## 2020-B-1
## Transfer Buff-fronted Foliage-gleaner *Philydor rufum* to the genus *Dendroma* (as *D. rufa*)

**YES**. The well supported phylogeny necessitates this change.

**YES**. Non-controversial, and we should follow SACC.

**YES**. This is a pretty clear-cut case, and we should align with SACC.

**YES**. Requires fewer name changes; leaves the name *Ancistrops strigilatus* intact.

**YES**. Following SACC, this seems the most prudent solution to deep polyphyly in *Philydor*.

**YES**. This seems straightforward for us. *Philydor* is polyphyletic, and transferring *rufum* to *Dendroma* is the answer for us with this taxon. The treatment of the other two taxon is not our decision, but the treatment of rufa in *Dendroma* is consistent with SACC.

**YES**. Option A seems like a reasonable way to go, given the long branch between *Philydor rufum* (plus *P. erythropterum*) and *Ancistrops.*

**YES**. I assume that Slaty-winged Foliage-gleaner remains in the genus *Philydor.*

**YES**. Option A best reflects the age of the split. Looks like there are several other genus-level issues on this tree.

**YES**. Though outside our purview, I prefer option B rather than have still another monotypic genus.

**YES**. This is an arbitrary decision given phenotypic similarities among the three, but looking at the time-calibrated phylogeny, treating *Ancistrops* as separate from *Dendroma* appears to me to be the better decision; this was also the view of SACC as a whole.

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## 2020-B-2

## Treat American Comb-Duck *Sarkidiornis sylvicola* as a separate species from *S. melanotos*

**YES**. Original reason for lumping (mating in captivity) not applicable to modern BSC.

**YES**. I would like to see more data on differences in phenotypic and behavioral traits as well as genetics, but the original rationale for lumping them was weak (hybridization in captivity). I don't see any reason not to go with the SACC recommendation.

**YES**. While I don't feel this is the strongest candidate for splitting, the reason these taxa were lumped in the first place is very weak. The fact that two waterfowl species hybridize in captivity is fairly meaningless, given the propensity of numerous waterfowl taxa to hybridize, even across genera. Given that this is a species mostly restricted to South America, I also feel we should defer to SACC in this case, andthey have already voted to split.

**YES**. The evidence here is not great, but this is primarily a SACC species and we should follow their lead here.

**YES**, following SACC for a species that is widespread in South America, but only has a small range in our area (eastern Panama). The data supporting the split is marginal.

**YES**. The lump was never supported by any evidence of lack of reproductive isolation. In addition, the species is barely in our area (only in the Darién of eastern Panama), so it seems best to follow the SACC here.

**YES**. Following SACC, I agree that reproductive viability via captive breeding is not a valid criterion for lumping under the BSC.

**YES**. I vote YES largely because the initial rationale for the lump was based on nearly irrelevant captive breeding. By the way, this one is screaming out for a genetic analysis, not for classification but for estimating the age of the split. These two really do not seem to differ very much, phenotypically, thus suggesting a relatively recent split, i.e. transoceanic dispersal. I wish we had comparative information on displays and voice on which to evaluate this one in terms of species rank.

**YES**, though a weak one. It seems like we're splitting this just because we think lumping them in the first place was wrong, not with any new data to test that hypothesis.

**YES** (but borderline). Few waterfowl are naturally as widespread as *Sarkidiornis*, but another example is Fulvous Whistling-duck, and White-faced Whistling-duck and Southern Pochard are nearly so. This and the fact that *Sarkidiornis* is strongly dispersive mean that the range discontinuities are not especially meaningful --- Asian and African populations are not even separated subspecifically! Nor are vocalizations particularly helpful in this case, and I take it that genetic divergence level is unknown.

Thus, we are left with morphology, mainly the dramatic difference in flank color, plus minor size differences (the sexes being highly size-dimorphic complicates this). Having just looked at many images, I'm unconvinced that there is any real difference in comb shape. It varies tremendously in males and can be high and rounded or squared off in both taxa.

That said, there are other waterfowl species that differ less strongly in plumage, and the original rationale for lumping was ill-founded, so we should continue our policy of following SACC for marginal NACC-region species.

**NO**. This is a borderline situation. I am sympathetic with the sentiment that the initial lump was arbitrary and was based on hybridization of the two in captivity, but splitting here seems arbitrary too. The differences on the males involve only a color difference on the flanks. The females are very similar between the two, though maybe *sylvicola* has darker gray flanks. The size differences are slight. As for the vocalizations, Madge and Burn (1988) says "relatively silent, but sometimes utters a low croak when flushed. During breeding season several short wheezy whistles, grunts and hisses may be given in display or aggression." There is a comment by Madge and Burn (1988) under Population that *sylvicola* has been "little studied in the field." Madge (1988) also points out that the world range of this species is similar to Fulvous Whistling-Duck *Dendrocygna bicolor* which is now treated as a monotypic species. Unless someone can demonstrate there is something truly different about these two types, other than flank color, I'd feel better maintaining the status quo for now as one polytypic species. Madge, S. and H. Burn. 1988. Waterfowl. Houghton Mifflin Company.

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## 2020-B-3
## Transfer White-shouldered Tanager *Tachyphonus luctuosus* to the genus *Loriotus*

**YES**. This is necessary because of priority.

**YES**. Seems required by the rules of nomenclature.

**YES**. Based on priority for *Loriotus*.

**YES**. Necessary change by ICZN.

**YES**. Unfortunately, this needs to be *Loriotus* to be consistent with ICZN.

**YES**. The ICZN rules are fairly straightforward in this case, and there really is no other option but to adopt *Loriotus* for this species, as has been done by SACC.

**YES**. A straightforward case of priority under the Code.

**YES**. This assumes that White-lined Tanager (*Tachyphonus rufus*) and Tawny-crested Tanager (*Tachyphonus delatrii*) remain in *Tachyphonus*, although this is unclear in the motion? In fact it is confusing as it states that White-lined is the only species in our area. Tawny-crested and White-lined are also in Central America.

**YES**. Priority of *Loriotus* is clear, *Islerothraupis* has a very short history of usage, and IUZN rules dictate that we use *Loriotus.*

**YES**. Following ICZN rules, *Loriotus* has clear priority.

**YES**. There is seemingly no question that *Loriotus* has priority.

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## 2020-B-4a

## Revise the taxonomy of species currently placed in *Locustella*: Transfer *L. ochotensis* to *Helopsaltes*

**YES**. Fascinating group.

**YES**, mainly because this is a group outside our area and we should follow the lead of relevant authorities. In general, however, I am not a fan of changing generic names unless absolutely necessary based on phylogenetic topology (and to a lesser extent age).

**YES**. This is a reasonable treatment for reasons given in the proposal.

**YES**. The phylogenetic evidence is clear-cut, so the question is where to draw the name boundaries, and as is often true there are alternative viable options. As these are vagrants in our area we should follow the lead of other authorities that have already adopted these changes.

**YES**. One would assume that if the Pallas's Grasshopper-Warbler (*L. certhiola*) is accepted (fall 2019 record from Gambell) it too would be placed in *Helopsaltes*, as it is closely related and apparently hybridizes with *ochotensis.*

**YES**. For consistency in crown-group ages and differences in vocalization complexity, it makes sense to follow recommendations of Alström et al. (2018) to transfer *L. ochotensis* to *Helopsaltes*. Will also promote congruence among taxonomic authorities (i.e., IOC).

**YES.** Recognize *Helopsaltes*, given the depth of the split and the diagnosably different songs of members of this clade.

**YES**. As outlined in the proposal, two genera are warranted to maintain consistent group ages to facilitate comparative biology.

**YES**. This seems a little weak.

**YES** (weakly). Maintaining *Locustella* would be more stable, and the morphological, and behavioral differences seem quite weak to warrant separation as different genera. Nonetheless, the well supported phylogeny indicates a rather deep break between the two clades, and it may be useful to have that knowledge reflected in the taxonomy.

**YES** (weakly). Given that this is a group that largely occurs outside of our area, I agree with others that we should follow their lead on these species. However, I generally prefer to keep monophyletic groups together in a single genus; I'm not a huge fan of using divergence times for these types of decisions, especially in a group of birds that are fairly morphologically uniform. The song data, however, is fairly compelling.

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**2020-B-4b**

**Revise the taxonomy of species currently placed in *Locustella*: Revise the linear sequence of species**

**YES** - 7 without comment.

**YES**. Sequence needs to be changed to be consistent with our methodology.

**YES**. The linear sequence issue is straightforward based on the phylogeny.

**YES**. Linear sequence should be revised regardless of whether genus transfer is voted in or not based on new phylogenetic information.

**YES**. Reflect the phylogeny as opposed to guesswork.

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**2020-B-5a**

**Change the taxonomy of the Phasianidae: Eliminate subfamilies**

**YES** - 1 without comment.

**YES**. Thanks to Terry for working through this one.

**YES**. Nice series of papers resolving a lot in an important group.

**YES**. While we could recognize two or more subfamilies, the line between what is and what is not a subfamily has to be drawn arbitrarily somewhere, and in this case not recognizing them is as good a solution as any, especially given our regional mandate.

**YES**. The phylogenetic data do not support our current classification.

**YES**. Subfamily ranks clearly no longer justified based on recent genetic data. Thanks to Terry for taking care of this one, which was overdue.

**YES**. I agree that the subfamilies as currently organized are not valid, and it's not very meaningful to subdivide Phasianidae just to retain Tetraoninae and Meleagridinae. Plus, as was brought up in the proposal, it is largely out of our place to subdivide the family into multiple groups that are all found outside of our area. I could be in favor of recognizing the two subfamilies, Phasianinae and Rollulinae, as in the most recent Howard and Moore Checklist (2014), but it doesn't seem like an important step for us to take at this point.

**YES**. Eliminate subfamilies because recognizing them leaves smaller clades in need of new names.

**YES**. The current sequence and subfamily taxonomy is completely at odds with recent phylogenies. Using subfamilies in our context does not add anything useful to the classification.

**YES**. Subfamilies are only a useful taxonomic rank if there are multiple subfamilies within a family, so given that current subfamilies are not monophyletic and other global references do not recognize any subfamilies, it makes sense to me to abolish subfamilies within Phasianidae.

**NO**. It is clear that our current treatment cannot be maintained, but I am not convinced the best way forward is dropping all the subfamilies. It looks like maybe a different 3-way split would tell us useful information about the structure of the family, I am thinking about recognizing Rollulinae, Phasianidae, and then the Coturnix to end (not sure what the name would be, but I suspect one exists) I am sad to lose the basically New World Grouse + Turkey clade, but there doesn't appear to be a way to rescue it.

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**2020-B-5b**

**Change the taxonomy of the Phasianidae:** Revise the linear sequence of species

**YES** - 5 without comment.

**YES**. This is overdue, and this sequence looks good to me.

**YES**. Linear sequence needs revising based on new phylogeny.

**YES**. The linear sequence seems fine with me.

**YES**. Linear sequence should be updated to reflect our improved knowledge of phylogenetic relationships.

**YES**. Non-controversial.

**YES**. We definitely need to rearrange the sequence of genera.

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## 2020-B-6
## Revise the linear sequence of the macaws (*Ara* spp.)

**YES** - 2 without comment.

**YES**. The new data support this change.

**YES**. This seems like the best sequence given what we currently know.

**YES**. New linear sequence necessary based on new topology.

**YES**. A minor change based on molecular phylogenetics that also accommodates uncertainty by recognizing a polytomy btwn *macao* + *chloropterus* + *militaris/ambiguous*.

**YES**. This seems like a fairly straightforward case, and the reasons laid out in the proposal are very solid and fully support this decision.

**YES**. Not too surprising that the much smaller and West Indian *A. tricolor* is not closely related to other red macaws. The phylogenies, though not very robust, are at odds with our current sequence. Kind of odd that they have complete mtDNA sequences of the extinct *tricolor*, but incomplete sequences of extant *chloropterus* and *ambiguus*, the former which is widely kept in captivity.

**YES**. Assuming the phylogenies are free of major confounding issues, this is clear-cut.

**YES**. Hopefully someone will publish a phylogeny soon that resolves the relationships among the extant large red/green macaws better.

**YES**. Straightforward changes required by latest phylogenetic data, the results of which had been anticipated by several earlier authors. No surprises here.

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## 2020-B-7a
## Revise the taxonomy of hummingbird genera *Atthis* and *Selasphorus*: Merge *Atthis* into *Selasphorus*

**YES** - 2 without comment.

**YES**. Well-supported by the phylogeny.

**YES**. Much better to merge in this kind of situation.

**YES**. The phylogenetic data clearly support the inclusion of *Atthis* in *Selasphorus.*

**YES**. Despite the behavioral/display differences, the phylogeny clearly shows that *ellioti* and *heloisa* are within *Selasphorus.* I much prefer keeping all within *Selasphorus* then separating out the three clades as genera.

**YES**. Merging *Atthis* into *Selasphorus* is the simplest and most straightforward way to reconcile the phylogeny with classification.

**YES**. Straightforward change required by latest phylogenetic data.

**YES**. Merger favored as *Atthis* position as currently recognized renders *Selasphorus* paraphyletic.

**YES**. A straightforward solution to paraphyly. The morphological diagnosis of *Atthis* is not very compelling in terms of the characters being obviously generic-level, and any other solution requires naming new genera.

**NO**. I am uneasy about the expanding genus *Selasphorus.* I was not comfortable with the merging of *Stellula* given the distinct vocal and behavioral differences, and this continues the trend. As the authors of the proposal state *Selasphorus* is paraphyletic and the alternative course is recognizing three genera, including Broad-tailed in its own genus. I'd like to consider that option before further expanding the genus. I have long heard grousing from Michael Retter and others that Glow-throated Hummingbird *Selasphorus ardens* isn't a valid taxon. Any thoughts on this issue?

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**2020-B-7b**

**Revise the taxonomy of hummingbird genera *Atthis* and *Selasphorus*: Change the linear sequence of species in these genera**

**YES** - 6 without comment.

**YES**. Well-supported by the phylogeny.

**YES**. Necessary based on the phylogeny.

**YES**. Change sequence to match phylogeny.

**YES**. The linear sequence seems fine.

**NO** - 1 without comment.

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**2020-B-8**

**Split *Aegolius acadicus brooksi* from Northern Saw-Whet Owl *A. acadicus acadicus***

**YES**. This is a well written and well formulated motion. My view on this is colored from my time in Costa Rica a little more than a year ago (January 2019) in Costa Rica. Up in the Talamanca we heard an Unspotted Saw-whet Owl (*Aegolius ridgwayi*) sing for over an hour. I heard pretty much continuous tooting along with screams and other cat calls. I know the vocalizations of Northern Saw-whet Owl well and I couldn't hear a bit of difference between these two recognized species. Here, we have a similarly allopatric population that shares, with Unspotted, a distinct morphology. As indicated in the motion, 7 of 120+ specimens from Haida Gwaii (nearly 6%) are nominate *acadicus*, the rest the expected *brooksi*. That's a large sample, and none show intergrade characteristics. As pointed out by the authors of the motion, nominate *acadicus* is resident in the Alexander Archipelago on Forrester Island, some 50 miles from the northern end of Haida Gwaii. I would imagine that *brooksi* Northern Saw-whets, start territorial "singing" (tooting) by February. It would appear that no or few *acadicus* have been lured and pair-ponded with *brooksi,* as indicated by no intergrade specimens. Yes, these fall/winter *acadicus* might be programmed to return off the island come spring, but in a sense they are less allopatric from each other than Unspotted and Northern Saw-whet. The authors mention the possibility that *brooksi* may be partly marine in its ecology. This is interesting and would be a useful adaptation to an island environment. Dan Gibson had mentioned to me that many (most?) of the specimens were taken from the fringe road (presumably hit by cars) near the ocean. I wonder if there has been any analysis of stomach content from the specimens. I note the comments about the calls. For what it's worth, Weidensaul (2015) says they are said to have higher pitched vocalizations, but no citation is given.

My view is that if you don't recognize *brooksi* as a separate species, you might as well go and lump Unspotted Saw-whet. Other than maintaining stability, is there any other reason why *brooksi* shouldn't be recognized, but Unspotted Saw-whet should?

**NO**. It would really help to have more information on actual or potential reproductive isolation. The genetic evidence is interesting, but it is unclear whether it results from simple geographic isolation or from a more biological cause. We all know what would happen if we were to raise to species status every isolated population with some reduction in gene flow.

**NO**. I think the absence of distinct voice in these two populations makes it hard to split them, despite the plumage differences.

**NO**. This is an interesting and challenging case. As Van wrote, the lack of vocal divergence is a strong reason to reject splitting as separate species. The importance of using vocalizations to identify species limits in owls and other night birds cannot be overstated. In contrast, the within-population variability in plumage in many species limits the utility of plumage as a criterion for identifying species limits. I am surprised that there is any gene flow, given that *acadius* is only a winter visitor to Haida Gwaii. Playback experiments would be very interesting.

**NO**. This is a difficult case because the species do not overlap during the breeding season, so "potential to interbreed" has to be inferred from other characters. The plumage differences are compelling, but these probably don't relate to reproductive isolation. The plumage differences and genetic differences together make a strong case for lack of, or very limited, gene flow. Thus, these two forms would easily be considered separate species under several other definitions of species. Given that the checklist committee uses the biological species concept, I would argue we need to consider the differences as subspecific.

**NO**. While this is a very interesting case, I would like to see some additional research on this intriguing system, including playback experiments and diet studies that look at **both** *acadius* and *brooksi* from Haida Gwaii showing that they forage in different habitats when they co-occur. Certainly, the diet evidence suggests that *brooksi* has a different foraging niche, but those papers also point out there is very little known about coastal *acadius* populations. Since the two do overlap for at least part of the year, it could afford us with the opportunity to study how the two subspecies interact, if at all, when they co-occur. Does *brooksi* have a distinct breeding season that may further strengthen reproductive isolation between the taxa? The genetic data and morphology is not quite enough for me. Especially for an owl, I would want to see a deeper dive into analysis of vocalizations.

**NO**. This is an interesting case, and *brooksi* is certainly diagnosable in plumage, but I don't see evidence yet for elevating it to species. The proposal states that "A rigorous comparative investigation of the advertising calls of *brooksi* and *acadicu*s has not been undertaken, but based on published pitch and frequency information they do not appear to be appreciably different." Vocal differences are clearly important in owl systematics, and so I'd like to see a rigorous analysis to confirm the lack of differences (or not). Playbacks also would help elucidate species limits in this case. I find it interesting that gene flow appears to be higher from *brooksi* into *acadicus* (than the reverse) despite the fact that *brooksi* is more sedentary. These taxa appear to be in the process of incipient speciation, but I'm comfortable keeping them as subspecies for now.

**NO**, although this is an interesting borderline situation. Vocal analyses and playback experiments might further bolster the case. Nevertheless, I don't think that allopatric owls must necessarily be vocally distinct to be separate species---after all, there are only so many ways to hoot, and if they are separated geographically they can differentiate in other ways to species level---but in this case, there is some gene flow and their divergence is very recent. That said, *brooksi* is impressively divergent in plumage, and although some owl taxa do have multiple morphs, most species otherwise have fairly to very limited plumage variation, and *brooksi* seems to form an exception to that pattern.

**NO**. The DADI models based on 1000s of UCE loci clearly favor scenarios with ongoing gene flow between *A. a. brooksi* and *A. a. acadicus*, the number of immigrants per generation is low, and there is clear evidence of phenotypic differentiation / diagnosability. How much gene flow is too much to recognize a split will forever be up for debate, but in this case, I think *brooksi* and *acadicus* are best treated as subspecies that exhibit geographic differentiation in phenotype and allele frequencies rather than full species split. Detailed vocal / playback analyses would be very useful in determining the current degree of reproductive isolation.

**NO**. Kevin and colleagues have done a great job in highlighting the unique features of this population. However, species limits in owls (and nocturnal birds in general) are nearly universally defined by voice, not plumage. In fact, many owls have two or more color morphs within a local population, much less a species; *Glaucidium brasilianum* in particular is remarkable in having dramatic individual variation. Of course, a fixed paedomorphic plumage is not the same as a color morph, but nonetheless we have no evidence that plumage variation of any kind in owls is relevant to species limits. We do know, however, that vocal differences play key roles in defining species, as in Eastern vs. Western screech-owls. Species limits in owls are consistently defined on that basis. As noted in the proposal, there are no known consistent vocal differences between *brooksi* and the mainland N. Saw-whet populations. Therefore, in my opinion, there is no reason to change species limits. The only rationale for ignoring voice, as outlined in the proposal, is that *A. ridgwayi*, treated as a separate species by us and most sources, seems not to differ dramatically in voice from *A. acadicus.* This is the strongest point in the proposal in my opinion. However, this suggests to me that our current treatment of *A. ridgwayi* needs to be re-evaluated. In fact, as noted in the proposal, there are no rigorous analyses of the songs of all three taxa; should such studies show differences comparable to other sister taxa of owls, then I reverse my vote. Better yet, how about some playback trials under Kroodsma-endorsed protocols?

As for the other evidence used to support species rank for *brooksi*:

1. Low gene flow. If the taxa were sympatric or parapatric during the breeding season, then these data would provide overwhelming evidence for species rank. But *brooksi* is sedentary and endemic to those islands, whereas nominate birds are known only from their non-breeding season. Therefore, assessments are in my view irrelevant. In fact, that there is evidence for <u>some</u> gene flow is further evidence in my opinion for subspecies rank because opportunities for gene flow are so tenuous. My only real quibble with the proposal is the following statement: *"These results show that despite opportunity for gene flow, it is occurring at remarkably low rates."* What opportunity is there for gene flow if nominate birds are not known to breed there regularly? Given that nominate birds do not breed there regularly, my interpretation is that *gene flow is occurring at remarkably <u>high</u>, not low, rates.* The BSC framework treats *brooksi* and nominate *acadicus* as allopatric, so direct assessment of reproductive isolation by gene flow is not possible and must be inferred from comparisons to known, reproductively isolated taxa in the same group. Yes, *brooksi* is certainly on a separate evolutionary trajectory, but under a BSC framework, it hasn't reached species rank yet (roughly consistent with the estimate of only 16K years of separation). "Separate evolutionary trajectory" itself is difficult to define because in theory any sedentary island colonist could be considered to be on that trajectory on Day 1 of successful breeding.

2. Sedentary vs. migratory. This is not a character that defines species limits. Hundreds of species of birds are partially migratory, with no sign of reproductive isolation between populations. American Robin, Blue Jay, American Crow, N. Mockingbird, etc. etc. have migratory and sedentary populations. This is not to say that such differences might not eventually contribute to cessation of gene flow, as potentially in *brooksi* (and well-documented in *Sylvia atricapilla* by Helbig 1991, Rolshausen et al. 2013), but differences themselves are not sufficient for assigning species rank. Zink (2011, *BJLS*) showed that migration as a trait shows idiosyncratic patterns within a phylogeny and that this trait is highly labile (and I strongly recommend Bob's paper in general for anyone assessing the phylogenetic interpretation and significance of migration).

**ABSTAIN** - 1.

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## 2020-B-9a
## Change the generic taxonomy of Puerto Rican Screech-Owl *Megascops nudipes*: Remove it from the genus *Megascops*

**YES**. See comments for B.

**YES** to removing *M. nudipes* from *Megascops*.

**YES**. Removing *nudipes* from *Megascops* seems like a better option then merging Flammulated Owl into that genus (recognizing the differences noted in the proposal).

**YES**, given the great depth of the *flammeolus/nudipes* and *Megascops* clades.

**YES**. I am ok with this, although I think merging them all to *Megascops* would require the fewest name changes (only *Psiloscops* would need to be changed). In general, when new topologies conflict with classification, I would prefer to change as few names as possible to preserve stability. However, I appreciate the argument that the time of divergence of *Psilocops/Gymnasio* is much older than the species within the *Megascops* clade. And keeping *Megascops* as a clade preserves the integrity of 'screech-owls'.

**YES**. This move seems makes the most sense to me to rectify paraphyly of *Megascops* as currently defined while still recognizing the phenotypic distinctiveness of *Psiloscops*.

**YES**. One of these changes is clearly necessary based on the phylogenetic evidence. But I think that 2a (Merge Puerto Rican Screech-Owl and Flammulated Owl into *Gymnasio*) is also a good option, since it would highlight this affinity. I suspect we would do 2a if *Psiloscops* had priority over *Gymnasio*.

**YES**. It certainly doesn't look like any *Megascops* I've ever seen. It does look somewhat like the Bare-legged Owl from Cuba for which I've seen many. I would certainly not favor putting it in *Psiloscops.*

**YES**. The phylogenies clearly show that *nudipes* should be removed from *Megascops*. Although *nudipes* could be placed with Flammulated Owl, they are very divergent morphologically and it is a quite old split, thus I strongly prefer that they be kept in separate genera.

**YES**. A generic realignment is required by published phylogenetic data, and placement of Flammulated Owl and Puerto Rican Screech-Owl in the same genus would defy all phenotypic standards for delimiting owl genera. Also, the estimated age of divergence at 12.5 MYA is at the far end, at best, of taxa considered to be congeners. (Tangentially, looking at Fig. 1, *Megascops* itself should be split into two genera in my opinion.)

**YES**. I think adopting the proposed treatment of monotypic genera for *nudipes* and *flammeolus* is the best treatment for these odd small owls.

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## 2020-B-9b
## Change the generic taxonomy of Puerto Rican Screech-Owl *Megascops nudipes*: Place it in a monospecific *Gymnasio*

**YES** - 5 without comment.

**YES**. See comment above.

**YES**. This is a tricky situation, but I really don't like adding more monotypic genera to the mix. I'd prefer combining Flammulated and Puerto Rican Screech-Owl into *Gymnasio*, despite the instability it causes with Flammulated Owl. In this case, I think it's more useful to have a larger *Gymnasio* that also includes Flammulated Owl, as two monotypic genera don't tell us very much about the evolutionary history of these owls; combining them into *Gymnasio* is a nod to their sister relationship, but also recognizes that they are quite different from the rest of the screech-owls in *Megascops*.

**YES**. The genus *Gymnasio* for *nudipes* is appropriate.

**YES**, given the 12-13 my divergence, very different morphology, and extremely different vocalizations of *flammeolus* vs. *nudipes*. Revision to common name needed.

**YES**. I think restricting Screech-Owl to *Megascops* makes the most sense, although in principle we could instead return to using Screech-Owl for Flammulated Owl.

**NO** to erecting another monotypic genus, so let's have a two-species *Gymnasio* (= YES to option 2a.).

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## 2020-B-10
## Revise the linear sequence of *Megascops* and related genera

**YES** - 4 without comment.

**YES**. This is a clean-cut case and a well laid out proposal.

**YES**. This sequence matches what I came up with.

**YES**. Sequence looks good following our protocols.

**YES**. Thanks to Max for working through this.

**YES**. It does seem that there is a slight conflict between the phylogeny and the current sequence with regard to *cooperi/kennicottii/asio*, but I agree that without *seductus* in the analysis it's nevertheless best to leave that part of the sequence unaltered for now.

**YES**. Clearly, a sequence change is required. From Fig. 1, I independently constructed a sequence using standard conventions and produced a sequence identical to the one in the proposal.

**NO**? Basically I agree that *Megascops* should be rearranged to reflect the taxonomy of Dantas et al. But I don't think this sequence is quite right based on our conventions. As I read the phylogeny in Dantas and our taxonomy, we recognize 3 species in the *M. guatemalae* clade guatemalensis, centralis and the extralimital *roraimae*. The *M. asio* clade has 4 species, *asio, kennicotti, seductus* and *cooperi*. I think that means the *guatemalae* clade should precede the *asio* clade, not follow it. That would mean the sequence of *Megascops* should be:

- *Megascops trichopsis*
- *Megascops clarkii*
- *Megascops choliba*
- *Megascops barbarus*
- *Megascops guatemalae*
- *Megascops centralis*
- *Megascops kennicottii*
- *Megascops asio*
- *Megascops seductus**
- *Megascops cooperi*

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## 2020-B-11
## Split *Formicarius moniliger* from Black-faced Antthrush *F. analis*

**YES**. Vocal differences indicate they would likely behave as separate species if they were in contact; genetic differences are also compelling. Mayan Antthrush seems like a good choice.

**YES**. This seems straight-forward, particularly given the vocal differences.

**YES**. The vocal differences, combined with phenotypic and genetic differences, support elevating *moniliger* to species. I agree with Patten that playback experiments would be interesting, especially given the lack of an apparent contact zone. Mayan Antthrush is a fine name.

**YES**. Seems warranted by multiple lines of evidence. Very well crafted proposal on a complicated situation.

**YES**. The analysis of vocal differences, plumage differences, and genetic differences all support splitting these two taxa. The work to document that vocal differences are maintained as one approaches the range edges of these species is particularly compelling evidence that they likely exhibit reproductive isolation. I would like to see some playback experiments near where their ranges come close, but, otherwise, this seems like a very strong case for a split. I vote to adopt the name Mayan Antthrush for this group for the reasons laid out in the proposal.

**YES**. Good work on this proposal.

**YES**. Several different sets of data correspond to indicate the *moniliger* should be split from *analis*. Mayan Antthrush is a good name and an improvement on previously suggested Mexican Antthrush.

**YES**. Splitting *moniliger* from the rest makes a lot of sense, given the vocal differences (especially because they are sub-oscines) and the lack of any changes close to the area where they are geographically closest. It would be nice to figure out the *hoffmanni/analis* split, but that appears to be much trickier. Mayan Antthrush is a great name, only lacking in longevity for a perfect choice.

**YES**. This is already adopted in e.g. IOC World Bird List and other sources. Note that the proposal's Fig. 2 caption should read "Honduras" instead of "Guatemala". I favor adoption of Mayan as the common name of the *moniliger* group, as its range is largely coincident with the Mayan civilization; it is otherwise not that widespread in Mexico but also occurs in much of Guatemala, all of Belize, and western Honduras; and "Mayan Antthrush" has also gained familiarity recently through use on other lists. I favor tentatively retaining Black-faced Antthrush for the remaining groups until we hear back from SACC. Much better not to fuss with that name until there is hope for some stability.

**YES**. Although, I would really like to see genetic data from Honduras / nearby populations of *moniliger* and *analis* accompanied by playback to be definitive. But given the integrative data at hand, it seems the populations are readily diagnosable in multiple traits, exhibit substantial genetic divergence, and do not occur in sympatry. Mayan Antthrush seems a good solution to the issue of English names, but a full SACC proposal seems due soon after this.

**YES**. Although the new evidence is from a field guide, an unpublished dissertation, and an online-only non-peer-reviewed source, together I think the evidence is so strong and from enough independent sources that we should overlook our usual rules on this and adopt the split, which Steve Howell was on to 25 years ago. Collectively, the new data place burden-of-proof on a single species treatment. As for English names, YES on Mayan Antthrush as a tentative solution, but a full proposal on this, which includes a compound name option (e.g. Mayan Black-faced Antthrush) etc. is advisable once SACC deals with *hoffmanni-analis*, which needs to happen soon.