While the relationships of these grosbeaks are clearly unresolved, the evidence for removing *abeillei* and *vespertinus* from *Coccothraustes* is not compelling to me; further, while not part of the proposal and outside the scope of the NACC, to overcome the potential paraphyly of identified in Zuccon et al. (2012), perhaps a better move would be to merge both *Eophona* and *Mycerobas* into *Coccothraustes*, as they share many similarities to the taxa we currently recognize in *Coccothraustes* (the *Mycerobas* grosbeaks being very similar to *abeillei*, and the *Eophona* grosbeaks being similar in respects to *coccothraustes*).

NO. I would rather not make a change based on an assumption (*abeillei* and *vespertinus* are sisters). This can easily be resolved with additional taxon sampling and analyses.

NO. The molecular phylogeny does not provide strong evidence for the non-monophyly of *Coccothraustes* and *Hesperiphona*. Only the nuclear tree in Fig. 2 of the proposal shows this relationship, and it's not strongly supported. Therefore, changing the genera is not necessarily. There may be other reasons (morphology, vocal, etc.), but these are not presented in the proposal. I understand that the switch was made in the 6th edition without comment, but that doesn't necessarily mean there wasn't a reason.