AOU Classification Committee – North and Middle America

Proposal Set 2014-A

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02	02	Transfer *Spinus psaltria, S. lawrencei,* and *S. tristis* to *Sporagra* or to *Astragalinus*
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1: Transfer *Spinus notatus, S. xanthrogastrus,* and *S. cucullatus* to *Sporagra*

2: Transfer *Spinus psaltria, S. lawrencei,* and *S. tristis* to *Astragalinus* or to *Sporagra*

These proposals would change the classification and nomenclature of most species of North American siskins and goldfinches, currently placed in the genus *Spinus*, either by transferring species to the genus *Sporagra* or by transferring some species to *Sporagra* and others to *Astragalinus.* Three species, in addition to type species *S. spinus*, would be left in *Spinus*.

Votes of NO on either proposal would leave the relevant taxa in *Spinus*.

Background:

Until recently, most post-Peters references lumped the North American siskins and goldfinches into an expanded version of the genus *Carduelis.* Chesser *et al.* (2009) returned the native North American species (as well as introduced species *cucullatus* and accidental species *spinus*) to the genus *Spinus*, based on the mtDNA phylogeny of Arnaiz-Villena *et al.* (2008), leaving only the introduced European Goldfinch in *Carduelis*.

New Information:

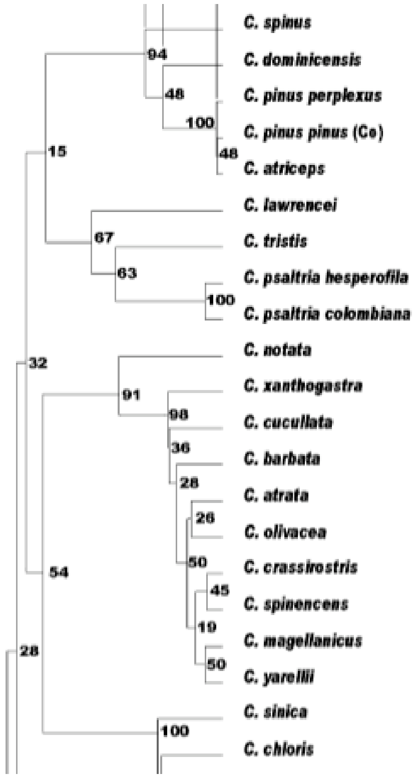
Nguembock et al. (2009), in a phylogenetic study of the Fringillidae based on data from five genes (three nuclear, two mitochondrial), found that the type species of *Spinus* (the Eurasian Siskin *S. spinus*) is not closely related to the New World members of this genus that they sampled, but instead is more closely related to species of *Acanthis* and *Loxia*. They recommended that the species of Neotropical siskin that they sampled, which included most species that occur mainly or exclusively in South America, be moved to the genus *Sporagra*, which appears to be the oldest name for this group of species. Based on this paper, the SACC transferred all species of siskin in their area to *Sporagra*, and proposed moving the Lesser Goldfinch *S. psaltria* to either *Sporagra* or *Astragalinus*, pending action on this issue by the NACC (SACC proposal 488).

More recently, Zuccon et al. (2012), in another study of the Fringillidae, also based on data from five genes (three nuclear, two mitochondrial), found that all species of *Spinus* sampled, including *S. spinus* and several species proposed for transfer to *Sporagra* or *Astragalinus* (as above) formed a reasonably well-supported monophyletic group.

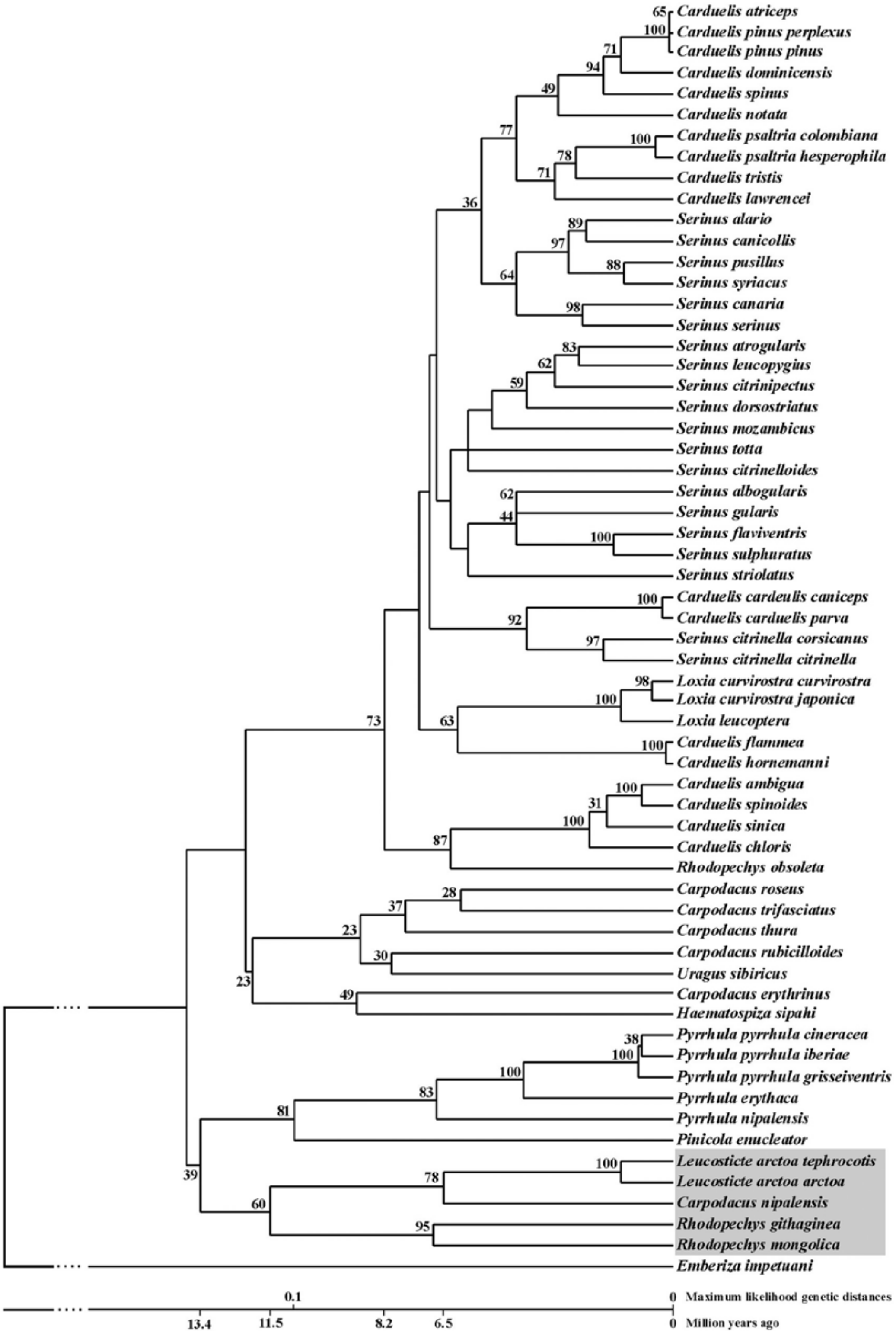
For North American species of *Spinus*, neither Nguembock et al. (2009), Zuccon et al. (2012), nor the earlier papers of Arnaiz-Villena et al. (2007, 2008) are as helpful as they might be. The taxon sampling in Arnaiz-Villena et al*.* (2007), a phylogenetic study of *Carduelis sensu lato*, was excellent (all native North American species sampled, in addition to the accidental and introduced species) and that in the more expansive 2008 paper was nearly as good, but the amount of data gathered for both studies (924 bp of cytochrome-*b*) was rather small. In contrast, Nguembock et al. (2009) and Zuccon et al. (2012) gathered much more data but sampled considerably fewer species of *Spinus*. Nguembock et al. (2009) sampled only two of the eight native North American species (*psaltria* and *xanthrogastrus*) along with *spinus* and *cucullatus* (sequence of one gene for *pinus* was downloaded from GenBank) and six South American species, whereas Zuccon et al. (2012) sampled only three of the eight native North American species (*pinus*, *psaltria*, and *tristis*), *spinus*, *cucullatus*, and three South American species.

The mitochondrial data from Arnaiz-Villena et al. (2007) indicated that the three North American goldfinches (*psaltria*, *tristis*, and *lawrencei*); the Pine, Antillean, and Black-capped siskins (*pinus*, *dominicensis*, and *atriceps*); and *notatus* + the two largely South American siskins that also occur in our area (*xanthrogastrus* and *cucullatus*) belong to three separate clades, and that relationships both among these clades and with other species of *"Carduelis"* were poorly resolved. The *notatus-xanthrogastrus-cucullatus* clade also included six species endemic to South America. The Eurasian Siskin *S. spinus* was sister to the *pinus*, *dominicensis*, and *atriceps* clade. Support for the monophyly of these clades was mediocre to strong (67% bootstrap for *psaltria-tristis-lawrencei*, 48% for *pinus-dominicensis-atriceps*, 94% for *pinus-dominicensis-atriceps-spinus*, and 91% for *notatus-xanthrogastrus*-*cucullatus*; see the 2007 tree below). The clades taken together did not form a monophyletic group, although support at deeper levels of the tree was poor.

Here's the relevant part of the likelihood tree from Arnaiz-Villena *et al.* (2007):



... and the likelihood tree from Arnaiz-Villena *et al.* (2008), with the relevant taxa at the top (see discussion below):



Taxon sampling for Arnaiz-Villena et al. (2008), which was based on the same segment of mitochondrial DNA, was much more extensive and included many species of *Serinus*, *Carduelis sensu stricto*, *Loxia*, *Acanthis*, etc., but for some reason omitted *xanthrogastrus* and *cucullatus*. Not surprisingly, they recovered the same *psaltria-tristis-lawrencei* (71% bootstrap) and *pinus-dominicensis-atriceps* (now also up to 71% bootstrap) clades as in the 2007 paper, and recovered *spinus* as sister to the latter clade (94% bootstrap) and *notatus* as sister to the *pinus-dominicensis-atriceps-spinus* clade (see the 2008 tree below). In this paper, the *psaltria-tristis-lawrencei* clade was reconstructed as sister to the *pinus-dominicensis-atriceps-spinus-notatus* clade, with reasonable bootstrap support of 77%. Thus, the New World species of *Spinus* sampled + *spinus* formed a monophyletic group in the 2008 paper.

For species occurring in North America, the concatenated tree of Nguembock et al. (2009) had data only for *psaltria*, *xanthrogastrus*, *cucullatus* (a captive individual), and *spinus*. They found *psaltria* to be sister to, but quite divergent from, a clade consisting of Neotropical siskins, including *xanthrogastrus* and *cucullatus* and all South American endemics sampled, whereas *spinus* was sister to a clade consisting of *Loxia* and *Acanthis*, although support for this was mixed (1 post. prob., <70% bootstrap). Support for the monophyly of the Neotropical siskin clade was strong (1 post. prob., 100% bootstrap), but support for the *psaltria*-Neotropical siskin clade was mixed (1 p.p., <70% bootstrap). The branch length between *psaltria* and the Neotropical siskin clade was roughly the same as that between *Loxia* and *Acanthis*, and Nguembock et al. (2009) recommended that *psaltria* be placed into a separate genus, for which the name *Pseudomitris* was noted to be available.

Complicating interpretation of the unusual result of a sister relationship between *S. spinus* and *Loxia-Acanthis* is the fact that none of the individual gene trees in Nguembock et al. (2009) have this result. For example, in the ATPase 6 tree, *spinus* is sister to *S. pinus* (this is the sequence from GenBank), and these two are sister to their Neotropical siskin clade, which is very similar to the mtDNA results in Arnaiz-Villena et al. In the TGF-beta2 intron 5 tree, *spinus* is sister to *Loxia* but *Acanthis* (*hornemanni*) is only distantly related.

The study of Zuccon et al. (2012) included *spinus*, *pinus*, *psaltria*, *tristis*, and *cucullatus* (again a captive individual), as well as three South American species, and determined that all of these species formed a monophyletic group with reasonable support (1 p.p., 79% bootstrap). This result was present in both the mitochondrial and nuclear trees. Within this group, the South American endemics + *cucullatus* formed a clade that was sister to a clade consisting of *pinus* + *spinus*, and these two clades in turn were sister to a clade consisting of *tristis* + *psaltria*. These individual clades and the sister relationship of the S.Am + *cucullatus* clade with the *pinus* + *spinus* clade were strongly supported (minimum 1 p.p. and 99% bootstrap). In contrast to the result of Nguembock et al. (2009), all branch lengths within the *Spinus* clade were noticeably shorter in the Zuccon et al. (2012) tree than the branch length between *Loxia* and *Acanthis*. Zuccon et al. (2012) noted that their ND3 sequence for *S. spinus* was identical to that of Nguembock et al. (2009), but that the myoglobin sequence used by Nguembock et al. was very similar to the *Loxia* sequence of Zuccon et al., and suggested that at least some of

Nguembock's sequence of *spinus* was not of this species. Zuccon et al. (2012) recommended that all species sampled, and presumed close relatives not sampled, be placed in *Spinus*.

Here's the concatenated Bayesian tree from Ngeumbock et al (2009) – see discussion above. New World taxa are identified by brackets labeled C2:

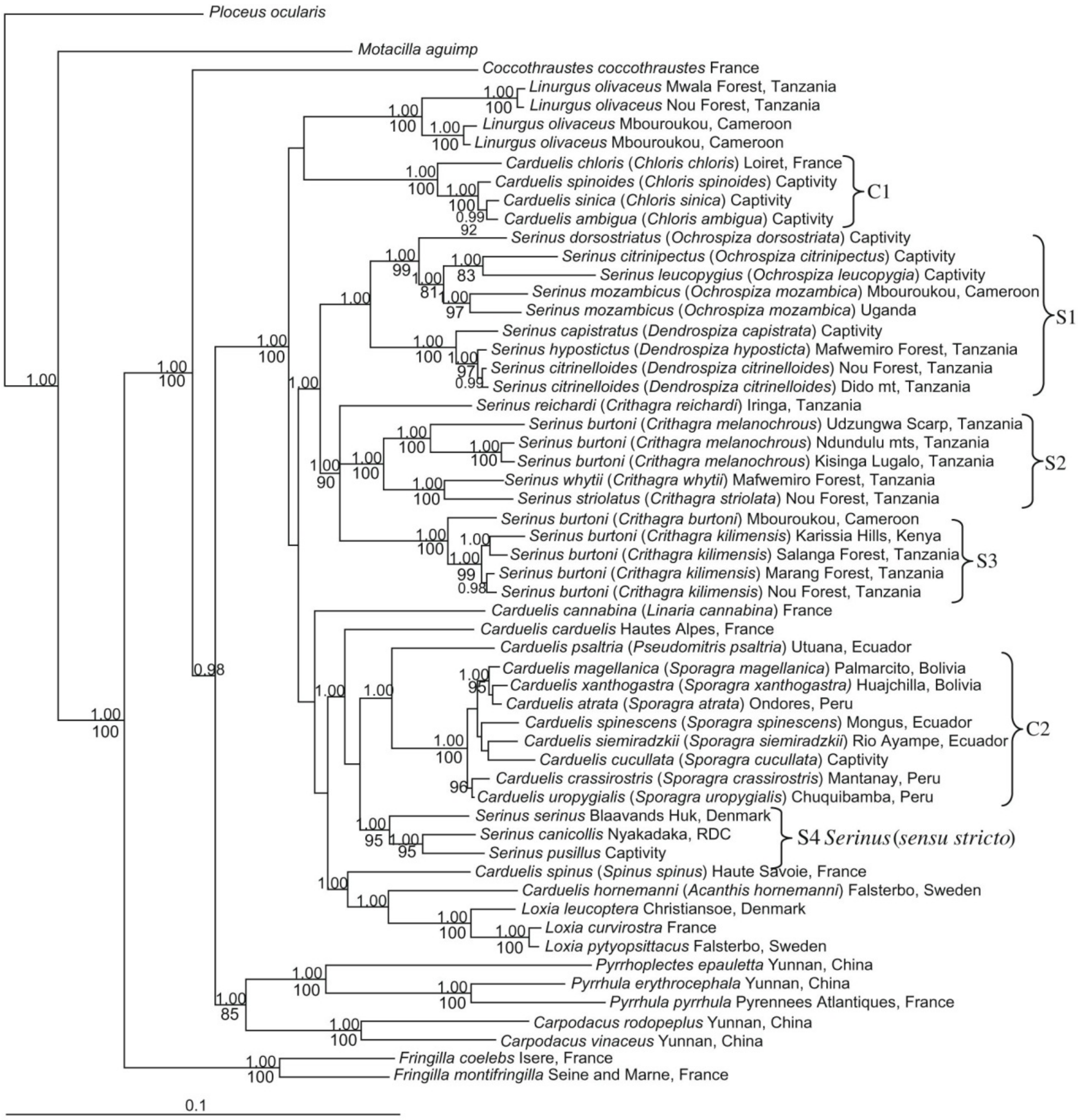
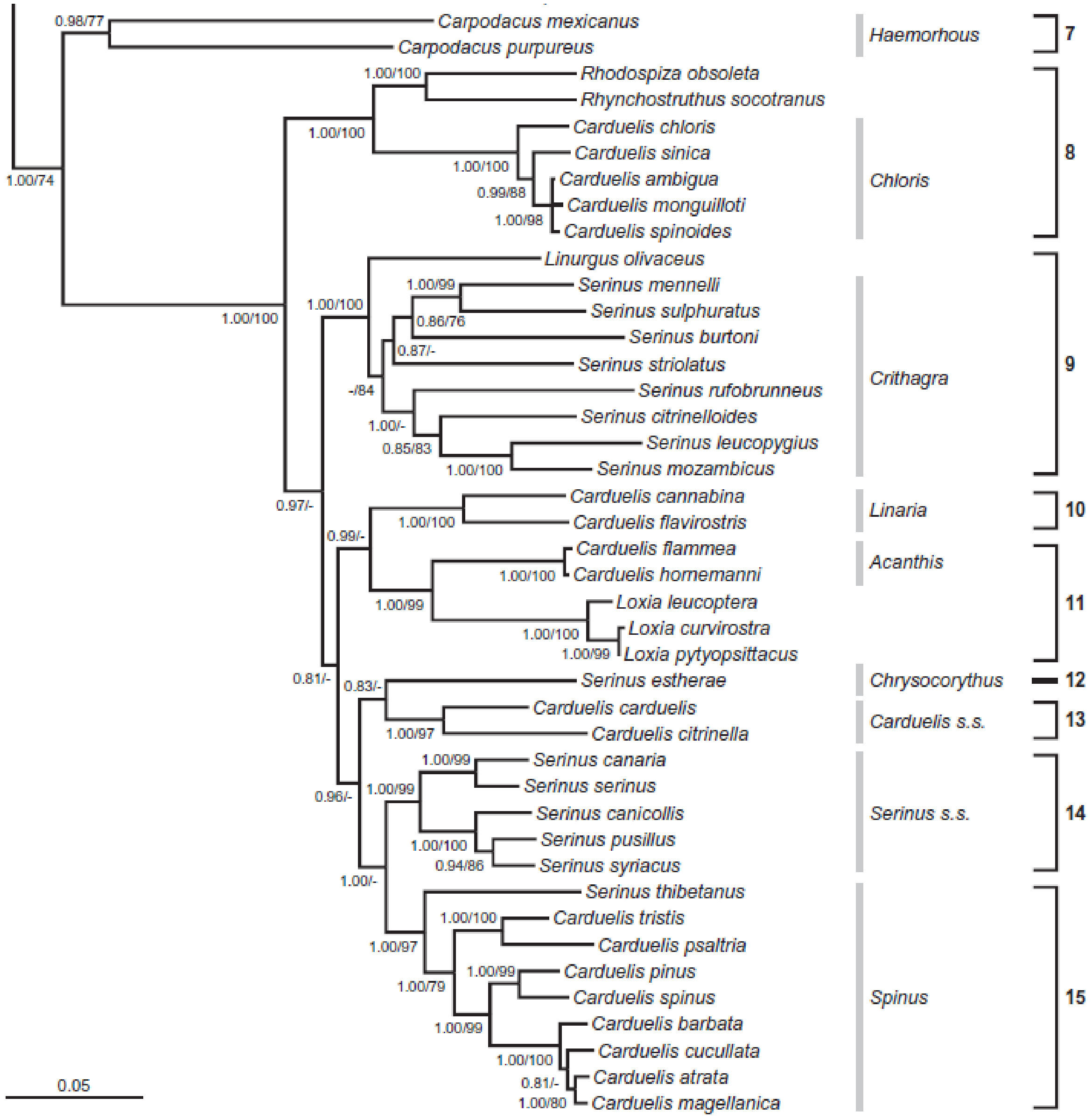


Fig. 4. The concatenated majority rule consensus tree. The 50% majority rule consensus tree obtained from the Bayesian analyses of the concatenated data set (mean log-likelihood value = 19296.56 ± 2.45). The optimal parameterization as estimated by MrMODELTEST was assumed for each of the eleven partitions. Posterior probabilities (0.95⩾) are indicated above the nodes, and PhyML bootstrap values (⩾0.70) below the nodes. Sn and Cn mean *Serinus* and *Carduelis* clades, respectively, and brace brackets show limits of these. Names between brackets correspond to those suggested by Wolters (1980) and rehabilitated for some by Ryan et al. (2004) and for others by this study.

... and the relevant part of the combined-data Bayesian tree of Zuccon et al. (2012). *Spinus* is at the bottom of the tree (clade 15):



Recommendation:

Sampling and support in these papers are not ideal. Nevertheless, all papers identify, within the limits of their sampling and with varying levels of support, three clades within what we currently consider *Spinus*: (1) type species *spinus* and *pinus-dominicensis-atriceps*, (2) *psaltria-lawrencei-tristis*, and (3) *notatus-xanthrogastrus*-*cucullatus* + the South American endemics. The issue before us is whether the data suggest that either of the latter two clades should be split from *Spinus.*

The primary support for splitting *Spinus* comes from Nguembock et al. (2009), whose results indicated that *Spinus*, as we currently recognize it, was not monophyletic. Instead, they found *spinus* (their only representative of clade 1 except for *pinus*, for which they had sequence for a single gene) to be sister to *Acanthis*+*Loxia*. They also found a relatively long branch length between *psaltria* (their only representative of clade 2) and their representatives of clade 3, and suggested that these taxa be placed in separate genera. However, both of these results were contradicted by Zuccon et al. (2012), who found all sampled species of *Spinus*, including species from all three clades, to form a reasonably supported monophyletic group containing relatively short branch lengths. Arnaiz-Villena et al. (2008), using more extensive sampling but sequencing fewer genes, had also recovered a reasonably supported clade consisting of all sampled species of *Spinus*.

At this point, we recommend NO votes on both 2014-A-1 and 2014-A-2. We recommend retaining the species listed in these proposals, along with *S. spinus, S. pinus, S. atriceps,* and *S. dominicensis*, in the genus *Spinus*, pending further data.

Literature Cited:

Arnaiz-Villena, A., V. Ruiz del-Valle, J. Moscoso, J. I. Serrano-Vela, and J. Zamora. 2007. MtDNA phylogeny of North American *Carduelis pinus* group. *Ardeola* 54: 1-14.

Arnaiz-Villena, A., V. Ruiz del-Valle, J. Moscoso, J. I. Serrano-Vela, and J. Zamora. 2008. Mitochondrial DNA phylogenetic definition of a group of ‘arid-zone’ Carduelini finches. *Open Ornithology Journal* 1: 1-7.

Nguembock, B., J. Fjeldså, A. Couloux, and E. Pasquet. 2009. Molecular phylogeny of Carduelinae (Aves, Passeriformes, Fringillidae) proves polyphyletic origin of the genera *Serinus* and *Carduelis* and suggests redefined generic limits. *Molecular Phylogenetics and Evolution* 51: 169-181.

Zuccon, D., R. Prys-Jones, P. C. Rasmussen, and P. G. P. Ericson. 2012. The phylogenetic relationships and generic limits of finches (Fringillidae). *Molecular Phylogenetics and Evolution* 62: 581-596.

Submitted by: Terry Chesser and Jim Rising

Date of Proposal: 8 May 2013

Proposal (488) to South American Classification Committee

Resurrect *Sporagra* for South American goldfinches and siskins

<u>Effect on SACC</u>: This would change the genus name from *Carduelis* to *Spinus* for all South American species in that genus (but would retain *Carduelis* for introduced *C. carduelis* and resurrect *Chloris* for introduced *C. chloris*).

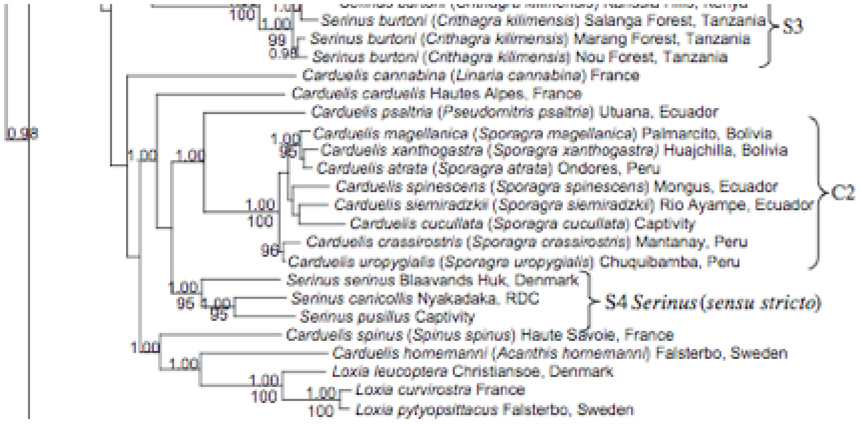
<u>Background</u>: These species were all in the proposed genera until Howell et al. (1968) and Mayr & Short (1970) lumped them all in one massive *Carduelis* with no explicit rationale, much less analysis or data. SACC and everyone else followed that classification.

<u>New information</u>: Arnaiz-Villena et al. (2007) sequenced 940 bp of cyt-B and found that broad *Carduelis* was polyphyletic. My screen grab of their complete tree is too fuzzy to be readable, so let me now if you need a pdf. Here is part of it (maximum likelihood):

[tree reproduced above in NACC proposal]

The North American Classification Committee (Chesser et al. 2009) voted to restore the pre-Peters generic classification based on those data; although NACC clearly recognized that such a single-locus study has potential problems, the committee largely agreed that those new data were at least sufficient to return to the previous classification, e.g. *Spinus* for our goldfinches and siskins and *Chloris* for the greenfinches, with *Carduelis* remaining for *C. carduelis*. There's no point in repeating all the details of the NACC proposal – you can access it the NACC proposal website. Note that the Neotropical taxa are in a different group from the primarily North American goldfinches (including *psaltria*).

Then, Nguembock et al. (2009) sampled 5 genes (including one nuclear, two nuclear introns, and two mitochondrial) to examine relationships of carduelines. Although their taxon-sampling was weaker for the New World than that of the previous study, their gene-sampling was much stronger. Broadly, they found similar results (e.g., only *C. carduelis* retained in *Carduelis*, *Chloris* for *chloris*) except that *Spinus* was also paraphyletic with respect to true *Serinus* and *Loxia*. [Arnaiz-Villena et al. (2007) did not sample much beyond the goldfinch-siskin group, and so their analysis would not have been able to reveal this.] Nguembock et al.'s results are below (Bayesian analysis, majority rule consensus tree, concatenated data); their analyses of single genes such as ND2 did not show the paraphyly of *Spinus*.



Here's what our current Note says:

"3. New World members of the genus *Carduelis* were formerly (e.g., Hellmayr 1938, Phelps & Phelps 1950a, Meyer de Schauensee 1966, 1970) placed in the genus *Spinus,* but recent authors (e.g., AOU 1983, 1998, Ridgely & Tudor 1989) have followed

Howell et al. (1968) in merging *Spinus* into *Carduelis*. <check Ackermann J. Orn. 108: 430-473, 1967>. Recent genetic data (Arnaiz-Villena et al. 2007, Nguembock et al. 2009) found that *Carduelis* as currently constituted is not monophyletic and that resurrection of *Spinus* is required, and Chesser et al. (2009) followed this by placing all New World goldfinches and siskins in *Carduelis*. Arnaiz-Villena et al. (2007) also showed that the Neotropical species of *Carduelis* likely form a monophyletic group that might not include *C. psaltria*, which forms a strongly supported group with the two North American goldfinches, *C. tristis* and *C. lawrencei*. Nguembock et al. (2009) found that *C. psaltria* was sister to the Neotropical group (but did not sample *C. tristis* or *C. lawrencei*); they also found that *Spinus* was more closely related to *Loxia* than to the New World goldfinch-siskin group, and that the latter was more closely related to true *Serinus* (at least in their concatenated data set). Therefore, they recommended that *Sporagra* Reichenbach, 1850, be resurrected for this group."

Nguembock et al.'s (2009) recommendation to recognize *Sporagra* was "temporary," evidently because of missing taxa in the New World.

Recommendation: Although the data from the new analyses are not ideal, they are clearly superior to the data-less classification used previously. Minimally, we should follow NACC by resurrecting *Spinus* for the New World group. However, Nguembock et al. (2009) was not available to Chesser et al. (2009), and I think the data are sufficient for going one step further by resurrecting *Sporagra* for the South American taxa, including *psaltria*. *Sporagra* would presumably also include North American *tristis* and *lawrencei*, which were found to form a group with *psaltria* by Arnaiz-Villena et al. but with no real support, as well as any the South American endemics not sampled by one or both studies. Therefore, I recommend (YES vote) we use *Sporagra* for all species on our list except the two introduced species, *Chloris chloris* and *Carduelis carduelis* (and *Spinus* would by implication be restricted to *spinus*, *pinus*, *atriceps*, and *dominicensis* on the NACC list). A NO vote would be to retreat to broadly defined *Spinus* (or even *Carduelis*) until more data are available.

Note on English names: If this proposal passes, then the names "goldfinch" and "siskin" not longer have any phylogenetic significance. Rather than tweak the names to reflect generic boundaries (difficult with the only "true" goldfinch being "the" goldfinch *C. carduelis*), I think it's better for stability to just add goldfinch and siskin to the growing list of names that indicate morphotypes groups rather than phylogenetic groups.

References:

ARNAIZ-VILLENA, A., V. RUIZ-DEL-VALLE, J. MOSCOSO, J. I. SERRANO-VELA, AND J. ZAMORA. 2007. MtDNA phylogeny of North American *Carduelis pinus* group. Ardeola 54: 1-14.

HOWELL, T.R., R. A. PAYNTER, JR., AND A. L. RAND. 1968. Subfamily Carduelinae. Pp. 207-306 in "Check-list of birds of the World, Vol. 14" (Paynter, R. A., Jr., ed.). Museum Comparative Zoology, Cambridge, Mass.

MAYR, E., AND L. L. SHORT. 1970. Species taxa of North American birds. Publ. Nuttall Orn. Club 9.

NGUEMBOCK, B. J. FJELDSÅ, A. COULOUX, & E. PASQUET. 2009. Molecular phylogeny of Carduelinae (Aves, Passeriformes, Fringillidae) proves polyphyletic origin of the genera *Serinus* and *Carduelis* and suggests redefined generic limits. Molecular Phylogenetics and Evolution 51: 169–181.

Van Remsen, June 2011

Comments from Nores: "YES**.** It is evident in the analyses by Arnaiz-Villena et al. (2007) and Nguembock et al. (2009) that the South American species form a well-separated clade."

Comments from Stiles: "At least a partial YES. I see no problem with *Sporagra* for the bulk of the South American species; the possible exception is *psaltria*. The A&V study places this species with *tristis* and *lawrencei* in a separate group from *Sporagra*; the N et al. study places it near *Sporagra* but the split here looks to be deep: the branch lengths between *psaltria* and the *Sporagra* group are much longer than those between *Spinus*, *Acanthis*, and *Loxia*, maintained as separate genera in this study (justifiably, in my opinion: *Loxia* in particular is highly distinctive). To be consistent with this, and assuming that more genetic data will support the close relationship of *psaltria*, *tristis* and *lawrencei* - as seems likely given the good agreement between the two studies in other aspects - it might be best to separate the latter three species from *Sporagra*, as N et al. do for *psaltria* (they didn´t sample *tristis* and *lawrencei*). They placed *psaltria* in *Pseudomitris* (type species *psaltria*). However, if these three species are indeed congeneric, as the A&V study strongly suggests, *Pseudomitris* Cassin 1865 should be regarded as a synonym of *Astragalinus* Cabanis 1851 (type species *tristis*). Given the combined results of the two studies, I suggest that the best course would be to use *Sporagra* Reichenbach 1850 for all of the South American (exclusively Neotropical) species and *Astragalinus* for *psaltria*, *tristis* and *lawrencei*, which are North American (only *psaltria* also occurs widely in the Neotropics as well but is probably of northern origin where it is more racially and morphologically diverse; only a single subspecies occurs in South America and southern Middle America).:

Comments from Remsen: "Given Gary's comments above, let's change the proposal to exclude *psaltria* – that one is more appropriate for NACC to decide anyway."

Comments from Pacheco: "YES, com as necessárias alterações sugeridas por Stiles."

Comments from Zimmer: "YES for resurrecting *Sporagra* for all of the exclusively South American species of siskins & goldfinches. I would agree with not messing with the English names of "siskin" and "goldfinch", recognizing that those names reflect morphotypes and not phylogenetic groups."

Comments from Robbins: "YES. I agree with Gary's comments concerning not including *psaltria* within S*poragra*. Otherwise, it seems straightforward in placing the remaining Neotropical "siskins" within *Sporagra*, if indeed that is the oldest name available."

Split the Variable Seedeater *Sporophila americana*

This proposal is based largely on a proposal that has already passed the SACC that recognizes 4 species in the *Sporophila americana* superspecies. Only one of these taxa, *corvina*, is found in our area. This work is based on Stiles (1996), which I have not seen.

A YES vote would split what we currently recognize as *S. americana* into 2 species, *S. corvina* (Variable Seedeater), and *S. americana* (Wing-barred Seedeater), only one of which occurs in our area. The suggested sequence of *Sporophila* in our list would be *schistacea, corvina*, *torqueola*, *nigricollis*, and *minuta*.

Background:

The taxonomy of seedeaters of this group has often been based on the coloration of the adult males, mostly gray or black-and-white. This, however, does not appear to be a useful way to separate these taxa, and some taxa occur parapatrically with little or no interbreeding, indicating close ecological similarities and exclusion. See the proposal to SACC below.

Recommendation: The proposal to the SACC, including these changes, was accepted unanimously by that committee, and I recommend that we accept this change. The proposed English names seem acceptable and appropriate.

Submitted by: Jim Rising

Date of proposal: 9 May 2013

Proposal (#287) to South American Classification Committee

Recognize four species of *Sporophila* within the *Sporophila americana* superspecies

This proposal would change our current list in two respects: it would place *S. intermedia* (Gray Seedeater) between *S. corvina* (Variable Seedeater, previously called *S. aurita*) and *S. americana* (Wing-barred Seedeater); and would recognize as a species distinct from the latter *S. murallae* (Caquetá Seedeater). The detailed justification for this treatment is presented in Stiles (1996); I summarize the main arguments here.

Classification of *Sporophila* seedeaters has in the past largely been based upon the coloration of the adult males; in particular, among the species of Central and northern South America, two main species groups have been recognized with male plumage being mostly gray vs. black-and-white. In this paper I argue that a close relationship exists between a black-and-white species (*corvina*) and a gray species (*intermedia*), based upon previously unappreciated similarities in plumage pattern, plumage sequences, distribution, biometrics and two localized zones of at least sporadic hybridization involving different races of both species. *S. intermedia* and *americana* are apparently parapatric in coastal NE Venezuela and W Guyana and appear to replace each other on Trinidad and Tobago, suggesting that they are too similar ecologically to coexist. No hybrids are known between these two, and they appear less closely related than *intermedia* is to *corvina* based on plumage pattern. The range of *americana* continues along the coastal lowlands of South America to the mouth of the Amazon and thence eastward along the Amazon (and apparently one or more of its northern tributaries in E Brazil) to the region of Manaus; Amazonian birds may differ in plumage from those of the coastal regions and have been named as a separate subspecies *dispar*, although this has not been accepted by all authors. Separated from this population by ca. 500 km is *murallae*, an isolated upper Amazonian derivative of *americana.* This form had been considered intermediate between *corvina* and *americana* by Meyer de Schauensee (1952) and this was used by some authors, notably Olson (1981) to lump *corvina* with all its races into *americana.* I demonstrate that this is incorrect, and that except for its lesser development of wing-bars there is no justification for allying *murallae* with *corvina*; in numerous features its affinities clearly lie with *americana.* However, it differs from *americana* in several plumage characters (and more from the Amazonian populations of the latter, if the characters of *dispar* are correct). It also differs most strikingly in biometrics, such that I consider it less close to *americana* than *corvina* is to *intermedia*, and thus deserving of species rank. These four should be placed in the following order in our list: *corvina, intermedia, americana* and *murallae.*

Considering all of these forms as a single superspecies appears justified based on the overall distribution of all forms. At the center of the distribution is *intermedia*, with the black-and-white forms occurring around the periphery, generally in areas of higher rainfall (as might be expected by Gloger's rule). No member of this group appears to occur on the Guyana shield.

I note in passing that, as Olson had earlier suggested, the name *aurita* is unidentifiable as its type came from the stable hybrid swarm between the races *corvina* and *hicksii*. The type has disappeared, and it is impossible to assign this name to either of the parental populations. The oldest name in this group that clearly refers to a definite population is *corvina*; hence the Variable Seedeater should be called *S. corvina*. (Olson did not do this as he considered all the black-and-white forms to be races of *americana*)*.* I also note that Dickinson and Ridgely & Greenfield recognize *murallae* as a species separate from *americana*. I recommend a YES vote on this proposal.

References:

Meyer de Schauensee, R. 1952. A review of the genus *Sporophila*. Proc. Acad. Natl. Sci. Phila. 104:153-196.

Olson, S. L. 1981. The nature of variability in the Variable Seedeater of Panama. Proc. Biol. Soc. Wash. 94:380-390.

Stiles, F. G. 1996. When black plus white equals gray: the nature of variability in the Variable Seedeater complex (Emberizidae: *Sporophila*). Orn. Neotrop. 7:75-107.

Gary Stiles, June 2007

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Comments from Robbins: "YES for now in recognizing four species within the *Sporophila americana* complex. I would like to see a molecular data set, not only for this group but for all of *Sporophila*, before I become fully convinced of species limits within this complex."

Comments from Zimmer: "YES. A confusing group to be sure, but Gary's arguments are convincing."

Comments from Nores: "YES, aunque no muy covencido. Este es un caso en el cual un análisis molecular sería fundamental. Además, Ridgely y Tudor señalan que las vocalizaciones de todas las poblaciones son similares."

Comments from Jaramillo: "YES - Although I imagine that eventually we may have some more re-shuffling in this genus. I concur with others that this genus is screaming out for a molecular analysis."

Comments from Pacheco: "YES. Estou ciente das dificuldades do complexo *Sporophila americana*; todavia, entendo que o arranjo proposto por Gary é melhor que o tradicional."

Replace the family name Megaluridae with Locustellidae

Background:

The family name Megaluridae was introduced in the AOU Check-list of North American Birds with the 51st Supplement (Chesser et al. 2010) as a result of publications by Alström et al. (2006) and Johansson et al. (2008). These authors had defined Megaluridae as a family encompassing *Megalurus*, *Locustella*, *Bradypterus* and *Dromaeocercus*, and had taken its name from Sibley and Monroe (1990).

In 2011, Alström et al. (2011) published additional information on this same family, but this time under the name Locustellidae. There they acknowledged that Locustellidae Bonaparte, 1854 has priority over Megaluridae Blyth, 1875 when the family includes *Locustella* Kaup [see also Bock (1994)]. They also acknowledged that the Megalurinae of Sibley and Monroe (1990) did not include *Locustella*.

Since *Locustella* is the only genus of this new family recorded in the AOU Check-list of North American Birds, there is little doubt that Locustellidae is indeed the correct name. Sangster et al. (2010) have independently come to the same conclusion in an Old World context.

Recommendation:

Replace the family name Megaluridae with Locustellidae in the AOU Check-list of North American Birds.

Literature Cited:

Alström, P., P. G. P. Ericson, U. Olsson, and P. Sundberg. 2006. Phylogeny and classification of the avian superfamily Sylvioidea. Molecular Phylogenetics and Evolution 38:381-397.

Alström, P., S. Fregin, J. A. Norman, P. G. P. Ericson, L. Christidis, and U. Olsson. 2011. Multilocus analysis of a taxonomically densely sampled dataset reveal extensive non-monophyly in the avian family Locustellidae. Molecular Phylogenetics and Evolution 58:513-526.

Bock, W. J. 1994. History and Nomenclature of Avian Family-Group Names. Bulletin of the American Museum of Natural History 222.

Bonaparte, C. L. 1854. Conspectus systematis ornithologiae. Annales des sciences naturelles, Série 4, Zoologie 1:105-152.

Chesser, R. T., R. C. Banks, F. K. Barker, C. Cicero, J. L. Dunn, A. W. Kratter, I. J. Lovette, P. C. Rasmussen, J. V. Remsen, Jr., J. D. Rising, D. F. Stotz, and K. Winker. 2010. Fifty-first supplement to the American Ornithologists' Union Check-list of North American Birds. Auk 127:726-744.

Johansson, U. S., J. Fjeldså, and R. C. K. Bowie. 2008. Phylogenetic relationships within Passerida (Aves: Passeriformes): A review and a new molecular phylogeny based on three nuclear intron markers. Molecular Phylogenetics and Evolution 48:858-876.

Sangster, G., J. M. Collinson, A. G. Knox, D. T. Parkin, and L. Svensson. 2010. Taxonomic recommendations for British birds: Sixth report. Ibis 152:180-186.

Sibley, C. G., and B. L. Monroe. 1990. Distribution and Taxonomy of Birds of the World. Yale University Press, New Haven, CT.

Submitted by: Michel Gosselin, Canadian Museum of Nature

Date of proposal: 21 May 2013

Elevate *Rallus longirostris crepitans*, *R. l. obsoletus*, and *Rallus elegans tenuirostris* to species rank

Background:

In the most recent checklist (AOU 1998:131), there is a discussion of hybridization between *Rallus longirostris* and *R. elegans* in the eastern and southern United States. There is a suggestion to merge the entire complex into a superspecies, but phylogenetic and detailed hybridization studies of the group have not been published until now (Maley 2012; Maley and Brumfield 2013). Taxonomy has always been difficult in this group given plumage variation, morphologically distinct allopatric populations, and uncertainty in the degree of hybridization between populations currently in contact. For example, *R. elegans* of the eastern US are bright rufous ventrally and breed in freshwater marshes, whereas *R. longirostris* of the eastern US are duller ventrally and breed in saltmarshes. Very similar allopatric birds of the southwestern US and northwestern Mexico are bright rufous ventrally and breed primarily in saltmarshes, making their classification into either species difficult (Olson 1997).

New Information:

A phylogenetic study using mitochondrial and nuclear markers found discordance between genetic relationships and current classification (Maley and Brumfield 2013). *Rallus elegans*, as currently recognized, is paraphyletic with respect to *R. longirostris*. Genetic lineages correspond roughly to geography instead of current species limits. The *R. l. obsoletus* subspecies group found in California, Arizona, and northwestern Mexico was discovered to be sister to *R. e. tenuirostris* of the highlands of Mexico instead of previously suggested sister relationships to either *R. l. crepitans* or *R. e. elegans* of eastern North America (Hellmayr and Conover 1942; Ripley 1977; Olson 1997). Additionally, the lineages of the *R. l. crepitans* group and *R. e. elegans*, which are known to hybridize in eastern North America (Olson 1997), are in the same clade (Maley and Brumfield 2013). This pattern of hybridization apparently also occurs on Cuba (Olson 1997) between members of these same two lineages (Maley and Brumfield 2013). This clade also includes birds from throughout the Caribbean (Fig. 1). Detailed investigations of hybridization using morphological, ecological, and genetic (mitochondrial and nuclear) characters in Louisiana reveal that strong selection against hybrids is likely preventing the fusion of these lineages (Maley 2012). Members of the nominate *R. l. longirostris* group of South America were found to be genetically distinct and sister to Caribbean and eastern North American birds (Fig. 1B). In the study the authors were unable to obtain samples of *R. l. longirostris*, instead sampling two members of the group *R. l. cypereti* and *R. l. phelpsi*. The following recommendations would remove *R. longirostris* from the checklist, because members of this subspecies group have not been documented in North America.

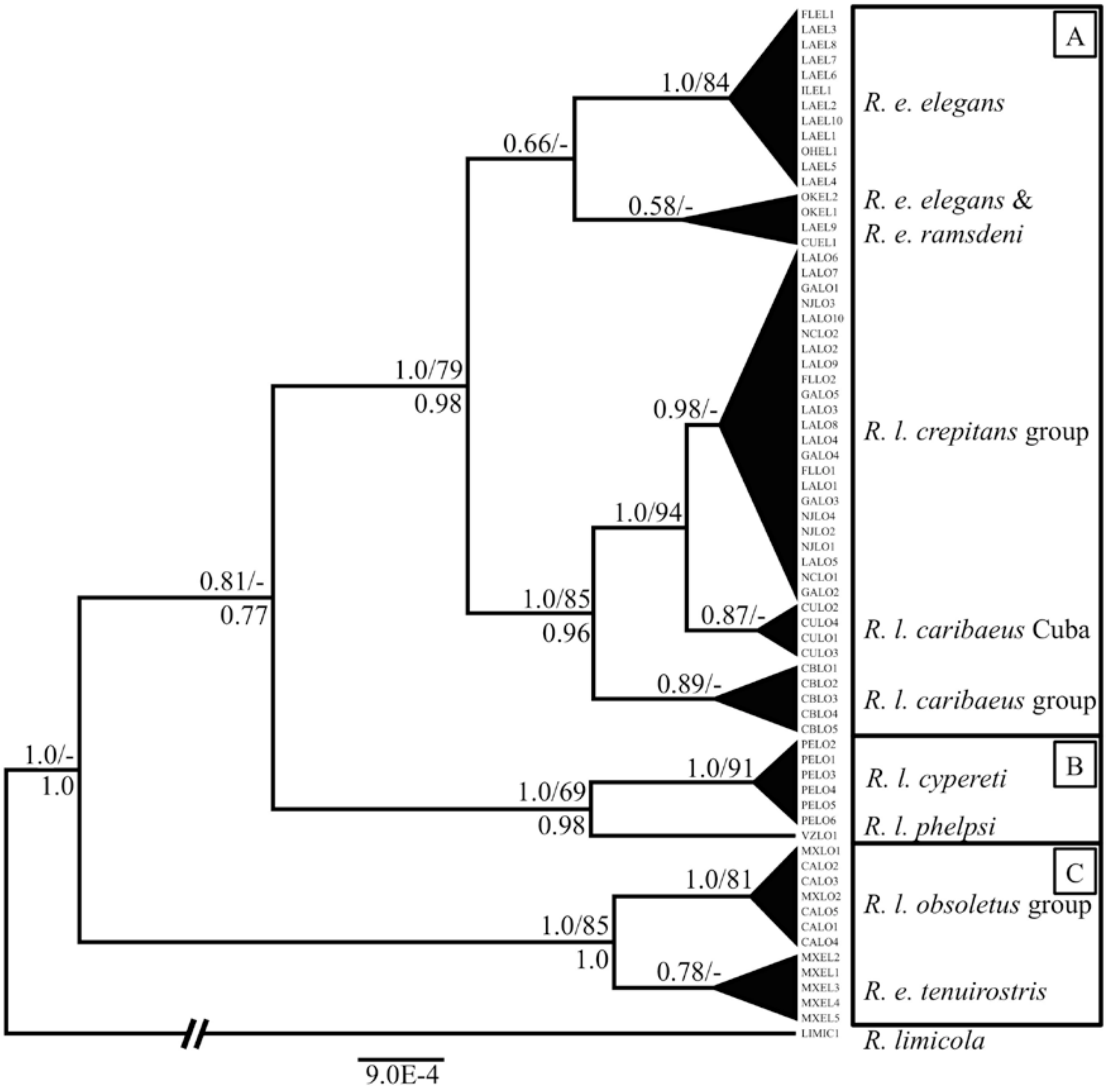

Figure 1. Maximum Clade Credibility gene tree of ND2 inferred in Beast (Drummond and Rambaut 2007). The labels above nodes are the posterior probability followed by the bootstrap support value (if greater than 65) for that node. The labels below nodes are the posterior probability for that node in the estimate of the species tree; this label is not included if the value was below 0.95. Each of the three major clades is outlined and labeled by geography, with clade A comprising eastern North American and Caribbean birds, clade B comprising South American birds, and clade C comprising birds of western North America, including Mexico.

Two members of the complex are in extensive secondary contact in eastern North America and Cuba, but have not fused despite hybridization (Olson 1997). The morphological and genetic characterization of the hybrid zone in Louisiana (Maley 2012) found that it is very narrow (~ 4.2 km wide), with selection against hybrids acting to prevent fusion. These data suggest there is strong, albeit incomplete, reproductive isolation between these species in Louisiana. There is no evidence of population genetic structure within *R. longirostris* in the eastern US, and very little within *R. elegans*, so we extrapolate these results for the entire distribution in the eastern and southeastern US. Extending these results to the remaining taxa and considering the differential level of morphological, ecological and genetic divergence between previously identified subspecies groups, we conclude that at least five species should be recognized in this complex. This treatment would be consistent with recent genetic analyses of other members of the family showing similar levels of divergence (Tavares et al. 2010; Goodman et al. 2011). The most divergent clade within the complex, according to mtDNA data, represents a pair of subspecies groups from both currently recognized species (*R. l. obsoletus* group and *R. e. tenuirostris*). This pair shares the same pattern observed in the birds of eastern North America, where individuals of one group are relatively smaller than those of the other and are found primarily in saltmarshes (*R. l. obsoletus* group), whereas the other is relatively larger, brighter, and found in freshwater habitats (R. e. tenuirostris, Olson 1997).

Recommendation:

We propose species rank for five members of the complex described below. These taxonomic recommendations are based primarily on two factors: 1) there is strong but incomplete reproductive isolation between parapatric populations based on hybrid zone analyses, 2) that each of the species represents a morphologically and genetically distinct group within the complex that is at least as distinct from other members of the complex as members that are currently in contact but showing evidence of reproductive isolation.

We propose recognizing as a species the nominate form *R. longirostris* Boddaert, 1783, plus the subspecies *phelpsi* Wetmore, 1941, *margaritae* Zimmer and Phelps, 1944, *pelodramus* Oberholser, 1937, *cypereti* Taczanowski, 1877, and *crassirostris* Lawrence, 1871. These birds are relatively very small, dull-breasted, robust-billed, and restricted to mangroves (Eddleman and Conway 1998), which is why we propose to give them the English name Mangrove Rail. This lineage is morphologically, genetically, and vocally distinct from all other members of the complex, and far more distinct from the rest of the complex than the members that are currently in contact are from one another.

The second species we propose is *R. tenuirostris* Ridgway, 1874, which includes the population of birds inhabiting the highland freshwater marshes of Mexico. Individuals are large, very bright rufous ventrally, and have diffuse flank banding (Meanley 1992). They are found almost entirely within the former Aztec Empire and are not the only member of the complex found in Mexico; thus we propose the English name Aztec Rail. They are distinct morphologically, genetically, and ecologically from their closest relative, in that they breed exclusively in freshwater marshes as opposed to saltmarshes, which is the same reproductive isolating mechanism as found in other lineages within the complex.

The third species we propose is *R. obsoletus* Ridgway, 1874, which includes the populations that occur along the Pacific Coast of North America. This species would include the subspecies *levipes* Bangs, 1899, *beldingi* Ridgway, 1882, *yumanensis* Dickey, 1923, *rhizophorae* Dickey, 1930, and *nayaritensis* McLellan, 1927. This group is characterized by their relatively small body size (although larger than South American birds), by a bright rufous breast, and by their occurrence primarily in saltmarshes (Eddleman and Conway 1998). Because Robert Ridgway contributed a significant amount of work on the complex, including describing *R. l. obsoletus* and *R. l. beldingi*, we propose the English name Ridgway's Rail in his honor. We propose species rank using a comparative approach: because this lineage is as distinct morphologically, genetically, and ecologically from its closest relative (*R. e. tenuirostris*) as are other members of the complex in contact known to be reproductively isolated.

The fourth species in the complex we propose is *R. elegans* Audubon, 1834, comprised of two subspecies, *R. e. elegans* and *R. e. ramsdeni* Riley, 1913, while excluding *R. e. tenuirostris* (as described above). We propose retention of King Rail as the English common name. This species is distinct from its closest relatives ecologically, morphologically, and genetically. Despite hybridization, they are reproductively isolated from their closest relative in contact, members of the *R. l. crepitans* group, apparently due to ecological differences (Maley 2012).

The fifth species proposed is *R. crepitans* Gmelin, 1789, comprised of the eastern North America group of *R. l. crepitans*, including the subspecies *waynei* Brewster, 1899, *scotti* Sennett, 1888, *insularum* Brooks, 1920, and *saturatus* Ridgway, 1880, as well as the birds of the Caribbean and Yucatan, including *R. l. caribaeus* Ridgway, 1880, *pallidus* Nelson, 1905, *grossi* Paynter, 1950, *belizensis* Oberholser, 1937, *leucophaeus* Todd, 1913, and *coryi* Maynard, 1887. These birds are intermediate in size, and the breast spans a range of colors from very dull, silvery-gray, to dull rufous. They breed in saltmarshes and saltmeadows of the Atlantic and Gulf Coasts of North America, as well as mangroves in the Yucatan, extreme southern Florida, Louisiana, and Texas, and throughout the Caribbean (Eddleman and Conway 1998). We propose to retain Clapper Rail as the English common name to avoid confusion. They are distinct morphologically, genetically, and ecologically. Despite hybridization, they are reproductively isolated from the other members of the complex they are in contact with, *R. e. elegans* and *R. e. ramsdeni* (Maley 2012).

Based on the phylogeny (Fig. 1), the linear classification in the North American Checklist for members of the *Rallus longirostris/elegans* complex should be:

Rallus obsoletus Ridgway. Ridgway's Rail.
Rallus tenuirostris Ridgway. Aztec Rail.
Rallus elegans Audubon. King Rail.
Rallus crepitans Gmelin. Clapper Rail.

Literature Cited:

Drummond, A. J., and A. Rambaut. 2007. BEAST: Bayesian evolutionary analysis by sampling trees. BMC Evolutionary Biology 7:214.

Eddleman, W. R., and C. J. Conway. 1998. Clapper Rail (*Rallus longirostris*). . in The Birds of North America, Inc. (A. Poole, and F. Gill, Eds.), Philadelphia, PA.

Goodman, S. M., M. J. Raherilalao, and N. L. Block. 2011. Patterns of morphological and genetic variation in the *Mentocrex kioloides* complex (Aves: Gruiformes: Rallidae) from Madagascar, with the description of a new species. Zootaxa 2776:49-60.

Hellmayr, C. E., and H. B. Conover. 1942. Catalogue of birds of the Americas. Part 1, no. 1. Field Museum of Natural History Zoological Series 13.

Maley, J. M. 2012. Ecological Speciation of King Rails (*Rallus elegans*) and Clapper Rails (*Rallus longirostris*). Ph.D. dissertation, Louisiana State University, Baton Rouge.

Maley, J. M., and R. T. Brumfield. 2013. Mitochondrial and next-generation sequence data used to infer phylogenetic relationships and species limits in the Clapper/King rail complex. The Condor 115:316-329.

Meanley, B. 1992. King Rail. *in* The Birds of North America, vol. 3 (A. Poole, P. Stettenheim, and F. Gill, Eds.). The Academy of Natural Sciences, Philadelphia, PA.

Olson, S. L. 1997. Towards a less imperfect understanding of the systematics and biogeography of the Clapper and King rail complex (*Rallus longirostris* and *R. elegans*). *in* The Era of Allan R. Phillips: A Festschrift. (R. W. Dickerman, Ed.). Horizon Communications, Albuquerque, NM.

Ripley, S. D. 1977. Rails of the world: a monograph of the family Rallidae. M. F. Feheley Publishers, Toronto.

Tavares, E. S., G. H. J. de Kroon, and A. J. Baker. 2010. Phylogenetic and coalescent analysis of three loci suggest that the Water Rail is divisible into two species, *Rallus aquaticus* and *R. indicus*. BMC Evolutionary Biology 10:226.

Submitted by: James M. Maley and Robb T. Brumfield

Date of proposal: 3 June 2013

Split Guadalupe Junco *Junco insularis* from Dark-eyed Junco *J. hyemalis*

The current (7th Edition) of the Check-list considers the Guadalupe Junco to be included in the Dark-eyed Juncos, probably close to the *oregonus* group. This proposal is to place it as a separate species, *Junco insularis*.

Background:

The Guadalupe Junco (*J. insularis*) has variously been considered to be a species of junco or a subspecies of the widespread "dark-eyed" junco (*J. hyemalis*), close to the *oreganus* group (esp. the "pink-sided" junco, *J. h. mearnsi*, which it closely resembles in appearance).

New Information:

Aleixandre et al. (2013) used mtDNA sequence of the control region and COI from 87 juncos, including 34 Guadalupe Juncos, and eight morphometric features to study the relationships between Oregon Junco (*mearnsi, oreganus, caniceps*) and Yellow-eyed Junco (*J. phaeonotus*, from La Cima, DF, Mex.). They also analyzed some song data. They concluded that the Guadalupe Juncos represent "…a well-differentiated 'cryptic' lineage adapted to the insular environment through long-term isolation, with plumage coloration a result of evolutionary convergence…." They recommend full species recognition of this population.

Recommendation:

I find this a difficult study to assess. Their genetic data seem to be derived from blood samples, and their measurements from living birds; apparently no specimens were taken. Aleixandare et al. (2013) have sequence of two mtDNA markers in 87 juncos (*oreganus, caniceps, mearnsi, phaeonotus, insularis*), resulting in 14 haplotypes. These data reveal two "highly divergent genetic lineages," *insularis* and *hyemalis* (including *phaeonotus*). One *insularis* individual falls into the *hyemalis* group. The morphometric data identify 3 phenetic clusters, *hyemalis*, *phaeonotus*, and *insularis*. The Guadalupe Island birds are larger, and have larger bills, although these differences are of the magnitude that one often (always?) finds in island populations of seed-eating island birds – not notably great. The songs differ significantly. I think that the decision as to whether or not recognize the island birds as a distinct species must be based on the molecular data, which I do not feel competent to assess. The authors argue that there is great diversity among the island birds – and that appears to be the case; thus, they argue that the population on Guadalupe must be old – they suggest 600 000 years. We, of course cannot know this. Generally, variability is lost randomly in small populations.

We don’t have data on population sizes here, but we do know (1) that the total size of their habitat on the island is something like 4 km square, and that habitat loss in recorded times has recently decreased this—i.e. the population has been recently bottlenecked; and (2) that at least one of 32 Guadalupe haplotypes that they found was on the mainland. This suggests that gene flow among these populations may be greater than one might suppose.

They did a song analysis based on DFA of 6 song variables of 30 songs (11 *hyemalis* from Mt. Laguna and U C San Diego, 12 *insularis* from I. Guadalupe, and 7 *phaeonotus* from Chiapas & DF, Mex.), and *insularis* differed from the others, especially with respect to number of different syllables, max. frequency and peak frequency. The songs among these three groups differ significantly.

Size variation on the magnitude shown is not surprising in an island isolate – in fact, it is to be expected. Likewise, the song differences would be expected. I guess the question is how different do these birds need to be to be considered a separate species? The surprising thing is how variable they appear to be genetically – exactly the sort of variability that one would suppose to be lost by bottlenecking. Although there may be more gene flow between the mainland and island than one might suppose, the variability shown would not seem to be easily explained by gene flow: the haplotypes found on the island do not appear to be like the mainland ones. I am perplexed, but **I cannot be convinced that we should propose a change to the Check-list on the basis of these data.**

Literature Cited:

Aleixandre, P., Hernández Montoya, J. & Milá, B. 2013, Speciation on oceanic Islands: rapid adaptive divergence vs. cryptic speciation on a Guadalupe Island songbird (Aves: *Junco*). PLoS ONE 8:1-12.

Miller, A. H. 1941. Speciation in the avian genus junco. Univ. Cal. Publ. Zool., 44:173-434.

Submitted by: Jim Rising

Date of proposal: 31 July 2013

Change the English names of *Chlorospingus* species from “Bush-Tanager” to “Chlorospingus”

Note: an earlier version of this proposal passed the South American Classification Committee in July 2013, and is here modified for North America.

The English name “tanager” no longer has any phylogenetic meaning now that *Piranga*, *Habia*, and *Chlorothraupis* are in the Cardinalidae, *Chlorospingus* is now in the Emberizidae, and *Rhodinocichla* and *Mitrospingus* are definitely not members of the Thraupidae. In my opinion, the term “tanager” is best regarded as a vaguely defined ecomorph, one in which the bill is too thick to be called a “warbler” and too thin to be called a “finch” or “grosbeak”. It thus joins most other English names of New World 9-primaried oscines in carrying no exclusive taxonomic significance, at least at the global level, e.g., warbler, redstart, chat, finch, sparrow, bunting, grosbeak, cardinal, seedeater, blackbird, and oriole.

However, I think we could eliminate one of the “problems” by changing the English names of the *Chlorospingus* Bush-Tanagers to “Chlorospingus”. As reluctant as I am to meddle with traditional names, this change has five advantages: (1) eliminates the only “Tanager” English names in the Emberizidae, (2) reduces by one the number of non-thraupid families that include species called “tanagers”; (3) eliminates a misleading name – the *Chlorospingus* species I’m familiar with don’t really have anything to do with “bushes” per se; (4) prevents confusion with the unrelated (extralimital) *Cnemoscopus rubrirostris,* the Gray-hooded Bush Tanager; and (5) avoids our having to officially change the English name from “Bush-Tanager” to “Bush-tanager” because it is no longer a true tanager, which itself could be controversial given that “Tanager” is no longer restricted to Thraupidae. If we keep the names as they are, we would have misleading names such as “Common Bush [not really]-tanager [definitely not].”

We already use “Hemispingus” as an English name for South American *Hemispingus* tanagers and Chlorophonia for *Chlorophonia* finches, and so the roots and structure of the new English name would be familiar and pronounceable (i.e. be thankful we’re not dealing with *Schistochlamys, Catamblyrhynchus*, or my personal favorite, *Periporphyrus*). Also note that we changed the English names of the *Spindalis* group from “Tanager” to “Spindalis” to take care of an analogous problem.

If this passes, the six species of *Chlorospingus*, currently called Something Bush-Tanager, would be called Something Chlorospingus, i.e.:

Yellow-throated Chlorospingus
Ashy-throated Chlorospingus

Sooty-capped Chlorospingus
Tacarcuna Chlorospingus (would be my candidate for most-euphonious name on NACC list)
Pirre Chlorospingus
Common Chlorospingus

Submitted by: Van Remsen

Date of proposal: August 2013

Divide *Aratinga* into four genera

Note: This is a revision, tailored for NACC, of the proposal to SACC (#578), which passed unanimously.

Five recent studies using DNA sequence data have found that the genus *Aratinga*, as defined since Peters (1937), is polyphyletic; see Remsen et al. (2013) for summary. Although none on its own had extensive taxon-sampling, the combined datasets provide a reasonably complete view of the relationships among these parakeets, and the taxa still to be sampled are noncontroversial in terms of placement based on plumage and morphology. As has often been the case, Ridgway's (1916) classification is a much better match for the new data than that of Peters (1937). Although Peters provided not a phrase of justification for his merger of genera into his broad *Aratinga*, his classification has remained largely unchanged for 70+ years.

Rather than repeat the text in Remsen et al. (2013), please refer to that for details; if anyone needs a pdf, just let me know. Basically, maintaining broadly defined *Aratinga* sensu Peters would require the merger of at least 9 other parrot genera, including *Ara*, into a single genus, which is of course untenable. Also, monotypic *Nandayus* is embedded in *Aratinga* sensu stricto with strong support unless *Aratinga weddellii* is placed in a monotypic genus.

The current NACC classification is:

Aratinga holochlora (Green Parakeet)
Aratinga strenua (Pacific Parakeet)
Aratinga finschi (Crimson-fronted Parakeet)
Aratinga mitrata (Mitred Parakeet)
Aratinga chloroptera (Hispaniolan Parakeet)
Aratinga euops (Cuban Parakeet)
Aratinga nana (Olive-throated Parakeet)
Aratinga canicularis (Orange-fronted Parakeet)
Aratinga pertinax (Brown-throated Parakeet)

Our proposed new classification is given below. The positions of *chloroptera* and *euops* are switched so that the northwestern-most taxon comes first, as per convention for sister taxa or allospecies in superspecies. Gender changes force changes in variable endings in *Psittacara*.

Psittacara holochlorus (Green Parakeet)
Psittacara strenuus (Pacific Parakeet)

Psittacara finschi (Crimson-fronted Parakeet)
Psittacara euops (Cuban Parakeet)
Psittacara chloropterus (Hispaniolan Parakeet)
Psittacara mitratus (Mitred Parakeet)

Eupsittula nana (Olive-throated Parakeet)
Eupsittula canicularis (Orange-fronted Parakeet)
Eupsittula pertinax (Brown-throated Parakeet)

Thus, there are no true *Aratinga* in North America, other than exotics such as *Aratinga nenday*. If this proposal passes, we propose that the genera and species be listed consecutively and temporarily as per above until a second proposal on rearranging the sequence of New World parrot genera is produced. Although passing of this proposal depends on the point that these species do not form a monophyletic group and thus should not be listed together, we think that the actual sequence of genera merits a full proposal.

A minor point is that AOU (1998) treated *P. finschi* and South American *P. leucophthalmus* as a superspecies, citing Sibley & Monroe (1990). This is refuted by the tree in Kirchman et al. (2012), which shows that *finschi* and the *holochlorus* group are sister taxa; they are parapatric in Central America, and thus the superspecies should include those two, not distant *leucophthalmus*, which Kirchman et al. showed is sister to all other *Psittacara* sampled.

DNA-based studies that find Aratinga as non-monophyletic:

Kirchman, J.J., Schirtzinger, E.E. & Wright, T.F. (2012) Phylogenetic relationships of the extinct Carolina Parakeet (*Conuropsis carolinensis*) inferred from DNA sequence data. Auk, 129, 197-204.

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

Ribas, C.C., & Miyaki, C.Y. 2004. Molecular systematics in *Aratinga* parakeets: species limits and historical biogeography in the *solstitialis* group, and the systematic position of *Nandayus nenday*. Molecular Phylogenetics and Evolution, 30, 663-675.

Schirtzinger, E.E., Tavares, E.S., Gonzales, L.A., Eberhard, J.R., Miyaki, C.Y., Sanchez, J.J., Hernandez, A., Mueller, H., Graves, G.R., Fleischer, R.C., & Wright, T.F. 2012. Multiple independent origins of mitochondrial control region duplications in the order Psittaciformes. Molecular Phylogenetics and Evolution, 64, 342-356.

Tavares, E.S, Baker, A.J., Pereira, S.L., & Miyaki, C.Y. 2006. Phylogenetic relationships and historical biogeography of Neotropical parrots (Psittaciformes: Psittacidae: Arini) inferred from mitochondrial and nuclear DNA Sequences. Systematic Biology, 55, 454-470.

Urantówka, A. D., Grabowski, K. A. & Strzała, T. 2013. Complete mitochondrial genome of Blue-crowned Parakeet (*Aratinga acuticaudata*) -- phylogenetic position of the species among parrots group called conures. Mitochondrial DNA, 24, 336-338.

Submitted by: Van Remsen and Adam Urantówka

Date of proposal: October 2013

Lump *Rhynchopsitta pachyrhyncha* and *R. terrisi* into a single species

Background:

Rhynchopsitta pachyrhyncha and *R. terrisi* occur in Pine and Pine-Oak forests of the highlands of Mexico. The two taxa have been treated by various authors as either as separate species (e.g. Hardy 1967) or subspecies (e.g. Hardy and Dickerman 1955). The AOU checklist currently recognizes the two taxa as species. Hardy (1967) considered them reproductively isolated because he contended that, since phenotypic differences are socially reinforced in parrots, this would prevent interbreeding if the forms came into contact. Regardless of taxonomic rank, all authors consider them distinct taxa because they differ in plumage, size, and behavior (Juniper & Parr 1998; Forshaw 2010).

Taxon distributions:

R. pachyrhyncha (Swainson 1827) - highlands of north-western and central Mexico from the Sierra Madre Occidental in Chihuahua and eastern Sonora south over the central Plateau.

R. terrisi (Moore 1947) - Sierra Madre Oriental in central-west Nuevo Leon, Mexico.

New Information:

Urantówka et al. (2013) published a phylogenetic analysis of select Neotropical parrots with the goal of assessing the species status of *Rhynchopsitta pachyrhyncha and R. terrisi*. Using ND2 and phylogenetic inference they found that *R. pachyrhyncha and R. terrisi* were not genetically differentiated enough to be deemed separate species and suggest that *R. terrisi* be treated as a subspecies of *R. pachyrhyncha.* The two samples of *R. pachyrhyncha* included came from previously published phylogenetic studies on parrots by Wright et al. (2008) and Tavares et al (2006). The one individual of *R. terrisi* presumably came from a zoo in Puebla, Mexico. No information was provided about the sample in the methods and the only details about its origins were in the acknowledgements.

Recommendation:

The genetic data are insufficient to lump *R. pachyrhyncha* and *R. terrisi*. Based on the presented data it is unclear whether they actually obtained a sample from *R. terrisi*. In some cases captive birds are the only available sources of genetic material, but great caution needs to be taken when using zoo birds because hybridization is very common in captivity, especially in parrots. To minimize concerns about using captive birds the authors would have needed to include information on whether the bird was bred in captivity or taken from the wild, how long it has been captivity, how the zoo obtained the bird, and visual confirmation by the authors that it was the correct species. Poaching records suggest that the bird is more likely to be *R. pachyrhyncha* because *R. terrisi* nests in cliffs that are inaccessible to trappers (Cantu et al. 2007). Because of the uncertainty surrounding the *R. terrisi* sample and the absence of wet-lab methods reported in the paper there can be little confidence that the sample is actually *R. terrisi*.

The other issue is that only one individual of *R. terrisi* was included, so there is no context about the causes of the genetic similarity between the species. Does the presumed genetic similarity between the species represent a lack of genetic differentiation between the taxa, incomplete lineage sorting, a selective sweep, or gene flow? Distinguishing between these scenarios needs to be determined before taxonomic changes can be made. Additional work using comprehensive population-level sampling will be required to confirm the findings of Urantówka et al. (2013).

For the reasons stated above, I recommend that this proposal be rejected.

Literature Cited:

Cantu, J. C. G., Saldana, M. E. S., Grosselet, M., & Gamez, J. S. 2007. The illegal parrot trade in Mexico: a comprehensive assessment. *Mexico and Washington, DC: Defenders of Wildlife*.

Forshaw, J. M. 2010. Parrots of the World. Princeton University Press.

Hardy, J. W. 1967. *Rhynchopsitta terrisi* is probably a valid species: a reassessment. *The Condor*, *69*(5), 527-528.

Hardy, J. W., & Dickerman, R. W. 1955. The taxonomic status of the Maroon-fronted Parrot. *Condor*, *57*, 305-306.

Juniper, T., & Parr, M. 1998. Parrots: a guide to parrots of the world. A&C Black.

Tavares, E. S., Baker, A. J., Pereira, S. L., & Miyaki, C. Y. 2006. Phylogenetic relationships and historical biogeography of Neotropical parrots (Psittaciformes: Psittacidae: Arini) inferred from mitochondrial and nuclear DNA sequences. *Systematic Biology*, *55*(3), 454-470.

Urantówka, A. D., Strzala, T., & Grabowski, K. A. 2013. Complete mitochondrial genome of endangered Maroon-fronted Parrot (*Rhynchopsitta terrisi*)-conspecific relation of the species with Thick-billed Parrot (*Rhynchopsitta pachyrhyncha*). *Mitochondrial DNA*, (0), 1-3.

Wright, T. F., Schirtzinger, E. E., Matsumoto, T., Eberhard, J. R., Graves, G. R., et al. 2008. A multilocus molecular phylogeny of the parrots (Psittaciformes): support for a Gondwanan origin during the Cretaceous. *Molecular Biology and Evolution*, *25*(10), 2141-2156.

Submitted by: Brian Tilston Smith, Museum of Natural Science, Louisiana State University

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Split Arctic Warbler *Phylloscopus borealis* into three species

Background:

The Arctic Warbler *Phylloscopus borealis* has long been treated as a complex of several taxa breeding from Scandinavia through Japan and Alaska, and wintering marginally in S Asia (Andamans) and widely in SE Asia through the Philippines and Lesser Sundas. As summarized in Alström et al. 2011, there has been great variation in exactly how many taxa are recognized, and the ranges ascribed to each of them. HBW taxonomy (Clement in del Hoyo et al. 2006; HBW Alive, 25 Sep 2013) recognized three races: the widespread nominate (in which were synonymized the races *talovka* of the western part of the range, *transbaicalicus* of E Siberia and N Mongolia, and *hylebata* of N Manchuria and SE Russia to N Korea); *xanthodryas*, which breeds in NE Russia through Sakhalin, Kurile Is, and N Japan (with which *examinandus* of the S Kuriles and Japan was synonymized); and *kennicotti*, which breeds in W Alaska.

New Information:

Recent papers (Reeves et al. 2008; Saitoh et al. 2008, 2010; Alström et al. 2011) based on large datasets (e.g. 113 individuals from 18 populations in Saitoh et al. 2010) of mtDNA have shown that there are three major clades within *P. borealis*, and that these are genetically highly distinct as well as being vocally and morphologically diagnosable. These three clades do not correspond closely to HBW treatment, as the clades identified by DNA and vocal analyses are: *borealis* (including *kennicotti*) of most of the northern Palearctic; *examinandus* of S Kamchatka, Sakhalin, Hokkaido, and the Kuriles; and *xanthodryas* of Japan except Hokkaido. As with many other members of the genus *Phylloscopus*, great morphological similarity has long obscured the ancient divergences of these taxa. The Japanese taxon *xanthodryas* is postulated on the basis of its genetic distinctness to have diverged from the other two taxa 2.5–3.0 mya, near the end of the Pliocene or early in the Pleistocene, whereas northeastern *examinandus* and widespread *borealis* are somewhat more similar in mtDNA, and are estimated to have diverged in the early to mid-Pleistocene.

Alström et al. (2011) obtained mtDNA from the types (from non-breeding localities) of *xanthodryas* and *examinandus*, and were able to place these with confidence among samples from the respective breeding populations. However, there are issues with the type status of the three presumed syntypes of *xanthodryas*, and there is another name *hylebata* Swinhoe, 1861, that may be relevant, but for which no type specimen could be traced. Thus, further study may result in a nomenclatural change, but this seems rather unlikely. Further, there may well be a contact zone between *borealis* and *examinandus*, but this has not been studied.

Despite the high level of genetic differentiation between the three clades *borealis*, *examinandus*, and especially *xanthodryas*, the Alaskan breeding form *kennicotti* is very close to *borealis* genetically and vocally, as well as being only weakly morphologically differentiated. Thus, Alström et al. (2011) suggest its synonymization. However, other sources (e.g., Brazil 2009) mention the finer bill, brighter green upperparts, and yellower underparts of *kennicotti* as compared to the nominate, which suggests that perhaps *kennicotti* should be maintained until its status is more rigorously evaluated.

There is a detailed discussion of the taxonomic status of these forms on birdforum.net (http://www.birdforum.net/showthread.php?t=119101), most of it from prior to the publication of Alström et al. (2011). Many of the questions raised in the forum were addressed in the latter publication. The reason I mention this forum is that several observers have independently noticed the vocal distinctions documented in Alström et al. (2011), and Pete Morris did some brief playback experiments in which Honshu birds reacted strongly to playback from their population, but not to European birds.

Review of NA records:

According to ORNIS, there are at least three Aleutians specimens identified as subspecies *xanthodryas* at UAM. Given that the name *xanthodryas* has previously been applied to both E Asian taxa now split by other sources as *examinandus* and *xanthodryas*, it seems on geographical grounds much more likely to pertain to the species referred to by Alström et al. (2011) as *examinandus*. The odds of the northerly breeding *examinandus* occurring in the Aleutians are naturally high, while *xanthodryas* (as restricted in Alström et al. 2011), which breeds in central and southern Japan, would be an unlikely vagrant to the Aleutians. The identity of these specimens needs to be rechecked in light of this restriction of *xanthodryas*. According to ORNIS, there is also a specimen at UAM from Old Chevak, NW Alaska, identified as nominate *borealis*, but this would not affect the Check-list.

Arctic Warblers considered to be of the NE race *examinandus* have been recorded in rather large numbers on Shemya Island, with for example at least 10 recorded between 15 Sep to 18 Oct (Tobish 2006).

A well-documented sight record from Baja California (12 Oct 1991; Pyle and Howell 1993) was thought not to be *kennicotti*, but more likely one of the East Asian races, based on body size, bill size, plumage color, and long primary projection. However, these authors conceded that identification to race was not possible on knowledge at that time. Because this record is specifically mentioned in the Check-list, if the split is accepted we should probably mention somewhere that its allocation to one or another species is uncertain—it could be *examinandus*, although equally it could be nominate *borealis*.

The first record of Arctic Warbler from California (Big Sur River mouth, 13 Sep 1995) was measured and photographed, but there was no consensus on subspecies (http://www.wfopublications.org/Rare_Birds/Arctic_Warbler/Arctic_Warbler.html). California's second record (Pismo Beach, San Luis Obispo County, 28 Sep–1 Oct 1996) was photographed and "well-documented", but subspecies was not indicated (McCaskie and San Miguel 1999). The third California record (Mountain View, Santa Clara County, 7 Sep 2000) was a brief view that was only accepted by the committee after four rounds, so racial identity will doubtless remain unknown (Cole and McCaskie 2004). The fourth record of Arctic Warbler from California (Farallon Islands, 27 Sep 2005) was banded and measured, and its measurements were believed to be consistent with race *kennicotti* (Iliff et al. 2007). There are numerous photographs of another bird (7–9 Sep 2007, Galileo Hill, Kern Co.) on the web. In summary, without further critical review there is little or no evidence that any of these California records represent anything other than *kennicotti*.

Arctic Warblers (taxon unstated) are regular on Ashmore reef, Australia (Coates and Bishop 1997), so I suggest adding something about that to the account. They are vagrant elsewhere in Australia, New Guinea, and the Bismarck Archipelago, but this level of detail seems too great for extralimital areas.

Recommendation:

There are multiple options:

Option 1) Adopt a three-way split: Arctic Warbler *Phylloscopus borealis*; Japanese Leaf-Warbler *Phylloscopus xanthodryas*; and Kamchatka Leaf-Warbler *Phylloscopus examinandus*. This split has been adopted by Sangster et al. (2012) and the IOC World Bird List (Gill and Donsker 2013), among others.

Option 2): No change in taxonomy, but add a Note indicating that evidence suggesting there are multiple species has been published.

Option 3): Adopt a two-way split, into Arctic Warbler *P. borealis*, including *examinandus*; and splitting Japanese Leaf-Warbler *Phylloscopus xanthodryas*. This is by the far the best-corroborated split, being more ancient as judged by mtDNA; the morphological and vocal differences are greater; and there is not suspected to be a contact zone. If we adopt this treatment, we would not need a new account unless birds identified as *xanthodryas* are really this, not *examinandus*. If the *xanthodryas* records are really *examinandus* and if Option 1 is accepted, then I am happy to prepare a new account for that species.

The only form that breeds in the AOU-CLC area is *kennicotti*. One recommendation by Alström et al. (2011) would, if accepted, result in its synonymization with nominate *borealis*. Since *kennicotti* is not specifically mentioned in the Check-list, that doesn't concern us greatly here.

However, if the three-way split between *borealis*, *examinandus*, and *xanthodryas* is accepted, we will need to modify the Check-list account slightly. I've included an account with some suggested changes in red below. In this case we would also need a new account for one of the component taxa, probably *examinandus* (pending further examination, as outlined below).

Suggested changes to Check-list account, if Option 1 is approved:

Phylloscopus borealis (Blasius). Arctic Warbler.

Phyllopneuste borealis Blasius, 1858, Naumannia 8: 313. (ochotzkischen Meere = Sea of Okhotsk.)

Habitat.—Dense deciduous (willow, dwarf birch, alder) riparian thickets; in Eurasia, also open coniferous or mixed coniferous-deciduous forest.

Distribution.—*Breeds* in western and central Alaska from the Noatak Rover and western and central Brooks Range south to southwestern Alaska, the base of the Alaska Peninsula, the Alaska Range, and Susitna River highlands; and in Eurasia from Sweden, northern Russia, and northern Siberia south to central Russia, Mongolia, and Amurland. Recorded in summer north to Barrow, and on St. Lawrence and St. Matthew islands, and east to northern Mackenzie (Prince Patrick Island).

Winters from Andaman Islands, Southeast Asia, southeastern China and Taiwan south to eastern Indonesia and Ashmore Reef, Australia, and the Philippines.

Migrates through eastern Asia and the Commander Islands, casually the Aleutians.

Casual in California (Monterey, San Luis Obispo, Stanislaus, San Francisco, and Kern counties). A sight report from Baja California may represent one of the Asian taxa.

Notes.—Formerly included *P. examinandus* and *P. xanthodryas*, but song and mtDNA show that these are better treated as separate species. Specimens and other records from the Aleutians may pertain to *Phylloscopus examinandus*.

Literature Cited:

Alström, P., T. Saitoh, D. Williams, I. Nishiumi, Y. Shigeta, K. Ueda, M. Irestedt, M. Björklund, and U. Olsson. 2011. The Arctic Warbler *Phylloscopus borealis*—three anciently separated cryptic species revealed. Ibis 153:395–410.

Brazil, M. 2009. Birds of East Asia. China, Taiwan, Korea, Japan, and Russia. Princeton University Press, Princeton, NJ. 528 pp.

Clement, P. 2006. In del Hoyo et al., Handbook of the Birds of the World. Volume 11: Old World Flycatchers to Old World Warblers. Lynx Edicions, Barcelona.

Coates, B.J., and K.D. Bishop. 1997. A Guide to the Birds of Wallacea. Sulawesi, the Moluccas and Lesser Sunda Islands, Indonesia. Dove Publications, Alderley, Queensland. 535 pp.

Cole, L.W., and G. McCaskie. 2004. Report of the California Bird Records Committee: 2002 records. Western Birds 35:2–31.

Gibson and Byrd. 2007. Birds of the Aleutian Islands, Alaska. Nuttall Ornithological Club. 351 pp.

Gill, F., and D. Donsker (eds). 2013. IOC World Bird List (v 3.5). Available at http://www.worldbirdnames.org [Accessed 25 September 2013].

Iliff, M., G. McCaskie, and M.T. Heindel. 2007. The 31st report of the California Bird Records Committee: 2005 records. Western Birds 38:161–205.

McCaskie, G., and M. San Miguel. 1999. Report of the California Bird Records Committee: 1996 records. http://californiabirds.org/96report/96report.html#figure9 [Accessed 25 Sep 2013].

Pyle, P., and S.N.G. Howell. 1993. An Arctic Warbler in Baja California, Mexico. Western Birds 24:53–56.

Reeves, A.B., S.V. Drovetski, and V. Fadeev. 2008. Mitochondrial DNA data imply a stepping-stone colonization of Beringia by Arctic Warbler *Phylloscopus borealis*. Journal of Avian Biology 39:567–575.

Saitoh, T, Y. Shigeta, and K. Ueda. 2008. Morphological differences among populations of the Arctic Warbler with some intraspecific taxonomic notes. Ornithological Science 7:135–142.

Saitoh, T., P. Alström, I. Nishiumi, Y. Shigeta, D. Williams, U. Olsson, and K. Ueda. 2010. Old divergences in a boreal bird supports long-term survival through the Ice Ages. BMC Evolutionary Biology 10:35.

Sangster, G., J. M. Collinson, P.-A. Crochet, A. G. Knox, D. T. Parkin, and S. C. Votier. 2012. Taxonomic recommendations for British birds: eighth report. Ibis 154: 874–883.

Tobish, T. 2006. Alaska. North American Birds 60:119–123.

Submitted by: Pamela C. Rasmussen, Michigan State University

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Postscript: Numerous Aleutian Island specimens at the Alaska Museum, previously thought to be *examinandus* on morphological grounds, have now been positively identified as *examinandus* using DNA (J. Withrow, pers. comm.). All specimens from which genetic samples have been analyzed (12+ specimens from the Aleutians) have been confirmed as *examinandus*. In addition, Kenyon 1961 (Auk 78, pp. 322-323) previously published two specimens of *examinandus*(before Vaurie lumped this race with *xanthrodryas*) that are in the bird collection at the USNM. *Phylloscopus examinandus* has not been added to the Alaska list because they follow AOU taxonomy and it is only now being split. Ordinarily we would wait for the local committee to accept the records before we add the species, but in this case there are peer-reviewed published specimens at USNM, the Alaska Museum specimens have been confirmed as this species, and Dan Gibson has said that there will be no difficulty adding *P. examinandus* to the Alaska list, so the committee has voted to add this species to the AOU Check-list coincident with the splitting of this species from *P. borealis*.