

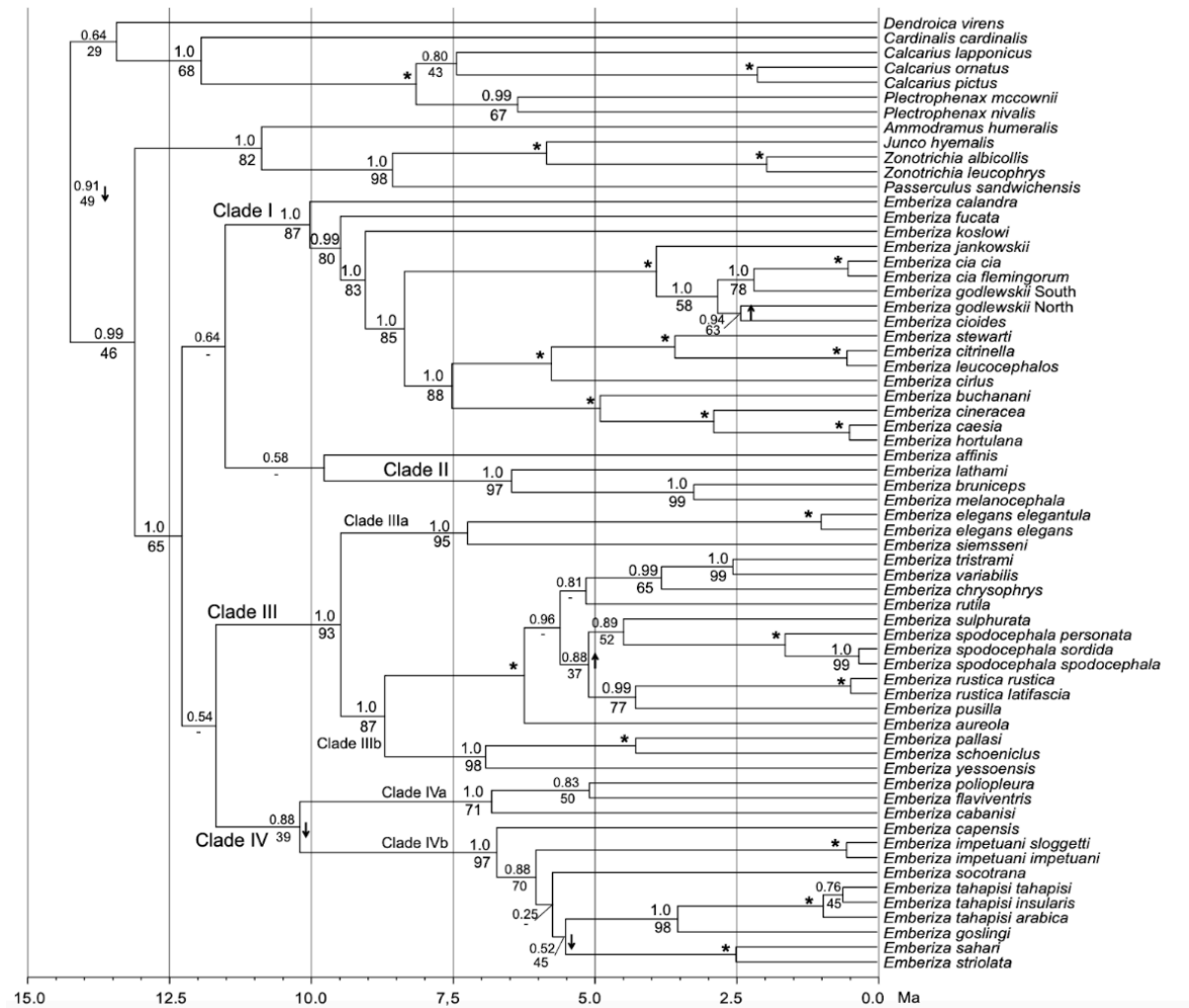
Emberizidae: split *Emberiza* into four genera

Background

Currently in AviList, all members of Emberizidae are included in a single genus, *Emberiza*, as is the case also in IOC, eBird/Clements and HBW/BirdLife. Previously, three additional monotypic genera were also recognised (*Miliaria*, *Latoucheornis* and *Melophus*), but were merged with *Emberiza* after genetics studies (Alström et al. 2008) showing them to be embedded. Howard & Moore, however, depart from the other taxonomic authorities by splitting *Emberiza* into five genera: *Melophus*, *Granativora*, *Emberiza* s.s. and *Schoeniclus*.

Available studies

Päckert et al. (2015) studied mitochondrial DNA (cytochrome-b) in 34 species of *Emberiza*. The phylogeny breaks up into four well separated clades, as seen below.



The results largely coincides with those of Alström et al. (2008). Compared to other genera sampled in the study, the four-way radiation is older than the *Calcaarius+Plectrophenax*-

split and the radiation of *Ammodramus+Passerella+Junco+Zonotrichia*, while being of about the same age as the split between *Cardinalis* and the longspurs.

Cai et al. (2021) sampled 43 out of 44 *Emberiza*-species, with a dataset including four mitochondrial and three nuclear loci. The phylogeny is similar to Päckert et al. (2015). The ages of the four clades are a bit younger, but they're still as old or substantially older than genera in closely related families. Unlike in Päckert et al. (2015), the arrangement of the four clades is robustly supported as a grade.

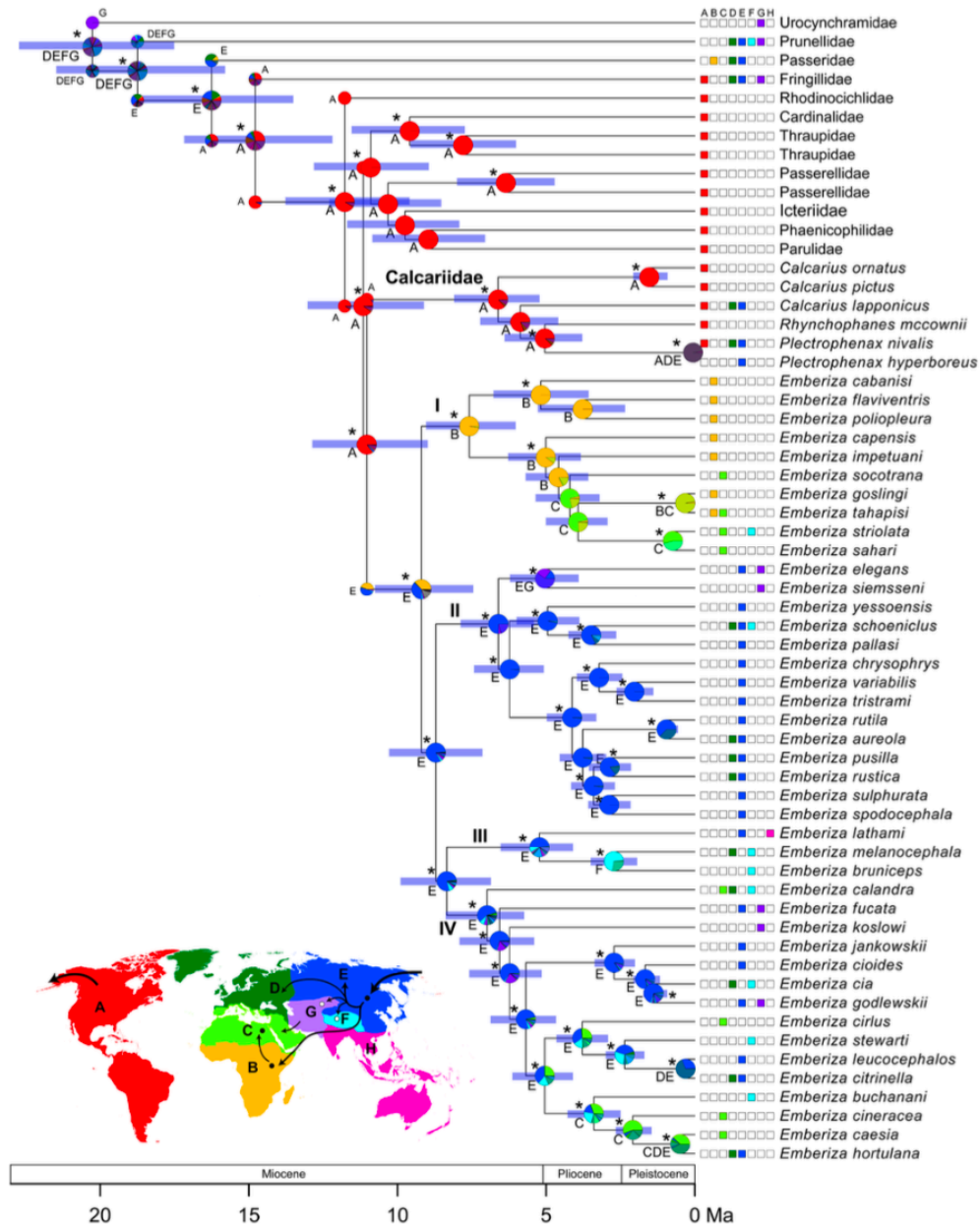


Figure 2. Time-calibrated phylogeny using a pruned DNA matrix with a rogue taxon excluded and ancestral area reconstruction for Emberizidae performed with BioGeoBEARS (Matzke 2014) based on the DEC+J model. The light blue bars at nodes in the phylogeny show the 95% highest posterior densities (HPDs) of divergence times estimated by two calibrations. The asterisks indicate Bayesian posterior probability (PP) ≥ 0.95 . The pie charts at the nodes represent the probability of regional occurrence, and the letters indicate the highest probability of ancestral regional states.

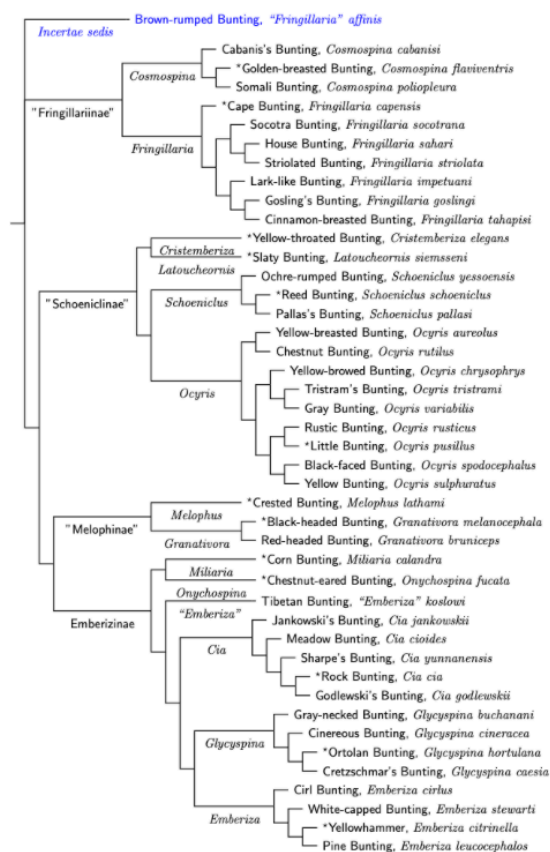
In Cai et al. (2021), the biogeographic history is described as such: “The group first dispersed from the New World to the northeast Palearctic, leading to a subsequent split between Calcaridae and Emberizidae. Then, the ancestral species of Emberizidae split

into two lineages: one lineage (clade I) mainly diversified in the African desert and savannah and the other (clades II, III and IV) mainly diversified in the eastern Palearctic, with several independent dispersals into the western Palearctic, QTP, mountains of central Asia and Saharo-Arabian-Mediterranean regions.” The four clades diverged from each other within a relatively short time period, with clades III and IV deriving from clade II at 9,8 Ma and clade IV splitting from clade III at 9,4 Ma.

If we were to recognize the four clades of *Emberiza* in Päckert et al. (2015) and Cai et al. (2021) as separate genera, the available names would be *Fringillaria* for clade I in Cai et al., *Schoeniclus* for clade II, *Melophus* for clade III and *Emberiza* for clade IV. This aligns with the taxonomy in Howard & Moore, save for their separation of *Granativora* constituting the Black-headed and Red-headed Buntings, while leaving Crested Bunting by itself in *Melophus*. As shown above, the split between them is relatively young.

There is some substructure below the four larger clades as well, some subclades being relatively old compared to other genera. John Boyd promotes the four genera as subfamilies and suggest the following names for younger clades:

Emberizidae: Buntings



KEY:
 DNA was available for each taxon.
 Blue = Position uncertain
 * = Type Species

Sources: Alström et al. (2008), Cai et al. (2021), Li et al. (2023), Olsson et al. (2013b), Päckert et al. (2015, 2020b), Ren et al. (2014), Schweizer and Kirwan (2014).

One surprising result in Päckert et al. (2015) was the position of Brown-rumped Bunting, *Emberiza affinis*. This African species is similar to other colorful representatives in the *Fringillaria* clade, but unexpectedly ends up as sister to *Melophus*. However, support

for this is low, without support from Bayesian posterior probabilities and in the maximum likelihood analysis with equally weak bootstrap support (27%). The position is commented as such: “This placement of *E. affinis* is highly doubtful because it received poor support in all analyses as it was based on evidence from two mitochondrial markers only. In fact, close affinities of *E. affinis* to other African species seem likely with respect to zoogeography but particularly with respect to strong similarities in external morphology with *E. flaviventris*, *E. cabanisi* and *E. poliopleura*.”

The issue is addressed in Cai et al. (2021) as well:

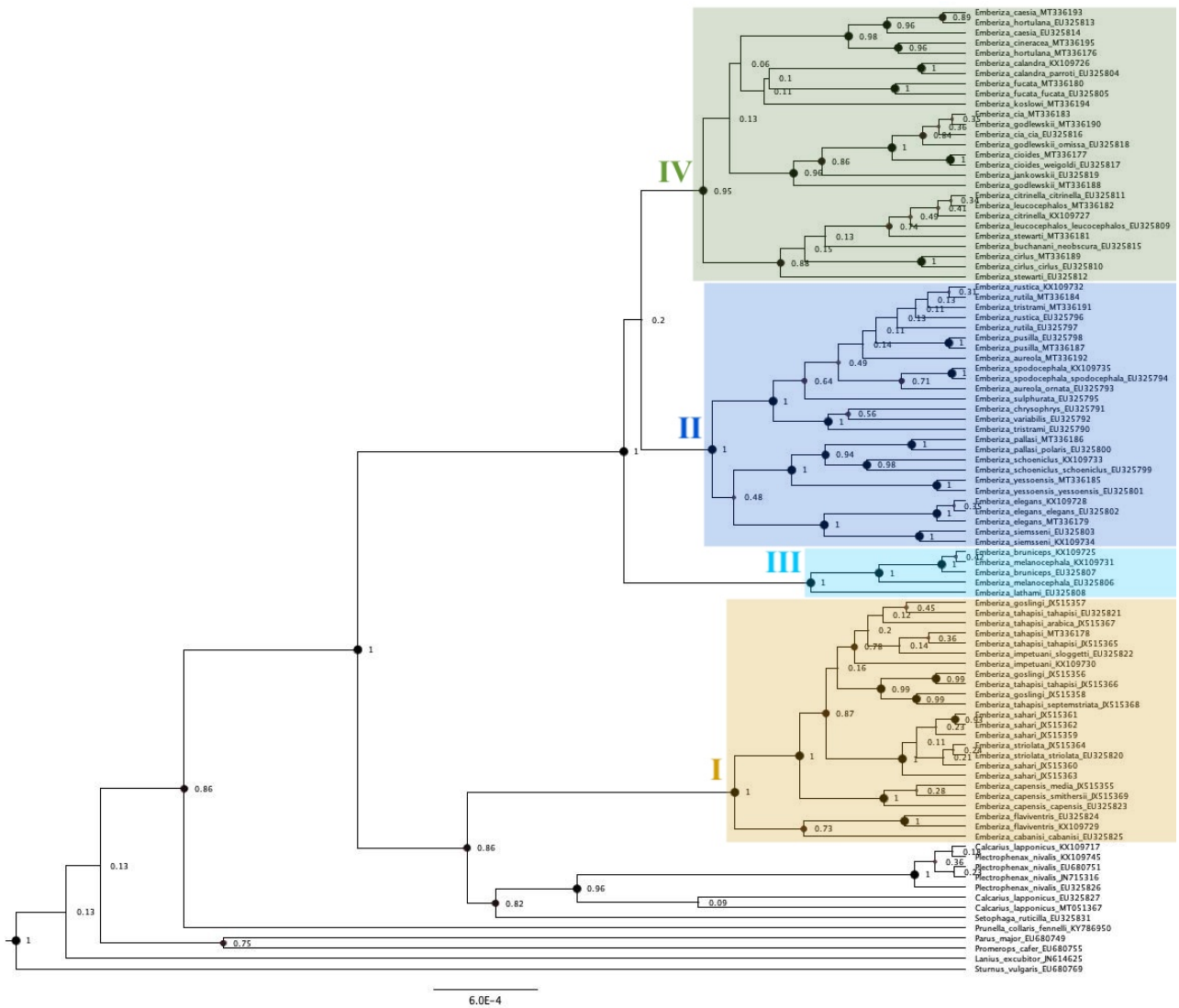
Our phylogenies based on a concatenated dataset of four mitochondrial and three nuclear markers suggested that the unsolved phylogenetic topologies of buntings in previous studies were probably caused by the inclusion of a rogue taxon *E. affinis* in phylogenetic analyses. For *E. affinis*, both Päckert et al. (2015, 2020) used the same short sequence of only one locus (Cytb, 672 bp) extracted from an old museum skin, which probably caused an unstable placement of taxa in their phylogeny (Moyle et al. 2012). Our phylogenetic analyses using the full DNA matrix (including this sequence) suggested four similar clades, as proposed by Päckert et al. (2015, 2020), but some of their internal relationships were poorly supported by the ML and BI trees (Supporting information). Subsequently, we identified *E. affinis* as a rogue taxon using RogueNaRok (Aberer et al. 2013) based on 1000 ML trees because *E. affinis* was placed in clades III, I and II in approximately 40, 30 and 20% of the trees, respectively. When *E. affinis* was excluded, the results strongly supported

Cai et al. (2021) states that *affinis* is “likely part of African buntings (clade I) instead of Eurasian buntings.”

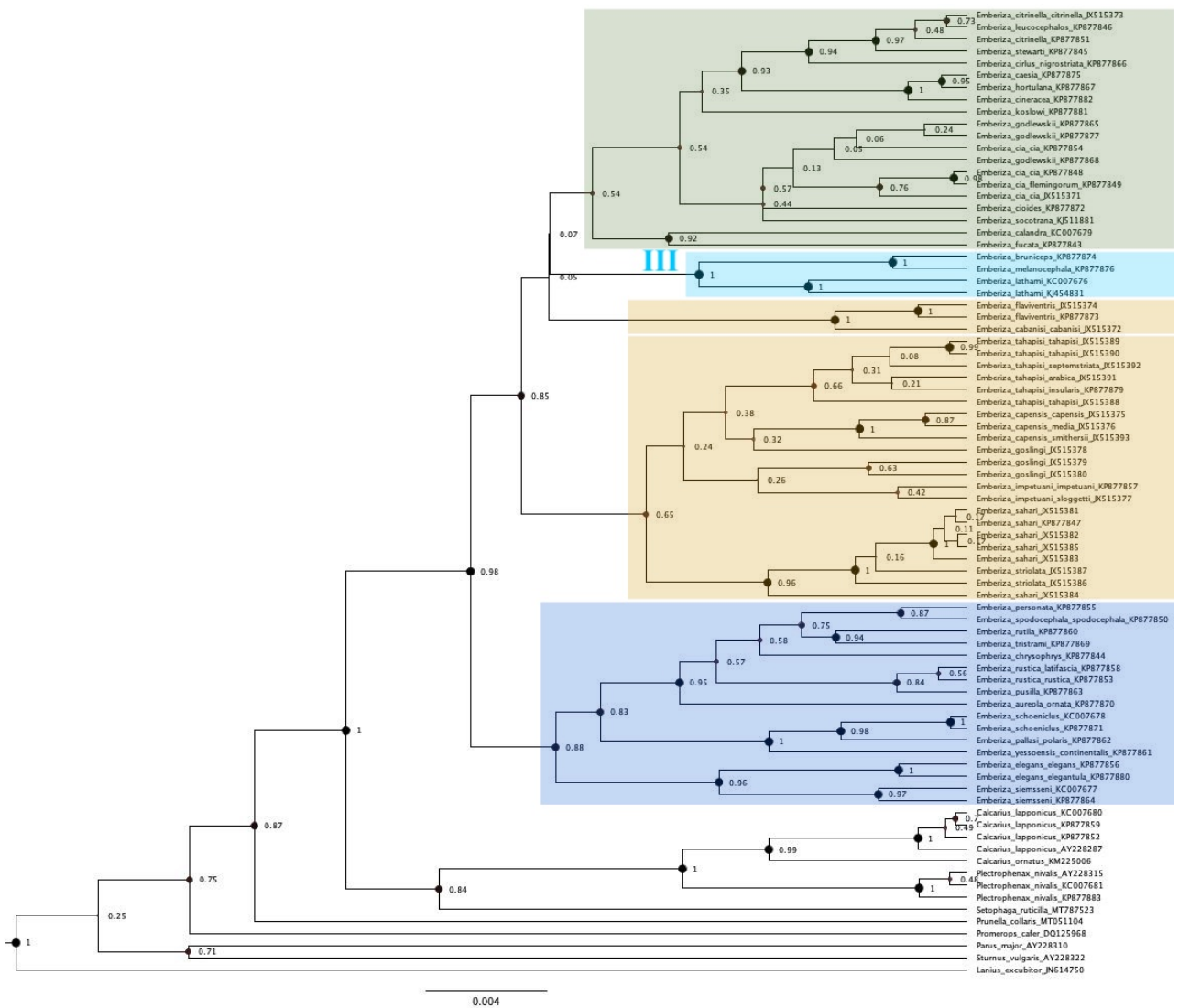
Further analyses

For this proposal, Martin Stervander downloaded sequence data from GenBank for the two nuclear markers that have best taxonomic coverage and performed alignment, partitioning according to intron/exon/codon position, ran model and evaluation partitioning (ModelFinder in IQ-TREE 2) and Bayesian phylogenetic analyses (Beast 2.7.8; receiving ESS>200 for all parameters). The results are rather relevant to the interpretation of the multilocus tree.

a. ODC introns 6+7 and exon 7 and partial 6+8 (two partitions: exons codon positions 1+2 JC+Γ; exons codon position 3+introns TPM+I) result in a phylogeny where the four clades discussed all are monophyletic and receive very strong support (posterior probability, PP, 0.95–1.0). The internal arrangement is not strongly supported, which is not particularly surprising, and Calcariidae (and the single parulid!) has been placed within Emberizidae as sister to clade I (*Fringillaria*). You may also see that neither do the very sparsely sampled more distant outgroups arrange quite as expected—again not very surprising for a single nuclear marker with no priors given on topology. All in all, it can be argued that this nuclear marker, comprising both coding and non-coding DNA, independently supports the results of the mitochondrial analyses.



b. Myoglobin intron 2 (single partition; K80+ Γ) results in a much less well-resolved phylogenetic tree. Clade III (*Melophus*) is the only well-supported clade with PP 1.0. Clades II (*Schoeniclus*) and IV (*Emberiza* s.s.) are recovered as monophyletic, but with low PP (0.88 and 0.54 respectively), while the clade comprising *E. flaviventris* and *E. cabanisi* has gone rogue from clade I (*Fringillaria*) though with exceedingly low node support. While the four clades do not receive strong support from Myoglobin analyses, they are still recovered with the exception of clade I, and—importantly—there are no strongly supported nodes that are incompatible with those clades.



Discussion

The aim of this proposal is to scrutinize whether or not *Emberiza* should be split up into smaller genera. Instead of arguing for or recommending a particular stance, we separate the pros and cons regarding the matter below.

Arguments for a split into four genera can be summarized as follows:

- * **Genetic support for four distinct clades corresponding to large phenotypic and ecological differences.** Available genetic data (mitochondrial and nuclear) support (or do not contradict) four distinguishable monophyletic clades (which make sense biogeographically). It is unlikely that recovering the four clades in the ODC analyses is a coincidence wrt the mitochondrial topology, which in turn indicates that it may likely represent a “true reflection of speciation” rather than results of introgression in secondary contact.
- * **Phylogenetic information.** A single broad *Emberiza* covering the entire family reveals no information about the internal structure.
- * **Age.** Although there is no universal yardstick concerning generic recognition, and while recognizing the current trend of lumping genera rather than splitting, *Emberiza* is an

excellent example of an overly broad genus in terms of age. It contains several ancient lineages branching off not far after the the entire family separated from its closest relatives.

- * **Consistency with genera in other families.** The ages of the larger clades are on par and sometimes even older than other clades in Passeroidea recognized as families. The inconsistencies are especially apparent when compared to the American Sparrows in Passerellidae, a family of similar age and with similar internal structure but divided into 30 genera. Current *Emberiza* s.l. is also older or comparable to, for example:

- a. *Pinicola*–*Pyrrhula*
- b. *Calcarius*–*Plectrophenax*
- c. all of Icteridae (31 genera, 108 spp)
- d. all of Parulidae (18 genera, 116 spp)
- e. all of the New World sparrows Paserellidae (30 genera, 138 spp)
- f. fringillid genera including *Chloris*, *Carduelis*, *Acanthis*, *Spinus*, *Loxia*, *Serinus*, *Crithagra*, *Linaria*
- g. a fringillid clade comprising *Bucanetes*, *Leucosticte*, *Rhodopechys*, and four additional monotypic genera
- h. five clades, which among them comprise all of Estrildidae (39 genera; 138 spp)
- i. the starling clade comprising genera *Sturnus*, *Pastor*, *Creatophora*, *Agropsar*, *Gracupica*, *Fregilupus*, *Leucopsar*, *Sturnia*, *Sturnornis*, *Spodiopsar*, and *Acridotheres*
- j. all of Zosteropidae (13 genera; 147 spp)

- * **Consistency with previous decisions.** Other relatively recent splits of genera have been adopted. A similar example is Sylviidae, previously monogeneric but split in two genera following genetic studies revealing ancient divergence.
- * **No complicated nomenclature issues.** The recognition of four genera for the prominent clades does not result in any monotypic genera, nor does it demand descriptions of new ones.

Arguments against a split can be summarized as follows:

- * **It isn't necessary.** *Emberiza* is monophyletic, which means the current arrangement isn't incorrect per se. There are also no universal yardsticks for genus delimitations and the members of *Emberiza* s.l. are also reasonably similar morphologically and/or ecologically.
- * **Stability is important.** There is a certain amount of frustration regarding the current state of flux of avian taxonomy. *Emberiza* is also a very well-known genus and a split would certainly affect a large part of the birding community. While this should not prevent us from making changes that are necessary when current taxonomy does not reflect the evolution of a given group, this should encourage us to exert caution and prioritize stability whenever we are facing a choice where the two options are equally in line with the evolutionary history of a group.
- * **Fewer genera is preferable to more.** Having one genus in Emberizidae but four in Calcariidae, for instance, makes no sense. But why not then lump *Calcarius*, *Rhynchophanes* and *Plectrophenax* instead? By always aligning the less split families with the most split families, we engage in a runaway process towards smaller and

smaller genera, which is an unnecessary and unwelcome development. And how can we justify lumping *Ixobrychus* with *Botaurus* but at the same time splitting *Emberiza* into four genera?

- * **Emberiza s.l. is not exceptionally old.** While there are a lot of younger genera, several others are of comparable age, such as *Carpodacus*, *Anthus*, *Prunella*, *Phoenicurus*, *Ficedula*, *Luscinia*, *Turdus*, *Sitta*, *Regulus*, and *Cisticola*.
- * **Unpublished studies.** The published studies are dominated by variation in mtDNA, which means we can't be sure they indeed reflect the evolutionary history. While Martin Stervander's further analyses do show that the clades are supported (or at least not contradicted by) ncDNA, there's a general reluctance to base decisions on unpublished data. However, the nuclear analyses are based on publicly available data and should reasonably have been included already in previously published studies running multilocus analyses.

Further division?

One could also argue splitting *Emberiza* further, into the younger clades described above. These do actually correspond quite well to natural groupings within *Emberiza* s.l., with diagnosable and readily recognized morphological, vocal and/or ecological traits. These clades are actually of an age corresponding to or even older than in other families, especially Passerellidae.

However, a division would require erecting several monotypic genera, primarily due to the grade-like structure in the *Emberiza* s.s. clade, which would hide phylogenetic information. Some of these are merely erections of previously used genera for quite characteristic species, like *Miliaria* for Corn Bunting and *Latoucheornis* for Slaty Bunting, but at least one name would have to be described.

Taxonomic implications for AviList

If *Emberiza* were to be split into four genera, as it is already arranged after Cai et al. (2021) in AviList, the order of species wouldn't change. An introduction of the four genera yields the following generic allocations:

- *Fringillaria* contains *cabanisi*, *flaviventris*, *poliopleura*, *affinis*, *capensis*, *impetuani*, *socotrana*, *sahari*, *striolata*, *goslingi* and *tahapisi*.
- *Schoeniclus* contains *siemsseni*, *elegans*, *yessoensis*, *pallasi*, *schoeniclus*, *chrysophrys*, *tristrami*, *variabilis*, *rutila*, *aureola*, *pusilla*, *rustica*, *sulphurata*, *personata*, and *spodocephala*.
- *Melophus* contains *lathamii*, *melanocephala* and *bruniceps*.
- *Emberiza* s.s. contains *calandra*, *fucata*, *koslowi*, *jankowskii*, *cioides*, *godlewskii*, *cia*, *buchanani*, and *cineracea*, *hortulana*, *caesia*, *cirlus*, *stewarti*, *leucocephalus* and *citrinella*.

Voting and recommendation

The subject of splitting *Emberiza* into four genera was put forth to RAG Palearctic, as item #42. All members voted on the matter, with 4 YES (Gustav Asplund, Erling Jirle, Markus Lagerqvist, Martin Stervander) and 4 NO (Pierre-André Crochet, Min Zhao, Paul Leader, Manuel Schweizer). RAG Sub-Saharan Africa were also invited to weigh in. 3 members voted, 2 YES (Gabriel Jamie and Roger Stafford) and 2 NO (Bob Dowsett and Françoise

Dowsett-Lemaire). See item #42 in the RAG-assessments repository on GitHub for the complete discussion.

There's no consensus among RAG Palearctic or RAG Sub-Saharan Africa on this issue. However, we still would like to put forth this proposal. Some of the basis for rejection pertains to a perceived lack of a policy on the matter. How important is genus name stability for AviList? What are the overall applied rules in AviList to designate genus level taxa? Although we do not think there should be a strict policy, we would appreciate if there were broad guidelines to guarantee some consistency among regional groups and taxa within AviList. We hope that this proposal could serve as a push in this direction.

References

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- Cai T, Wu G, Sun L, Zhang Y, Peng Z, Guo Y, Liu X, Pan T, Chang J, Sun Z and Zhang B. 2021. Biogeography and diversification of Old World buntings (Aves: Emberizidae): Radiation in open habitats, *Journal of Avian Biology* 52: e02672.
- Päckert M, Sun YP, Strutzenberger P, Valchuk O, Tietze DT and Martens J. 2015. Phylogenetic relationships of endemic bunting species (Aves, Passeriformes, Emberizidae, *Emberiza koslowi*) from the eastern Qinghai-Tibet Plateau. *Vertebrate Zoology* 65: 135–150.

This proposal was drafted by Gustav Asplund as pre-proposal, posted to RAG Palearctic on 19 October 2025 when co-signed by Erling Jirle, Markus Lagerqvist and Martin Stervander. It was augmented with further analyses by Martin Stervander, voting details and comments from the discussion from both RAG Palearctic members and members of RAG Sub-Saharan Africa.