

# BIRD FAMILIES OF THE WORLD

## AN INVITATION TO THE SPECTACULAR DIVERSITY OF BIRDS

**David W. Winkler**

*Professor, Curator of Birds, and Director of the Cornell University Museum of Vertebrates,  
Department of Ecology and Evolutionary Biology and Cornell Laboratory of Ornithology,  
Cornell University, Ithaca, NY 14853 USA*

**Shawn M. Billerman**

*Ph.D. Candidate, Department of Zoology and Physiology and Program in Ecology,  
University of Wyoming, Laramie, WY 82071 USA*

**Irby J. Lovette**

*Professor, Curator of Genetic Resources, Cornell University Museum of Vertebrates,  
Cornell Laboratory of Ornithology and Department of Ecology and Evolutionary Biology,  
Cornell University, Ithaca, NY 14853 USA*

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## Three new bird family names

By Jon Fjeldså<sup>1</sup>, Per G. P. Ericson<sup>2</sup>, Ulf Johansson<sup>2</sup>, Dario Zuccon<sup>3</sup>

Over the last two decades, many molecular phylogenetic studies have provided robust evidence for the phylogenetic placement of species, or species groups, which had previously been difficult to place in the taxonomic hierarchy. Many of these have in the past been appended to larger family groups, although they may in fact represent ancient relictual forms with no close relatives. Separate family group names were in many cases suggested to flag their isolated position. Cracraft (2014) suggested that, in order not to lose taxonomic hierarchy, they should be included in a more inclusive family, provided that there was strong support for a sister group relationship. However, such a practice would lead to loss of information about the uniqueness of taxa that represent the last surviving relictual members of ancient radiations. We believe that, in case of an assemblage of several species or genera, each of which represents a lineage that is as old as, or older than, other species-rich family groups, we should accept each lineage of that assemblage to be an independent family (and we could then create taxonomic hierarchy of superfamilies, as exemplified by Alström *et al.* 2014 and Barker 2014). Jönsson *et al.* (2015) demonstrated, for the crow-like passerine birds (cohort Corvides), that the current family-level classification was largely consistent with 30 million years of divergence. Although this may differ somewhat among avian groups, we will argue that terminal branches, even if they include only a single extant species, should be recognized as a separate family if its genetic divergence is consistent with ages of related families, according to molecular phylogenies calibrated against fossils (Alström *et al.* 2014, Ericson *et al.* 2014, Selvatti *et al.* 2015).

For some such small families suggested in recent years, the suggested name was not presented in accordance with the International Code of Zoological Nomenclature. Here we provide formal family group names for three such taxa. The evidence will generally come from molecular phylogenetic studies, as these groups appear to be characterized mainly by morphological traits that are plesiomorphic within the assemblage of most closely related families.

### Chaetopidae Fjeldså *et al.* Fam. Nov.

*Chaetops*, the rock-jumpers of South Africa, have in most earlier classifications been placed in the family Timaliidae (often together with the warbler *Achaetops pycnopygius*), or in the Turdidae. Sibley and Ahlquist (1990) included *Chaetops* in DNA-DNA hybridization experiments with *Picathartes* and representatives of several species of the Corvida and Passerida cohorts; they found that the closest taxon to *Chaetops* was *Picathartes* and they were placed together in a family Picarthartidae and Parvorder *incertae sedis*. Using nuclear and mitochondrial DNA sequences, Barker *et al.* (2004) and Beresford *et al.* (2005) recovered *Picathartes* and *Chaetops* as strongly supported sister-taxa in an ancient lineage that may have originated already in the Eocene (Ericson *et al.* 2014). Jönsson *et al.* (2007) expanded the analysis by adding the Oriental *Eupetes*, which was found to group with *Chaetops*, leaving *Picathartes* as a more distant relative. Cracraft (2014) proposed to include all three genera in a single family Eupetidae, but considering the Paleogene age of the *Picathartes-Chaetops-Eupetes* clade (Ericson *et al.* 2014), we

find it more reasonable to assign the three genera to separate families (which can then be assembled in a superfamily Eupetoidea). Family name Chaetopidae has been mentioned for instance by Collar and Robson (2007) and Alström *et al.* (2014), but has not been formally named yet. Here we formally name the taxon:

#### Chaetopidae, new family

Type genus: *Chaetops* Swainson, 1832.

Diagnosis: The most inclusive crown clade that contain the two *Chaetops* species *frenatus* and *aurantius* (considered subspecies of one species by some), but not *Eupetes macrocercus*, *Picathartes gymnocephalus* and *P. oreas*, or *Achaetops pycnopygius*. Medium-sized (21-25 cm) insectivorous and petrophilous ten-primaried oscine passerine birds distributed in the south of Africa. Bill medium long, slightly decurved, legs and feet strong; tail fairly long and graduated, blackish with white feather tips, often held upright; plumage with streaked grayish upper parts and rusty rump and body underparts, and long whitish malar stripe. According to the available anatomic evidence, characterized by plesiomorphic characters such as a single cup-like humeral fossa and generalized oscine configuration of the syrinx (Olson 1984).

### Hylocitreidae Fjeldså *et al.* Fam. Nov.

The species *Hylocitreia bonensis* has had a convoluted taxonomic history, but until recently it was placed in family Pachycephalidae (Mayr 1967, Morony *et al.* 1975), without much supporting evidence other than a general similarity and presumably also guided by its distribution (Sulawesi) within the geographical range of the Pachycephalidae, which are well represented across the Malesian island region. Based on nuclear and mitochondrial DNA data, Spellman *et al.* (2008) placed it with strong support in the superfamily Bombycilloidea (with Dulidae, Bombycillidae, Ptiliogonatidae, Mohoidae, and Hypocoliidae), but with low support for a sister-group relationship with *Hypocolius* within that superfamily. Using additional markers and a complete species dataset, the *Hylocitreia-Hypocolius* clade became fully supported (Zuccon, unpublished), with basal divergences within the superfamily estimated to have taken place within a narrow time window around 30 Mya. Cracraft (2014) placed *Hylocitreia* as *incertae sedis* within the superfamily Bombycilloidea, but considering the age of divergence, we propose family rank. Alström *et al.* (2014) referred to Family Hylocitreidae, but without formally describing the family, which we here formally describe:

#### Hylocitreidae, new family

Type genus: *Hylocitreia* Mathews, 1925.

Diagnosis: The most inclusive crown clade that contains one species *Hylocitreia bonensis* with two distinctive subspecies (or allospecies, *bonensis* and *bothaina*), but not *Hypocolius ampelinus*, *Dulus dominicus*, *Bombycilla* spp., *Phainoptila melanoxantha*, *Phainopepla nitens*, *Ptilogonys* spp., *Moho* spp. or *Chaetoptila angustipluma*. Medium-sized (14-15 cm) ten-primaried oscine passerine inhabiting montane forests of Sulawesi, Indonesia; plumage mostly gray and olive-brown,

<sup>1</sup> Natural History Museum of Denmark, Universitetsparken 15, DK-2100 Copenhagen, Denmark

<sup>2</sup> Swedish Museum of Natural History, P.O. Box 50007, Stockholm, SE-104 05, Sweden

<sup>3</sup> Muséum national d'Histoire Naturelle, Paris Cedex 05, France

with yellow-olive flanks and rump, resembling a diminutive female *Phainoptila melanoxantha* (unlike the more drab-gray *Hypocolius*); bill short, broad-based and slightly hooked and with short rictal bristles; legs short and feet small. By lack of anatomic specimens, no apomorphies have been identified, and external characters (including structure of plumage, bill and feet), frugivorous diet and high-pitched, buzzy vocalizations (Stresemann 1940) appear similar to other members of the Bombycilloidea assemblage.

### **Modulatricidae** Fjeldså *et al.* Fam. Nov.

Members of this group have had a tumultuous taxonomic history, being placed in various classifications as members of the Timaliidae *sensu lato*, Pycnonotidae or Turdidae. Using nuclear and mitochondrial DNA sequences, Johansson *et al.* (2008) demonstrated that *Modulatrix stictigula*, *Arcanator orostruthus*, and *Kakamega poliothorax* form a monophyletic group. Cracraft (2014) avoided erecting a family group for these three by placing them together with *Promerops* in the Promeropidae. This was justified by a strong support for monophyly based on RAG-1 and RAG-2 nuclear DNA (Barker *et al.* 2004, Beresford *et al.* 2005). However, RAG genes have given divergent results in some phylogenetic studies, and Johansson *et al.* (2008), adding other DNA markers, could not support this relationship. Further, the *Promerops* and *Modulatrix-Arcanator-Kakamega* lineages are estimated to have originated in the Oligocene (Alström *et al.* 2014), and before the divergence of the 26 other families in the Passeroidea radiation (*sensu* Barker 2014). The name Modulatricidae was mentioned (in quotation marks) by Fjeldså & Bowie (2008) and again by Alström *et al.* (2014). We here formally name the taxon:

#### **Modulatricidae, new family**

Type genus: *Modulatrix* Ripley, 1852.

Diagnosis: The most inclusive crown clade that contains the species *Modulatrix stictigula*, *Arcanator orostruthus* and *Kakamega poliothorax*, but not *Promerops cafer* or *gurneyi*. Medium-sized (15–19 cm) thrush-like passerine birds inhabiting the interior of Afromontane humid forest; feathering fine, close and dense, with uniform brownish dorsum and tail; further, the bill is fairly long, thin, and straight, rictal bristles reduced; legs long and feet large. We can confirm that details of tongue, jaw muscles, and structure of foot-pads, as described by Mann *et al.* (1978) for *Kakamega*, apply to all three species.

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