Nesotrochidae, fam. nov. – a new name for the New World cave rails *Nesotrochis* spp., sister taxon of the New Zealand adzebills (Aptornithidae)

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ABSTRACT: Recent studies led to dramatic taxonomic revisions of the relationships of various rail-like birds. This is particularly true for cave rails from the New World (*Nesotrochis* spp.), which were long presumed to belong to the cosmopolitan rail family (Rallidae). Analyses of morphological data and mitochondrial genomes have revealed that cave rails are instead more closely related to the predominantly African flufftails and forest rails (Sarothruridae). These latter birds were long also considered to belong within the Rallidae but have instead been shown to be more closely related to finfoots (Heliornithidae), with which they form the taxon Heliornithes. Palaeogenomic studies further suggested a placement of adzebills (Aptornithidae) from New Zealand into the Heliornithes. We reanalysed available mitochondrial data, complemented by two new mitochondrial assemblies for the sarothrurid genera *Rallicula* and *Mentocrex*, and found *Nesotrochis* to be the sister taxon of the Aptornithidae, with an estimated divergence in the late Eocene. *Nesotrochis* and Aptornithidae could be merged into an expanded, broader-sense Aptornithidae, but not least because *Aptornis* deviates dramatically in terms of morphology thereby supporting its own family-level taxon, we assign *Nesotrochis* spp. to Nesotrochidae, fam. nov.

KEYWORDS: Gruiformes, Rallidae, Sarothruridae, new family, phylogeny.

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INTRODUCTION

The cave rails were first described with *Nesotrochis debooyi* by Alexander Wetmore (1918) from midden deposits on St. Thomas (one of the Virgin Islands, Caribbean Sea), presumed to be a flightless New World member of the rail family Rallidae Leach, 1820. In 1974, Storrs L. Olson (1974) described another species from Hispaniola (Dominican Republic), *N. steganinos*, and reclassified *Fulica picapicaensis* Fischer & Stephan, 1971 from Cuba as *N. picapicaensis* (see Olson, 1974). The three species are only known from skeletal remains. They occurred in the Antilles islands (predominantly the Greater Antilles) of the Caribbean Sea and varied considerably in size. *Nesotrochis* carried cultural significance as a human food item and *N. debooyi* may have gone extinct as late as the end of the 19th Century (Olson, 1974).

Initially, Wetmore (1922) presumed *Nesotrochis* to be most closely related to the rallid genus *Aramides* Pucheran, 1845, but he later suggested it instead would be an aberrant gallinule of rallid subfamily Gallinulinae Goldfuss, 1820 (see Wetmore, 1937), a taxon corresponding to the present-day tribe Fulicini Nitzsch, 1820 (Kirchman *et al.*, 2021). This taxonomic placement was supported by Olson (1974). Livezey (1998), based on morphological phylogenetic analyses, deduced that *N. debooyi* (but not *N. steganinos*, which was unresolved

in a polytomy) is the sister taxon of "*Canirallus* (including *Mentocrex*)", the former now known to be a rallid (Boast *et al.*, 2019; Kirchman *et al.*, 2021), whereas *Mentocrex* Peters, 1932 belongs to the family Sarothruridae Verheyen, 1957. Notably, Garcia-R and Matzke (2021) concurred with Wetmore's initial conclusion, that *Nesotrochis* would be sister to *Aramides*, after analysing the trait data from Livezey (1998) with sequence data of rallids (though no sequence data of *Nesotrochis* were used).

De Pietri and Mayr (2014) noted that the tarsometatarsus of *Nesotrochis* shows a close resemblance in hypotarsus morphology to that of extant flufftails (*Sarothrura* spp.). *Sarothrura* Heine, 1890 was traditionally assigned to the Rallidae, but Mayr (2011: 66) showed that the unusual hypotarsus morphology of these birds closely resembles that of the Heliornithidae G.R. Gray, 1840 and for the first time highlighted the then uncommented-upon findings of sequence-based studies (Fain *et al.*, 2007; Hackett *et al.*, 2008) that found *Sarothrura* to be the sister taxon of the Heliornithidae. All subsequent recent molecular analyses have supported a clade formed by the Sarothruridae and Heliornithidae, which was termed Heliornithes by Mayr (2019); this clade is the sister taxon of the Rallidae, together with which it constitutes the gruiform superfamily Ralloidea Leach, 1820. Expanding the analyses of hypotarsus morphology, Mayr (2019) suggested *N. steganinos* would be part of Heliornithes. Hypotarsus morphology likewise suggested a placement of *Mentocrex* into Heliornithes (see Mayr 2019).

After extracting and sequencing ancient DNA (aDNA), Boast *et al.* (2019) analysed mitochondrial genomes, which surprisingly showed that the extinct New Zealand adzebills, family Aptornithidae Bonaparte, 1856, were the sister taxon of the Sarothruridae—although this was contested by Musser and Cracraft (2019), who used additional morphological data to suggest that Aptornithidae were instead the sister taxon of the Psophiidae Bonaparte, 1831 in the gruiform superfamily Gruoidea Vigors, 1825. However, as noted by Mayr (2019), hypotarsus morphology conforms to a placement of *Aptornis* Owen, 1848a [see also Owen, 1848b] into Heliornithes.

Oswald *et al.* (2021) succeeded in extracting and sequencing aDNA of *N. steganinos*, and analyses of mitochondrial genomes demonstrated with full statistical support that *Nesotrochis* formed a clade with Aptornithidae and Sarothruridae, although the topology among the three groups was effectively unresolved (Figure 1a). Analyses of their "Dataset 1" resulted in two different topologies (Figure 1b–c) yielding almost equal bootstrap support (52% vs 48%) whereas analyses of "Dataset 2" (trimmed of poorly aligning portions) yielded 58% bootstrap support for *Nesotrochis* being the sister-group to the clade of Aptornithidae and Sarothruridae (Figure 1b). The non-dated phylogenetic analyses were made with Maximum Likelihood methods and, importantly, Oswald *et al.* (2021) partitioned their molecular data in three categories (protein-coding sequences (CDS), rRNA and tRNA sequences, and non-coding sequences) seemingly without reporting any analyses to determine the best model-fitting and partitioning scheme.

The unresolved topology among *Nesotrochis*, Aptornithidae and Sarothruridae offers little guidance on how to classify the Caribbean cave rails and how to treat the three groups with respect to each other. All three clades could be merged into an Aptornithidae *sensu lato* (Figure 1b), but Aptornithidae *sensu stricto* is drastically different regarding morphology and ecology. If keeping Aptornithidae and Sarothruridae as separate families, the classification of *Nesotrochis* spp. depends on their exact phylogenetic placement (Figure 1). Here, we set out to reanalyse mitochondrial data in a more rigorous manner across order Gruiformes Bonaparte, 1854, to shed light on this question.

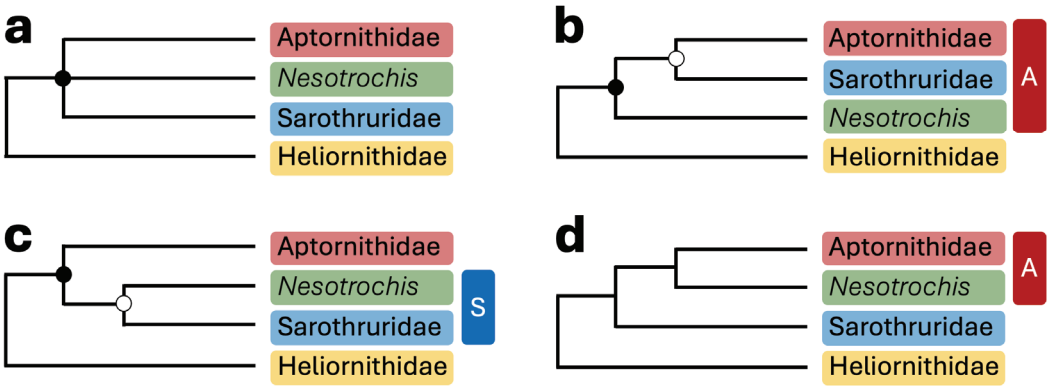

Figure 1. Potential and previously recovered phylogenetic scenarios within Heliornithes Mayr, 2019. Family Heliornithidae Gray, 1840 is known to be basal within the clade, but the relationships among families Sarothruridae Verheyen, 1957 and Aptornithidae Bonaparte, 1856, as well as genus *Nesotrochis* Wetmore, 1918 are unresolved. ● = full nodal support; ○ = low nodal support. Clade colours correspond to those of Oswald *et al.* (2021) as well as Figure 2. Vertical bars to the right of trees represent the necessary expansion of currently recognized families (S on blue = Sarothruridae; A on red = Aptornithidae), should *Nesotrochis* not be recognized to constitute a new family. (**a**) Present knowledge, based on Oswald *et al.* (2021), effectively reflects a hard polytomy, where Sarothruridae, Aptornithidae, and *Nesotrochis* form a well-supported clade, whose internal arrangement is unresolved. (**b**) The main tree ("Figure 1"; "Dataset 2") of Oswald *et al.* (2021) puts *Nesotrochis* basal relative to Sarothruridae and Aptornithidae as sisters, but the latter sister relationship only received bootstrap support of 58%. (**c**) The alternative tree ("Figure S1"; "Dataset 1") of Oswald *et al.* (2021) recovers *Nesotrochis* as sister to Sarothruridae, with Aptornithidae basal relative to them. However, the former sister relationship only received 52% bootstrap support. (**d**) The third possible topology, previously not recovered, would put Sarothruridae basal relative to the sister taxa *Nesotrochis* and Aptornithidae.

METHODS

In order to further explore the relationships between the three clades, and include them all in a dated phylogeny, we reanalysed 57 publicly available mitochondrial genomes of 50 gruiform species and four charadriiform outgroups (Appendix 1). While analysed by Oswald *et al.* (2021), mitochondrial sequence data of *Rallicula* Schlegel, 1871 from Garcia-R *et al.* (2020) are currently not publicly available; neither, currently, is the raw sequence data of *Mentocrex* produced by Kirchman *et al.* (2021). Given their crucial taxonomic placement in an expanded Sarothruridae/Aptornithidae (Boast *et al.*, 2019; Kirchman *et al.*, 2021; Oswald *et al.*, 2021) we created *de novo* mitochondrial assemblies for *Rallicula forbesi* Sharpe, 1887 (sample 150322_D1907007800) and *Mentocrex kioloides* (Pucheran, 1845) (sample B10K_D_MAD_206_D2212160148). We used the mitochondrial genome assembler NOVOPlasty (v2.7.2) (Dierckxsens *et al.*, 2017), which utilizes a seed-and-extend algorithm to assemble mitochondrial genomes from whole-genome sequencing data, and followed the the pipeline of Feng *et al.* (2020). In brief, mitochondrial genomes were assembled from all whole-genome sequencing reads using NOVOPlasty with default parameters, with the seed sequence derived from the complete mitochondrial genome of the Red Junglefowl *Gallus gallus* (Linnaeus, 1758) (GenBank accession no. NC_040902). Repeated trials using different K-mer sizes (39, 23 or 19) were conducted to obtain the circularized assemblies. The circularized mitochondrial sequence with fewer ambiguous bases was selected as the final mitochondrial genome of *M. kioloides*, and all contigs with non-circularized mitochondrial sequences were retained for *R. forbesi*. We annotated these

Table 1. Substitution models and partitioning scheme. I = invariant sites; Γ = rates follow a gamma distribution; uf = unequal base frequencies; ef = equal base frequencies.

Partition	Genes: codon position	Length (bp)	Best substitution model	Implemented model in BEAST
1	ND1: 1	318	GTR + I + Γ	GTR + I + Γ
2	ND1: 2, COX3: 2	578	TVM + I + Γ	TVM + I + Γ
3	All genes: 3	3205	TVM + Γ	TVM + Γ
4	ND5: 1, ND2: 1	943	GTR + I + Γ	GTR + I + Γ
5	ND2: 2	345	GTR + I + Γ	GTR + I + Γ
6	COX1: 1	515	GTR + I + Γ	GTR + I + Γ
7	COX1: 2	515	TVM + I + Γ	TVM + I + Γ
8	COX2: 1	226	GTR + I + Γ	GTR + I + Γ
9	COX2: 2	226	HKY + I + Γ	HKY + I + Γ
10	ATP8: 1	54	GTR + Γ	GTR + Γ
11	ATP8: 2	54	K81uf + I + Γ	TIM1uf + I + Γ (closest option)
12	ATP6: 1, ND4: 1, ND4L: 1, ND3: 1	891	GTR + I + Γ	GTR + I + Γ
13	ATP6: 2, ND4L: 2	322	TVM + I + Γ	TVM + I + Γ
14	COX3: 1	260	TVMef + I + Γ	TVMef + I + Γ
15	ND3: 2	115	TIM + I + Γ	TIM1 + I + Γ (identical)
16	ND5: 2, ND4: 2	1052	GTR + I + Γ	GTR + I + Γ

through lift-over from *Sarothrura ayresi* (Gurney, 1877) (GenBank accession no. KY075897) and manual curation in Geneious Prime v2023.1.2.

We opted to not include the control region, which is hard to reliably align (*cf.* Oswald *et al*., 2021), or RNAs. Instead, using Geneious Prime v2023.1.2 we aligned all coding mitochondrial genes except cytochrome b (for which *Nesotrochis* data are missing) from the 59 assemblies using the MAFFT v7.490 algorithm (Katoh, 2002; Katoh & Standley, 2013). After minimal manual curation (adjusting indels to align with full codons), we extracted the well-aligning core portions, excluding start and stop codons, and avoiding overlap between genes. This resulted in 11 mitochondrial genes comprising 9,615 bp.

Following Boast *et al.* (2019), because the third codon position was saturated with transitions, we recoded these into purines (R) or pyrimidines (Y) in Mesquite v3.81 (Maddison & Maddison, 2023) and kept them in a single combined partition, whereas we extracted first and second codon positions separately per gene. Using PartitionFinder2 v2.1.1 (Lanfear *et al.*, 2016), we evaluated the best substitution model with and without invariant sites (I) and the rate heterogeneity was modelled with a gamma distribution (Γ). We used the corrected Aikaike Information Criterion for selecting the best out of 256 models and partitioning scheme, applying the greedy algorithm (Lanfear *et al.*, 2012). This resulted in 16 partitions (Table 1), most commonly following the GTR+Γ+I model, which were implemented in BEAST v2.7.7 (Bouckaert *et al.*, 2014)—except for model K81 with unequal base frequencies, a proportion of invariant sites and mutation rate following a gamma distribution (K81uf + I + Γ), which was replaced by TIM1uf + I + Γ as the closest-fitting available model.

We dated the phylogeny by applying three well-characterised calibration points from Stiller *et al.* (2024): (1) crown Gruiformes as defined by the most recent common ancestor (MRCA) of Ralloidea [represented by *Laterallus rogersi* (Lowe, 1923)] and Gruoidea [*Grus grus* (Linnaeus, 1758)] at 55.6 Ma; (2) crown Jacanida Livezey, 2010 (*sensu* Černý & Natale, 2020) as defined by the MRCA of Rostratulidae Coues, 1888 + Jacanidae Des Murs, 1854 [*Jacana jacana* (Linnaeus, 1766)] and Thinocoridae Sundevall, 1836 + Pedionomidae Adams, Baikie & Barron, 1854 [*Pedionomus torquatus* Gould, 1840] with a minimum age of 29.5 Ma; and (3) crown Alcini Leach, 1820 (*sensu* Storer, 1960) as defined by the MRCA of *Alca* [*Alca torda* (Linnaeus, 1758)]

and *Uria* [*Uria aalge* (Pontoppidan, 1763)] with a minimum age of 15.97 Ma. For details of the fossils included, we refer to Stiller *et al.* (2024), while we implemented the calibration densities as log-normal distributions with mean 1.655, standard deviation 0.94, and offset 55.629 (Gruiformes); mean 1.08, standard deviation 0.965, and offset 29.513 (Jacanida); and mean 1.73, standard deviation 0.845, and offset 16.032 (Alcini).

We ran the phylogenetic analyses in BEAST, applying an optimised relaxed clock model and letting the speciation follow a birth–death prior. We optimised operators after preliminary runs for improved performance and ran two final replicates at different seeds for 100 million generations, sampling every 5,000 generations. Discarding the first 13% as burn-in, we observed stationarity, high effective sample sizes (ESS > 200), and between-replicate convergence for all parameters (with the exception of tree likelihood for partition 3, which had ESS < 200 in one run and was the only parameter to diverge slightly between runs) in Tracer v1.7.2 (Rambaut *et al.*, 2018). We obtained maximum clade credibility trees with divergence times (common ancestor, median, and mean node heights) with TreeAnnotator v2.7.1 (Drummond & Rambaut, 2007). Given the overall convergence (identical topology; node ages and posterior probabilities [PP] differing by ≤ 5%) we used a single replicate and drew it in R v4.3.0 (R Core Team, 2023) using the packages ape v5.3 (Paradis & Schliep, 2019) and phytools v0.6–99 (Revell, 2012). For full results of both replicate runs, see Data Availability.

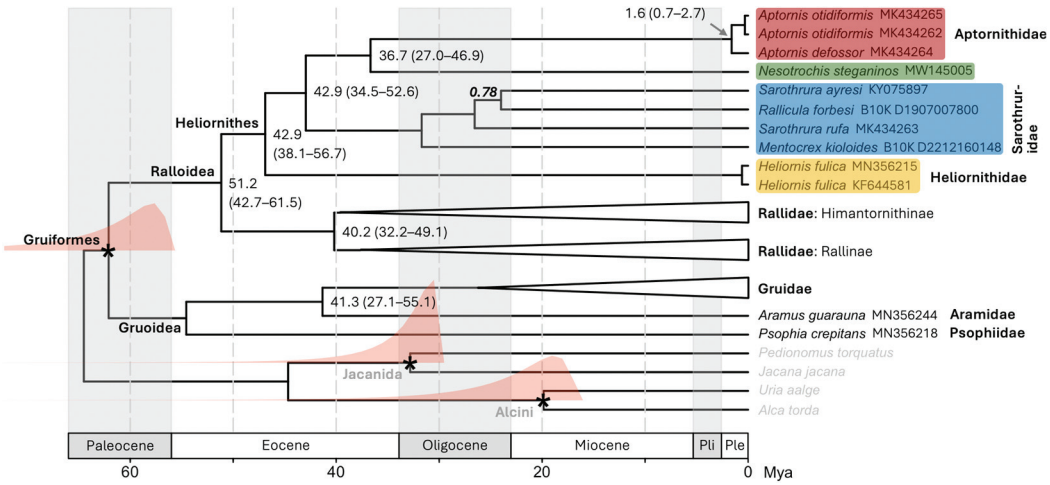

Figure 2. Dated phylogeny based on 9,615 base pairs mitochondrial DNA across Gruiformes, with charadriiform outgroups (in grey). With full posterior probability (PP = 1.0), the Cuban cave rail *Nesotrochis steganinos* Olson, 1974 is the sister taxon of the adzebill family Aptornithidae Bonaparte, 1856, from which it diverged 36.7 Ma. Their most recent common ancestor diverged from the flufftail family Sarothruridae Verheyen, 1957 at 42.9 Ma. Some key nodes are annotated tip-side of the node with the estimated and the 95% highest posterior density for divergence time. Nodes used for time calibrations are marked with asterisks and the calibration density distributions coloured in peach. All nodes shown have PP = 1.0 except one within Sarothruridae labelled with the PP value in bold italics on the root-side of the node. In the geological time scale, Pli = Pliocene, Ple = Pleistocene. Clade colours correspond to Figure 1 and Oswald *et al.* (2021). This tree is based on a single BEAST run comprising 100 million generations, with 13% burn-in and mean node heights. For other trees, see Data Availability.

RESULTS

The results of the phylogenetic analyses (Figure 2) are considerably more informative than those of Oswald *et al.* (2021) and demonstrate that cave rails *Nesotrochis* spp. are sisters to adzebills Aptornithidae, with full support (posterior probability [PP] 1.0), and that this clade is the sister taxon of the Sarothruridae (PP 1.0; Figure 2). The estimated divergence time between cave rails and adzebills is 36.7 [95% highest posterior density (HPD) 27.0–46.9] Ma (replicate 2: 36.6 [27.0–46.7] Ma), i.e. in the Priabonian stage of the late Eocene, and between them and sarothrurids 42.9 [34.5–52.6] Ma (42.9 [34.7–52.5] Ma), i.e. in the Lutetian stage of the mid-Eocene (Figure 2). This demonstrates a divergence time similar to that between Aramidae Bonaparte, 1849 and Gruidae Vigors, 1825 (41.3 [27.1–55.1] Ma) and older than that between *non-sister* outgroup families (Pedionomidae and Jacanidae; Figure 2), though also similar to the deepest divergence between subfamilies within Rallidae (Figure 2).

SYSTEMATIC ZOOLOGY

Nesotrochidae fam. nov.

Type genus: *Nesotrochis* Wetmore, 1918.

Differential diagnosis: Distinguished from Rallidae, Sarothruridae, and Heliornithidae in that the humerus has a large and ventrally protruding processus flexorius (Figure 3d). Further differs from Rallidae in that the hypotarsus has two dorsoplantarly staggered canals for the tendons of musculus flexor digitorum longus and musculus flexor perforans digiti II/m. flexor perforans et perforatus digiti II (Figure 3l). Distinguished from Heliornithidae in that the tarsometatarsus is much more slender. Differs from Aptornithidae in that the proximal end of the humerus is not reduced (Figure 3d, e), the hypotarsus has a sulcus for the tendon of musculus flexor hallucis longus (Figure 3l); hypotarsal canals not confluent (as they are in species of *Aptornis*; Figure 3m).

Contents: *Nesotrochis* Wetmore, 1918 with three species: *N. debooyi* Wetmore, 1918; *N. picapicensis* (Fischer & Stephan, 1971); *N. steganinos* Olson, 1974.

ZooBank LSID for new family: C10AEEC3-0BC0-4CE4-8035-369C9A624D5B

DISCUSSION

As an aside, Oswald *et al.* (2021) was first to show, with full bootstrap support (BS = 100%), that *Rallicula* was part of Sarothruridae based on mitochondrial data. The exact position within the family was effectively unresolved, with lower node support (BS = 75%) placing it nested within *Sarothrura*. Kirchman *et al.* (2021), based on nuclear genomic data from a different set of species, recovered *Rallicula* as sister to *Sarothrura* (BS = 100%). Our Bayesian mitochondrial analyses of the species covered by Oswald *et al.* (2021) yield full posterior probability (PP = 1.0) for placing *Rallicula* in a clade with *Sarothrura* (Figure 2), again nested within the latter with lower node support (PP = 0.78–0.79). A sister group relationship between the genera is compatible with all three studies and must be regarded as most likely. However, due to exceptional dispersal capability and pronounced convergent and divergent evolution within Ralloidea, geographic distributions and morphology have historically performed poorly as basis for inference of evolutionary relationships (*cf.*, e.g., Livezey, 1998; Boast *et al.*, 2019; Stervander *et al.*, 2019; Garcia-R *et al.*, 2020; Kirchman *et al.*, 2021; Oswald *et al.*, 2021). Should future phylogenomic

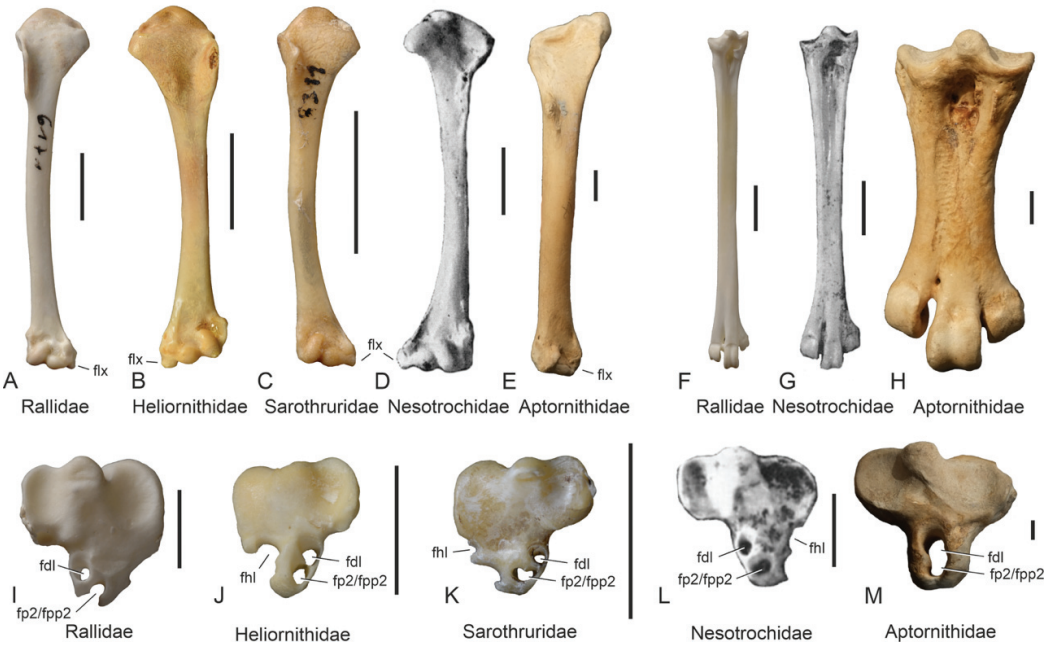

Figure 3. Humeri (A–E, cranial view), tarsometatarsi (F–H, dorsal view), and hypotarsi (I–M, proximal view) of the Rallidae (A, F, I), Heliornithidae (B, J), Sarothruridae (C, K), Nesotrochidae, fam. nov. (D, G, L), and Aptornithidae (E, H, M). A, *Aramides cajanea* (right side); F, I, *Aramides saracura* (right side); B, J, *Heliornis fulica* (all left side); C, K, *Sarothrura pulchra* (C: right side, K: left side); D, G, L, *Nesotrochis steganinos* (from Olson, 1974: figs. 1 and 2; D: left side, G, L: right side); E, H, M, *Aptornis defossor* (all right side). Abbreviations: fdl, sulcus/canal for tendon of musculus flexor digitorum longus; fhl, sulcus for tendon of musculus flexor hallucis longus; fp2, sulcus/canal for tendon of musculus flexor perforatus digiti II; fpp2, sulcus/canal for tendon of musculus flexor perforans et perforatus digiti II; flx, processus flexorius. The scale bars equal 10 mm in A–H and 5 mm in I–M; the scale bars for *N. steganinos* are approximate and based on measurements given by Olson (1974).

analyses with extended taxon sampling indeed render strong support for a topology yielding *Sarothrura* Heine, 1890 paraphyletic, the genus should be synonymised in *Rallicula* Schlegel, 1871.

As for *Nesotrochis*, the sister group relationship with Aptornithidae demonstrated here would offer the option to keep Sarothruridae *sensu stricto* (including *Sarothrura*, *Rallicula*, and *Mentocrex*) and to include *Nesotrochis* spp. in an expanded Aptornithidae. However, given the age of the three clades *Nesotrochis* spp., Aptornithidae, and Sarothruridae—combined with their geographic disparity and the pronounced phenotypic and ecological divergence of the Aptornithidae—we propose to instead make a new family-group name available under Article 13.1.1 (ICZN, 1999: 17) and Article 16.1 (ICZN, 1999: 19).

From a biogeographic point of view, it is notable that the West Indian Nesotrochidae are the sister taxon of the Aptornithidae from New Zealand, with the clade formed by these groups in turn being the sister taxon of the predominantly sub-Saharan Sarothruridae (which, in addition to *Sarothrura* now also includes the genus *Rallicula* from New Guinea and *Mentocrex* from Madagascar; Oswald *et al.*, 2021). This may suggest complex dispersal events, but we consider it more likely that these taxa are relics of a once more widespread radiation of heliornithine birds, which is supported by the fact that fossils from the early Miocene of Europe likewise show affinities to the Heliornithes (see De Pietri & Mayr, 2014), at the same period that aptornithids were present in New Zealand (Worthy *et al.*, 2011).

DATA AVAILABILITY

The mito-assemblies of *Mentocrex* and *Rallicula* and the maximum clade credibility trees of both replicate BEAST analyses, as well as alignments, XML specifications, and raw log and tree files, are freely available at Zenodo at https://doi.org/10.5281/zenodo.15727330.

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APPENDIX 1. The 53 publicly available gruiform and four outgroup charadriiform mitochondrial genomes included in this study, ordered alphabetically.

Taxon name	GenBank accession no.
Alca torda	MN356408
Amaurornis akool	KJ192198
Amaurornis phoenicurus	KJ874440
Antigone antigone	FJ769854
Antigone canadensis	FJ769855
Antigone rubicunda	FJ769853
Antigone vipio	FJ769852
Aptornis defossor	MK434264
Aptornis otidiformis	MK434262
Aptornis otidiformis	MK434265
Aramus guarauna	MN356244
Atlantisia rogersi	MH029238
Balearica pavonina	FJ769842
Balearica regulorum	FJ769841
Canirallus oculeus	MK434261
Coturnicops exquisitus	AP010823
Coturnicops noveboracensis	OM992117
Eulabeornis castaneoventris	KF644583
Fulica atra	KF644582
Gallicrex cinerea	KP057881
Gallinula chloropus	HQ896036
Gallirallus australis australis	KF425525
Gallirallus australis hectori	KF701060
Gallirallus striatus	MH219930
Grus americana	FJ769848
Grus carunculata	FJ769843
Grus grus	FJ769849
Grus japonensis	FJ769847
Grus leucogeranus	FJ769846
Grus monacha	FJ769850
Grus nigricollis	FJ769851
Grus paradisea	FJ769844
Grus virgo	FJ769845
Heliornis fulica	KF644581
Heliornis fulica	MN356215
Hypotaenidia okinawae	AP010821

Taxon name	GenBank accession no.
Hypotaenidia philippensis	KF701061
Jacana jacana	KJ631049
Laterallus jamaicensis jamaicensis	OM677841
Laterallus spilonota	MW067132
Lewinia muelleri	KF644584
Nesotrochis steganinos	MW145005
Pedionomus torquatus	MN356368
Porphyrio mantelli	OR753214
Porphyrio porphyrio	KF701062
Porzana paykullii	MG200164
Porzana pusilla	MW043485
Psophia crepitans	MN356218
Rallina eurizonoides sepiaria	AP010822
Rallus aquaticus	MH229988
Rallus indicus	OM837807
Rallus obsoletus yumanensis	OM992118
Sarothrura ayresi	KY075897
Sarothrura rufa	MK434263
Uria aalge	MN356418
Zapornia atra	MN356311
Zapornia fusca erythrothorax	LC541456