N&MA Classification Committee: Proposals 2009-C

- # Page Title
- 01 2 Create a new order, Phaethontiformes, for the Phaethontidae
- 02 4 Alter the traditional orders Pelecaniformes (excluding Phaethontidae) and Ciconiiformes to reflect new data on their relationships, and create a new order, Suliformes
- 03 7 Remove the Accipitridae from the Falconiformes, and create a new order, Accipitriformes
- 04 10 Elevate the Osprey to family status, Pandionidae
- 05 12 Create a new order, Eurypygiformes, for the Sunbittern (and Kagu)
- 06 14 Alter the traditional orders Apodiformes and Caprimulgiformes to reflect new data on their relationships
- 07 17 Elevate the New World barbets and *Semnornis* barbets to their own families (Capitonidae and Semnornithidae)
- 08 19 Recognize six families arising from the breakup of the Sylviidae
- 09 25 Alter the composition of the Timaliidae by merging *Zosterops* and moving the Wrentit *Chamaea fasciata* to the Sylviidae
- 10 28 Remove the longspurs (*Calcarius*) and snow buntings (*Plectrophenax*) from the Emberizidae and elevate them to the new family Calcariidae
- 11 30 Create a new family, Viduidae, for the indigobirds and whydas

Create a new order, Phaethontiformes, for the Phaethontidae

Description of the problem:

The tropicbirds (Phaethontidae), as currently recognized by the AOU, form part of the order Pelecaniformes. The traditional members of the Pelecaniformes, including the tropicbirds, share a number of morphological characters, including totipalmate feet, which occur only in the traditional Pelecaniformes (del Hoyo et al. 1992, Hedges and Sibley 1994, Kennedy and Spencer 2004). The traditional Pelecaniformes were also united by the placement of the salt gland and the lack of any brood patch, among other synapomorphies (Hedges and Sibley 1994). The monophyly of this group was questioned by Sibley and Ahlquist (1990) and again by Hedges and Sibley (1994) based on DNA-DNA hybridization work. However, even in the DNA-DNA hybridization-based reconstructions, the tropicbirds formed a monophyletic group with three other traditional families of Pelecaniformes: the cormorants (Phalacrocoracidae), anhingas (Anhingidae), and gannets and boobies (Sulidae) (Hedges and Sibley 1994).

New information:

Sequence-based molecular phylogenies provide a different perspective on relationships of the tropic birds. Kennedy and Spencer (2004), in a species-level phylogeny of the frigatebirds (Fregatidae) and tropicbirds, found that the tropicbirds are not closely related to the other Pelecaniformes, although their ability to fully explore this issue was compromised by limited sampling outside their focal groups. Molecular phylogenies with greater taxon sampling include Ericson et al. (2006), who, using five nuclear loci (~5000 base pairs of data), found that the tropic birds occupy a position in a basal clade ("Metaves") of the Neoaves where they are very distantly related to the other Pelecaniformes. A similarly distant relationship between the Phaethontidae and the other Pelecaniformes was recovered by Hackett et al. (2008), in a study using 19 nuclear loci (nearly 32,000 base pairs). Both of these studies placed the tropicbirds near the doves (Columbidae), mesites (Mesitornithidae), sandgrouse (Pteroclidae), and grebes and flamingos (Podicipedidae and Phoenicopteridae) (Ericson et al. 2006, Hackett et al. 2008). Although support for the separation of the Phaethontidae from the other Pelecaniformes was very strong in both studies, support for placement near the groups listed above was strong only in the Ericson *et al* study, where the result may be driven by a single atypical gene.

Recommendation:

It seems clear that the tropicbirds do not belong in or near the traditional Pelecaniformes. We propose recognizing a new order, the Phaethontiformes, already adopted by Christidis and Boles (2008) and Gill *et al.* (2009), and placing this new order before the Ciconiiformes (see Proposal 2009-C-02) in the linear classification.

Literature cited:

Christidis, L. and Boles, W.E. 2008. *Systematics and Taxonomy of Australian Birds*. CSIRO Publishing, Collingwood, Australia

Del Hoyo, J., Elliott, A. and Sargatal, J. eds. 1992. *Handbook of the Birds of the World*. Vol. 1. Lynx Edicions, Barcelona

Ericson, P.G.P., Anderson, C.L., Britton, T., Elzanowski, A., Johansson, U.S., Källersjö, M., Ohlson, J.I., Parsons, T.J., Zuccon, D., and Mayr, G. 2006. Diversification of neoaves: integration of molecular sequence data and fossils. *Biol. Lett.* **2** 543-547

Gill, F., M. Wright, and D. Donsker, D. 2009. IOC World Bird Names (version 2.0)

Hackett, S.J, Kimball, R.T., Reddy, S., Bowie, R.C.K., Braun, E.L., Braun, M.J., Chojnowski, J.L., Cox, W.A., Han, K., Harshman, J., Huddleston, C.J., Marks, B.D., Miglia, K.J., Moore, W.S., Sheldon, F.H., Steadman, D.W., Witt, C.C., and Yuri, T. 2008. A phylogenomic study of birds reveals their evolutionary history. *Science*. **320** 1760

Hedges, S.B. and Sibley, C.G. 1994. Molecules vs. morphology in avian evolution: The case of the "pelecaniform" birds. *Proc. Natl. Acad. Sci. USA*. **91** 9861-9865

Kennedy, M. and Spencer, H.G. 2004. Phylogenies of the frigatebirds (Fregatidae) and tropicbirds (Phaethontidae), two divergent groups of the traditional order Pelecaniformes, inferred from mitochondrial DNA sequences. *Molecular Phylogenetics and Evolution.* **31** 31-38

Sibley, C.G. and Ahlquist, J.E. 1990. Phylogeny and classification of birds. Yale. Univ. Press, New Haven, Connecticut

Name and affiliation of submitter: Shawn Billerman, Irby Lovette, Terry Chesser, NACC

2009-C-02 N&MA Check-list Committee

Alter the traditional orders Pelecaniformes (excluding Phaethontidae) and Ciconiiformes to reflect new data on their relationships, and create a new order, Suliformes

pp. 28-51

Description of the problem:

The AOU Check-list recognizes the Pelecaniformes and the Ciconiiformes as distinct orders. The Pelecaniformes (minus the Phaethontidae, see previous proposal), includes the following families:

Fregatidae (Frigatebirds) Pelecanidae (Pelicans) Phalacrocoracidae (Cormorants and Shags) Anhingidae (Darters) Sulidae (Gannets and Boobies)

and the Ciconiiformes consists of:

Ciconiidae (Storks) Ardeidae (Herons and Egrets Threskiornithidae (Ibises and Spoonbills) Scopidae (Hamerkop—not in AOU area) Balaenicipitidae (Shoebill—not in AOU area)

In the current check-list, these two orders are listed sequentially, reflecting their close relationship, as proposed in numerous studies (e.g., Sibley and Ahlquist 1990, Hedges and Sibley 1994, Van Tuinen *et al.* 2001, Ericson *et al.* 2006, Hackett *et al.* 2008). However, there is now substantial phylogenetic evidence for the paraphyly of these two groups, due to the Shoebill (*Balaeniceps rex*) being more closely related to the Pelecanidae than to the rest of the Ciconiiformes (Cracraft 1981, Livezey and Zusi 2001), or to the Pelecanidae being more closely related to the Shoebill and Hamerkop (*Scopus umbretta*) than to the rest of the Pelecaniformes (Van Tuinen *et al.* 2001, Ericson *et al.* 2006, Hackett *et al.* 2008).

The monophyly of the Pelecaniformes was questioned by Sibley and Ahlquist (1990) and again by Hedges and Sibley (1994) based on DNA-DNA hybridization work. The observed paraphyly of the Pelecaniformes with the Ciconiiformes led to placement of the Pelecaniformes, along with seven other closely related orders, in a greatly expanded Ciconiiformes (Sibley and Ahlquist 1990, Sibley and Monroe 1990, Hedges and Sibley 1994). However, we now know that this expanded Ciconiiformes is itself paraphyletic.

New information:

DNA sequence data suggest that neither the Pelecaniformes nor the Ciconiiformes is monophyletic, and generally support a close relationship

between the Pelecanidae and the Shoebill (Van Tuinen *et al.* 2001, Ericson *et al.* 2006, Hackett *et al.* 2008). Further, it appears that the Ciconiidae is not sister to the other families traditionally placed in the Ciconiiformes, but is instead sister to the remaining "Ciconiiformes"+Pelecaniformes (Hackett *et al.* 2008) or its relationship is unresolved (Ericson et al. 2006).

Given that the Pelecaniformes and Ciconiiformes are paraphyletic, there are three main alternatives to be considered. These would result in one, four, and three orders, respectively. The first would lump the Pelecaniformes (excluding the Phaethontidae) with the Ciconiiformes to create an expanded Ciconiiformes. The second would split the Pelecaniformes (again excluding the Phaethontidae) and Ciconiiformes into two orders apiece. Following the Hackett et al. (2008) phylogeny, the Pelecaniformes would be split into the Suliformes (Anhingidae, Phalacrocoracidae, Sulidae, Fregatidae) and the Pelecaniformes (Pelecanidae; Balaenicipitidae and Scopidae from outside our area), and the Ciconiiformes into the Ciconiiformes (Ciconiidae) and the Ardeiformes (Ardeidae, Threskiornithidae). The third option would split the Suliformes (as above) from the Pelecaniformes and the Ciconiidae from the rest of the erstwhile Ciconiiformes (as above), but would lump the Ardeiformes (as above) and the Pelecaniformes (as above), creating a revised Pelecaniformes (Ardeidae, Threskiornithidae, Pelecanidae; Balaenicipitidae and Scopidae from outside our area).

The genetic data provide the strongest support for the third option (three orders). In Hackett et al. (2008), the bootstrap value for a completely lumped Ciconiiformes (option 1) is 81%; this node is not present in the tree of Ericson et al. (2006), which means it received less than 0.95 posterior probability. The bootstrap value for a monophyletic Ardeiformes consisting of the Ardeidae and the Threskiornithidae (as in option 2) was 72% and the posterior probability for this node was again less than 0.95 (i.e., it was not present in the tree). In contrast, the three order-defining nodes in option 3 all receive 88-100% bootstrap support and more than 0.95 posterior probability. If we are reorganizing these orders based on genetic data, we would suggest option three as the best choice.

Recommendation:

We recommend altering the makeup of the Pelecaniformes and Ciconiiformes and creating the new order Suliformes, as specified in option 3 above. The order of taxa in the AOU area would be as follows, based on the phylogeny of Hackett *et al.* (2008).

Ciconiiformes Ciconiidae (Storks) Suliformes Fregatidae (Frigatebirds) Sulidae (Gannets and Boobies) Phalacrocoracidae (Cormorants and Shags) Anhingidae (Darters) Pelecaniformes Pelecanidae (Pelicans) Ardeidae (Herons and Egrets) Threskiornithidae (Ibises and Spoonbills)

Literature cited:

Cracraft, J. 1981. Toward a phylogenetic classification of the recent birds of the world (class Aves). *The Auk.* **98**(4) 681-714

Ericson, P.G.P., Anderson, C.L., Britton, T., Elzanowski, A., Johansson, U.S., Källersjö, M., Ohlson, J.I., Parsons, T.J., Zuccon, D., and Mayr, G. 2006. Diversification of neoaves: integration of molecular sequence data and fossils. *Biol. Lett.* **2** 543-547

Hackett, S.J, Kimball, R.T., Reddy, S., Bowie, R.C.K., Braun, E.L., Braun, M.J., Chojnowski, J.L., Cox, W.A., Han, K., Harshman, J., Huddleston, C.J., Marks, B.D., Miglia, K.J., Moore, W.S., Sheldon, F.H., Steadman, D.W., Witt, C.C., and Yuri, T. 2008. A phylogenomic study of birds reveals their evolutionary history. *Science*. **320** 1760

Hedges, S.B. and Sibley, C.G. 1994. Molecules vs. morphology in avian evolution: The case of the "pelecaniform" birds. *Proc. Natl. Acad. Sci. USA*. **91** 9861-9865

Kennedy, M. and Spencer, H.G. 2004. Phylogenies of the frigatebirds (Fregatidae) and tropicbirds (Phaethontidae), two divergent groups of the traditional order Pelecaniformes, inferred from mitochondrial DNA sequences. *Molecular Phylogenetics and Evolution.* **31** 31-38

Livezey, B.C. and Zusi, R.L. 2001. Higher-order phylogenetics of modern Aves based on comparative anatomy. *Netherlands Journal of Zoology*. **51**(2) 179-205

Sibley, C.G. and Ahlquist, J.E. 1990. Phylogeny and classification of birds. Yale. Univ. Press, New Haven, Connecticut

Sibley, C.G. and Monroe, B.L. 1990.

Van Tuinen, M., Butvill, D.B., Kirsch, J.A.W., Hedges S.B. 2001. Convergence and divergence in the evolution of aquatic birds. *Proc. R. Soc. Lond.* B. **268** 1345-1350

Name and affiliation of submitter: Shawn Billerman, Irby Lovette, Terry Chesser, NACC

Remove the Accipitridae from the Falconiformes, and create a new order, Accipitriformes

Description of the problem:

The Falconiformes have traditionally been considered to consist of the Cathartidae (New World vultures), Accipitridae (osprey, hawks, kites, and eagles), and Falconidae (falcons and caracaras) (e.g., Cracraft 1981, Sibley and Ahlquist 1990, Livezey and Zusi 2001). Although placement of the Cathartidae has been the subject of some controversy (e.g., Sibley and Ahlquist 1990, Hedges and Sibley 1994), a close relationship between the Falconidae and the Accipitridae has been generally accepted. A dissenting opinion came from Jollie (1977), who suggested, based on morphological characters, that the falcons were in fact not related to other diurnal raptors, but were more closely related to the parrots (Psittaciformes) and cuckoos (Cuculiformes).

New information:

Ericson *et al.* (2006), using molecular sequence data, also found that the Falconidae were not closely related to the Accipitridae. These families were separated by many nodes of high posterior probability. The relationships of the Cathartidae were essentially unresolved, although they grouped in the same large clade as the Accipitridae, not closely related to the Falconidae (and even less so to the Ciconiidae). The sister taxon to the Accipitridae could not be identified due to lack of resolution in the tree, but the Falconidae formed a well-supported clade with the parrots (Psittaciformes), seriemas (Cariamidae), and passerines (Passeriformes). Similar results were found by Griffiths *et al.* (2007) in her phylogeny of the Accipitridae. Their results indicated that the Falconidae were not related to the other diurnal raptors, but instead grouped with the parrot outgroup.

In Hackett *et al.* (2008), the Falconidae were placed well outside the traditional clade of diurnal raptors, forming a clade instead with the Psittaciformes, Cariamidae, and Passeriformes, although support for this clade was not strong (64% ML bootstrap). Within this clade, the Psittaciformes and Passeriformes were sister taxa (77%) and the Falconidae were sister to these (73%). The Accipitridae and Cathartidae were weakly supported sister taxa (61%) and were basal in the clade that was sister to the

Falconidae+Psittaciformes+Cariamidae+Passeriformes clade. The large clade including the Falconidae+Psittaciformes+Cariamidae+Passeriformes clade plus its sister clade (Accipitridae+Cathartidae+most "higher non-passerine landbirds") was reasonably well supported as sister to the Charadriiformes (81% bootstrap). The Falconidae, Accipitridae, and Cathartidae were all recovered as monophyletic with 100% support. These genetic studies are consistent in supporting the removal of the Accipitridae and Cathartidae from the Falconiformes, and congruent in placing the Falconidae closer to the Psittaciformes, Cariamidae, and Passeriformes than to the other diurnal raptors.

Recommendation:

We recommend that the Accipitridae and Cathartidae be grouped in a new order, the Accipitriformes. The new Accipitriformes would be listed prior to the Falconiformes and ordered as follows:

Cathartidae (New World Vultures) Accipitridae (Osprey, Hawks, Kites, Eagles, and Old World Vultures)

pending further developments concerning the placement and status of the Cathartidae.

Literature cited:

Cracraft, J. 1981. Toward a phylogenetic classification of the recent birds of the world (class Aves). *The Auk*. **98**(4) 681-714

Ericson, P.G.P., Anderson, C.L., Britton, T., Elzanowski, A., Johansson, U.S., Källersjö, M., Ohlson, J.I., Parsons, T.J., Zuccon, D., and Mayr, G. 2006. Diversification of neoaves: integration of molecular sequence data and fossils. *Biol. Lett.* **2** 543-547

Griffiths, C.S., Barrowclough, G.F., Groth, J.G., and Mertz, L.A. 2007. Phylogeny, diversity, and classification of the Accipitridae based on DNA sequences of the RAG-1 exon. *J. Avian Biol.* **38** 587-602

Hackett, S.J, Kimball, R.T., Reddy, S., Bowie, R.C.K., Braun, E.L., Braun, M.J., Chojnowski, J.L., Cox, W.A., Han, K., Harshman, J., Huddleston, C.J., Marks, B.D., Miglia, K.J., Moore, W.S., Sheldon, F.H., Steadman, D.W., Witt, C.C., and Yuri, T. 2008. A phylogenomic study of birds reveals their evolutionary history. *Science*. **320** 1760

Hedges, S.B. and Sibley, C.G. 1994. Molecules vs. morphology in avian evolution: The case of the "pelecaniform" birds. *Proc. Natl. Acad. Sci. USA*. **91** 9861-9865

Helbig, A.J., Kocum, A., Seibold, I., and Braun, M.J. 2005. A multi-gene phylogeny of aquiline eagles (Aves: Accipitriformes) reveals extensive paraphyly at the genus level. *Molecular Phylogenetics and Evolution*. **35** 147-164

Jollie, M. 1977. A contribution to the morphology and phylogeny of the Falconiformes. *Evolutionary Theory*. **1** 285-298; **2** 1-93; **3** 1-91; **4** 1-142

Livezey, B.C. and Zusi, R.L. 2001. Higher-order phylogenetics of modern Aves

based on comparative anatomy. Netherlands Journal of Zoology. 51(2) 179-205

Sibley, C.G. and Ahlquist, J.E. 1990. Phylogeny and classification of birds. Yale. Univ. Press, New Haven, Connecticut

Name and affiliation of submitter: Shawn Billerman, Irby Lovette, Terry Chesser, NACC

2009-C-04

Elevate the Osprey to family status, Pandionidae

Description of the problem:

The family-level classification of the Osprey (*Pandion haliaetus*) has varied across years and authorities. Currently, the Osprey is placed in its own family, Pandionidae, in several recent taxonomies (Clements *et al.* 2007, Gill *et al.* 2009, SACC 2009), whereas it is included in the larger Accipitridae in others (Dickinson 2003), including the most recent edition of the Check-list (AOU 1998). Through the 5th edition of the Check-list, the Osprey had been placed in its own monotypic family (AOU 1957, 1983).

New information:

Studies using mitochondrial and nuclear DNA sequence data consistently recover the Osprey as sister to the Accipitridae (provided the Sagittariidae is recognized as a separate family), with high support for the node that separates the Osprey from the rest of the Accipitridae (Helbig *et al.* 2005, Lerner and Mindell 2005, Ericson et al. 2006, Griffiths et al. 2007, Hackett et al. 2008). Two recent phylogenetic studies focused on the Accipitridae (Lerner and Mindell 2005, Griffiths et al. 2007) recommended placing the Osprey in its own monotypic family, and the genetic distances that separate the Osprey from the Accipitridae are similar to the distances between various other traditional families that are sister-clades (Hackett *et al.* 2008).

The recognition of Pandionidae is not mandated by any need to create monophyletic family-level taxa, but, given its position as the sister taxon to the other members of the Accipitridae and its numerous morphological adaptations, the Osprey is arguably distinct enough to warrant family status. The Osprey's unique morphological adaptations include spines, known as spicules, on its footpad for grasping fish, a reversible hallux (found in no other raptor), and nasal valves that close and prevent water from entering when the bird dives for fish (del Hoyo *et al.* 1994). In addition, the Osprey has dense, oily plumage that enhances water resistance when it dives (Poole *et al.* 2002).

Recommendation:

We recommend that the AOU revive the monotypic family Pandionidae, based on the available genetic evidence and morphological data. This return to the previous AOU classification is motivated largely by new phylogenetic evidence showing that the Osprey is sister to, and distinct from, the remaining Accipitridae.

If this proposal is passed, Pandionidae should be placed after the Cathartidae, but before the Accipitridae in the sequence of birds on the Check-list.

Literature cited:

American Ornithologists' Union. 1957. Check-list of North American birds. 5th edition. – American Ornithologists' Union, Washington, D.C.

American Ornithologists' Union. 1983. Check-list of North American birds. 6th edition. – American Ornithologists' Union, Washington, D.C.

American Ornithologists' Union. 1998. Check-list of North American birds. 7th edition. – American Ornithologists' Union, Washington, D.C.

Clements, J.F. 2007. *The Clements Checklist of Birds of the World*. Cornell University Press, Ithaca, NY.

Del Hoyo, J., Elliott, A. and Sargatal, J. eds. 1994. *Handbook of the Birds of the World*. **Vol. 2**. Lynx Edicions, Barcelona

Dickinson, E.C. ed. 2003. *The Howard and Moore Complete Checklist of the Birds of the World*. 3rd Edition. Christopher Helm, London

Ericson, P.G.P., Anderson, C.L., Britton, T., Elzanowski, A., Johansson, U.S., Källersjö, M., Ohlson, J.I., Parsons, T.J., Zuccon, D., and Mayr, G. 2006. Diversification of neoaves: integration of molecular sequence data and fossils. *Biol. Lett.* **2** 543-547

Gill, F., M. Wright, and D. Donsker, D. 2009. IOC World Bird Names (version 2.0)

Griffiths, C.S., Barrowclough, G.F., Groth, J.G., and Mertz, L.A. 2007. Phylogeny, diversity, and classification of the Accipitridae based on DNA sequences of the RAG-1 exon. *J. Avian Biol.* **38** 587-602

Hackett, S.J, Kimball, R.T., Reddy, S., Bowie, R.C.K., Braun, E.L., Braun, M.J., Chojnowski, J.L., Cox, W.A., Han, K., Harshman, J., Huddleston, C.J., Marks, B.D., Miglia, K.J., Moore, W.S., Sheldon, F.H., Steadman, D.W., Witt, C.C., and Yuri, T. 2008. A phylogenomic study of birds reveals their evolutionary history. *Science*. **320** 1760

Helbig, A.J., Kocum, A., Seibold, I., and Braun, M.J. 2005. A multi-gene phylogeny of aquiline eagles (Aves: Accipitriformes) reveals extensive paraphyly at the genus level. *Molecular Phylogenetics and Evolution*. **35** 147-164

Lerner, H.R.L. and Mindell, D.P. 2005. Phylogeny of eagles, Old World vultures, and other Accipitridae based on nuclear and mitochondrial DNA. *Molecular Phylogenetics and Evolution*. **37** 327-346

Poole, A.F., Bierregaard, R.O. and Martell, M.S. 2002. Osprey (*Pandion haliaetus*), The Birds of North America Online (A. Poole, Ed.). Ithaca: Cornell Lab of Ornithology

Name & affiliation of submitter: Shawn Billerman, Irby Lovette, Terry Chesser

2009-C-05 N&MA Check-list Committee p. 139

Create a new order, Eurypygiformes, for the Sunbittern (and Kagu)

Description of the problem:

The Gruiformes as traditionally recognized are an extremely diverse group, and there have been numerous suggestions that they are not monophyletic. For example, Cracraft (1981) recognized three particularly problematic families whose placement in the Gruiformes was tenuous; two of these taxa (the mesites, Mesitornithidae, and the bustards, Otididae) are still placed in the Gruiformes, whereas the third (the buttonquail, Turnicidae) is now generally recognized as belonging to the Charadriiformes. Additional taxa that are dubiously placed within the Gruiformes include the seriemas (Cariamidae), the Kagu (Rhynochetidae), and the Sunbittern (Eurypygidae).

Using cladistic analyses of morphological characters, Livezey and Zusi (2001, 2007) did not recover a monophyletic Gruiformes, but instead found Gruiform taxa spread across their phylogeny, with the Sunbittern, Kagu, bustards, mesites, rails (Rallidae), and sungrebes (Heliornithidae) all falling far outside a "core" Gruiformes consisting of the trumpeters (Psophiidae), cranes (Gruidae), Limpkin (Aramidae), and Hoatzin (Opisthocomidae). They found the Sunbittern and Kagu to be sister taxa, and used the name Eurypygae for a sub-order consisting of these taxa. In contrast, Sibley and Ahlquist (1990) recovered a monophyletic Gruiformes in their DNA-DNA hybridization-based study.

New information:

Recent phylogenetic studies based on mitochondrial and nuclear DNA sequences have provided new information on the relationships of these taxa (Fain and Houde 2004, Ericson *et al.* 2006, Hackett *et al.* 2008). There is increasingly strong evidence that the traditional Gruiformes is not a monophyletic group. Instead, only five of the nine families traditionally placed in the order (excluding buttonquail) appear to constitute a monophyletic core Gruiformes (cranes, Limpkin, trumpeters, rails, and sungrebes) (Fain and Houde 2004, Ericson *et al.* 2007, Hackett *et al.* 2008).

In both Ericson *et al.* (2006) and Hackett *et al.* (2008), the Sunbittern is sister, with strong support (>0.95 posterior probability, 100% bootstrap), to the Kagu (Rhynochetidiae). Together these sister taxa appear to represent a relatively ancient lineage that is not closely allied to any other group of extant birds (Fain and Houde 2004, Ericson *et al.* 2006, Hackett *et al.* 2008).

Recommendation:

We propose that the Check-list recognize the order Eurypygiformes for the Sunbittern (the Kagu, which occurs outside our area, would also be in this order). This name is new, and has been adopted by IOC check-list (Gill *et al.* 2009). We

recommend that the new order be placed immediately before the Gruiformes in the linear classification.

Literature cited:

Cracraft, J. 1981. Toward a phylogenetic classification of the recent birds of the world (class Aves). *The Auk*. **98**(4) 681-714

Ericson, P.G.P., Anderson, C.L., Britton, T., Elzanowski, A., Johansson, U.S., Källersjö, M., Ohlson, J.I., Parsons, T.J., Zuccon, D., and Mayr, G. 2006. Diversification of neoaves: integration of molecular sequence data and fossils. *Biol. Lett.* **2** 543-547

Fain, M.G. and Houde, P. 2004. Parallel radiations in the primary clades of birds. *Evolution*. **58**(11) 2558-2573

Fain, M.G., Krajewski, C., and Houde, P. 2007. Phylogeny of "core Gruiformes" (Aves: Grues) and resolution of the Limpkin-Sungrebe problem. *Molecular Phylogenetics and Evolution*. **43** 515-529

Gill, F., M. Wright, and D. Donsker, D. 2009. IOC World Bird Names (version 2.0)

Hackett, S.J, Kimball, R.T., Reddy, S., Bowie, R.C.K., Braun, E.L., Braun, M.J., Chojnowski, J.L., Cox, W.A., Han, K., Harshman, J., Huddleston, C.J., Marks, B.D., Miglia, K.J., Moore, W.S., Sheldon, F.H., Steadman, D.W., Witt, C.C., and Yuri, T. 2008. A phylogenomic study of birds reveals their evolutionary history. *Science*. **320** 1760

Livezey, B.C. and Zusi, R.L. 2001. Higher-order phylogenetics of modern Aves based on comparative anatomy. *Netherlands Journal of Zoology*. **51**(2) 179-205

Livezey, B.C. and Zusi, R.L. 2007. Higher-order phylogeny of modern birds (Theropoda: Aves: Neornithes) based on comparative anatomy. II. Analysis and discussion. *Zoological Journal of the Linnean Society*. **149** 1-95

Sibley, C.G. and Ahlquist, J.E. 1990. Phylogeny and classification of birds. Yale. Univ. Press, New Haven, Connecticut

Name and affiliation of submitter: Shawn Billerman, Irby Lovette, Terry Chesser, NACC

Alter the traditional orders Apodiformes and Caprimulgiformes to reflect new data on their relationships

Description of the problem:

The Caprimulgiformes traditionally comprises five families (Steatornithidae, Podargidae, Nyctibiidae, Caprimulgidae, and Aegothelidae), while the Apodiformes traditionally contains three (Apodidae, Hemiprocnidae, and Trochilidae). All but the Podargidae, Aegothelidae, and Hemiprocnidae occur in the AOU area.

There have long been competing hypotheses about the relationships of the Caprimulgiformes, with its sister group variously proposed to be the Strigiformes (Owls) or the Apodiformes (Swifts and Hummingbirds). Cracraft (1981) argued for a sister relationship between the Caprimulgiformes and the Apodiformes based on numerous shared morphological characters. However, some authors have suggested, based on morphology, that the Caprimulgiformes itself is paraphyletic (Livezey and Zusi 2001, 2007).

The affinities of the Apodiformes have not been investigated as thoroughly as those of the Caprimulgiformes. However, there is strong support for the sister relationship between the swifts (Apodidae and Hemiprocnidae) and the hummingbirds (Trochilidae) based on both morphological and molecular characters (Cracraft 1981, Sibley and Ahlquist 1990, Ericson *et al.* 2006, Hackett *et al.* 2008).

New information:

Recent molecular phylogenetic studies (Barrowclough et al. 2006, Ericson et al. 2006, Hackett et al. 2008, Braun and Huddleston 2009) provide strong support for the inclusion of the owlet-nightjars (Aegothelidae) in the Apodiformes, rather than in the Caprimulgiformes. This finding renders the traditional Caprimulgiformes paraphyletic. Hackett et al. (2008) found strong support for a clade consisting of the Caprimulgiformes plus the Apodiformes (98 % bootstrap); within this clade the Caprimulgidae was sister to the Apodiformes+Aegothelidae, the Podargidae was sister to this grouping, and a clade consisting of the potoos (Nyctibiidae) and Oilbird (Steatornithidae) was sister to this still larger clade. Ericson et al. (2006) also recovered a well supported clade of Caprimulgiformes+Apodiformes; however, the internal topology of the clade differed from that of Hackett et al. (2008). Nevertheless, in both studies the Apodiformes+Aegothelidae were found to occupy a derived position relative to the Caprimulgiformes. Barrowclough et al. (2006) and Braun and Huddleston (2009) did not recover monophyletic clades, likely due to relatively poor taxon and outgroup sampling and smaller numbers of loci (max of two). Both studies recovered trees with extensive polytomies.

Given that the traditional Caprimulgiformes is paraphyletic, there are two main modifications to be considered. One would lump the Apodiformes with the Caprimulgiformes. The other would split the Caprimulgiformes into multiple orders. If the Aegothelidae are merged into the Apodiformes, the Caprimulgiformes would need to be split into the Caprimulgiformes, Podargiformes, and either the Nyctibiiformes and Steatornithiformes or a combined order including both of these to maintain monophyletic groupings (following Hackett et al. 2008).

The support for a combined Apodiformes+Caprimulgiformes is strong (100% bootstrap, >0.95 post. prob.), but this creates an extremely heterogeneous order. Support for a combined Apodiformes+Aegothelidae is likewise strong (98% bootstrap, >0.95 post. prob.), but support for a Nyctibiiformes containing both the Nyctibiidae and Steatornithidae is poor (<70% bootstrap, <0.95 post. prob.). Indeed, support for relationships among any current families of Caprimulgiformes (except Aegothelidae) is poor. Neither solution is particularly good: one lumps extremely heterogeneous taxa into a single order, whereas the other creates 3-4 small (as small as one species) orders from the currently recognized order Caprimulgiformes.

Recommendation:

We recommend that both options above be rejected and, given the uncertainty about relationships among most families of the traditional Caprimulgiformes, that the Aegothelidae simply be moved from the Caprimulgiformes to the Apodiformes. No members of the Aegothelidae occur in our area, so this would have no effect on the Check-list.

Literature cited:

Barrowclough, G.F., Groth, J.G. and Mertz, L.A. 2006. The RAG-1 exon in the avian order Caprimulgiformes: Phylogeny, heterozygosity, and base composition. *Molecular Phylogenetics and Evolution*. **41** 238-248

Braun, M.J. and Huddleston, C.J. 2009. A molecular phylogenetic survey of caprimulgiform nightbirds illustrates the utility of non-coding sequences. *Molecular Phylogenetics and Evolution.* **53** 948-960

Cracraft, J. 1981. Toward a phylogenetic classification of the recent birds of the world (class Aves). *The Auk.* **98**(4) 681-714

Ericson, P.G.P., Anderson, C.L., Britton, T., Elzanowski, A., Johansson, U.S., Källersjö, M., Ohlson, J.I., Parsons, T.J., Zuccon, D., and Mayr, G. 2006. Diversification of neoaves: integration of molecular sequence data and fossils. *Biol. Lett.* **2** 543-547

Hackett, S.J, Kimball, R.T., Reddy, S., Bowie, R.C.K., Braun, E.L., Braun, M.J., Chojnowski, J.L., Cox, W.A., Han, K., Harshman, J., Huddleston, C.J., Marks, B.D., Miglia, K.J., Moore, W.S., Sheldon, F.H., Steadman, D.W., Witt, C.C., and Yuri, T. 2008. A phylogenomic study of birds reveals their evolutionary history. *Science*. **320** 1760

Livezey, B.C. and Zusi, R.L. 2001. Higher-order phylogenetics of modern Aves based on comparative anatomy. *Netherlands Journal of Zoology*. **51**(2) 179-205

Livezey, B.C. and Zusi, R.L. 2007. Higher-order phylogeny of modern birds (Theropoda: Aves: Neornithes) based on comparative anatomy. II. Analysis and discussion. *Zoological Journal of the Linnean Society*. **149** 1-95

Sibley, C.G. and Ahlquist, J.E. 1990. Phylogeny and classification of birds. Yale. Univ. Press, New Haven, Connecticut

Name and affiliation of submitter: Shawn Billerman, Irby Lovette, Terry Chesser, NACC

Elevate the New World barbets and *Semnornis* barbets to their own families (Capitonidae and Semnornithidae)

Description of the problem:

The classification of the barbets and toucans has a complicated history. One traditional approach placed all barbets in the family Capitonidae, while placing the toucans in the Ramphastidae (del Hoyo *et al.* 2002). Another approach lumped all barbets and toucans into a single family, an expanded Ramphastidae (Prum 1988, Sibley and Ahlquist 1990, Dickinson 2003). A third approach recognized three families: the African barbets (Lybiidae), Asian barbets (Megalaimidae), and the New World barbets + toucans (Ramphastidae) (Gill *et al.* 2009). The current AOU treatment places all New World barbets and toucans into the Ramphastidae (AOU 2009).

New information:

Two recent molecular studies clarify barbet and toucan relationships. The phylogenies of Barker and Lanyon (2000) and Moyle (2004), while differing as to the relationships of the Old World barbets, recover the same relationships between the New World barbets and the toucans. Barker and Lanyon used sequence data from cytochrome-*b*, whereas Moyle sequenced cyt-*b* and a nuclear locus, β -fibrinogen intron 7. In these reconstructions, the New World barbets are paraphyletic, with the *Semnornis* barbets sister to the clade that contains the rest of the New World barbets plus the toucans. Hence, the toucans are sister to the clade containing the *Eubucco* and *Capito* barbets.

Given these relationships, we could continue to place the New World barbets and the toucans into the same family, a large Ramphastidae (e.g, Gill *et al.* 2009). An alternative would divide these taxa among three families, the Semnornithidae (for *Semnornis*), Capitonidae (for *Eubucco* and *Capito*), and Ramphastidae (toucans) (Clements 2007). The latter option is reflected in the SACC list (Remsen *et al.* 2009).

Recommendation:

Given the morphological distinctiveness of the toucans and barbets, we propose splitting the Ramphastidae into the Semnornithidae, Capitonidae, and Ramphastidae *sensu stricto*, and thereby bringing the North and Middle American classification into agreement with the South American list. The toucans possess several unique morphological features not found in any barbet, including a serrated bill and the fusion of three tail vertebrae, which allows them to snap their tail forward while sleeping (del Hoyo *et al.* 2002). In addition, toucans differ from most barbets in their lack of sexual dimorphism, aerial displays, and cavity excavation behavior (del Hoyo *et al.* 2002).

The AOU list would be modified as follows:

Semnornithidae (*Semnornis*) Capitonidae (*Eubucco* and *Capito*) Ramphastidae (toucans and aracaris)

Literature cited:

Barker, F.K. and Lanyon, S.M. 2000. The impact of parsimony weighting schemes on inferred relationships among toucans and Neotropical barbets (Aves: Piciformes). *Molecular Phylogenetics and Evolution*. 15(2) 215-234

Clements, J.F. 2007. *The Clements Checklist of Birds of the World*. Cornell University Press, Ithaca, NY.

Del Hoyo, J., Elliott, A. and Sargatal, J. eds. 2002. *Handbook of the Birds of the World*. Vol. 7. Lynx Edicions, Barcelona

Dickinson, E.C. ed. 2003. *The Howard and Moore Complete Checklist of the Birds of the World*. 3rd Edition. Christopher Helm, London

Gill, F., M. Wright, and D. Donsker, D. 2009. IOC World Bird Names (version 2.0)

Moyle, R.G. 2004. Phylogenetics of barbets (Aves: Piciformes) based on nuclear and mitochondrial DNA sequence data. *Molecular Phylogenetics and Evolution*. 30 187-200

Prum, R.O. 1988. Phylogenetic interrelationships of barbets (Aves: Capitonidae) and toucans (Aves: Ramphastidae) based on morphology with comparisons to DNA-DNA hybridization. *Zool. J. Linn. Soc.* 92(4) 313-343

Remsen, J. V., Jr., C. D. Cadena, A. Jaramillo, M. Nores, J. F. Pacheco, M. B. Robbins, T. S. Schulenberg, F. G. Stiles, D. F. Stotz, and K. J. Zimmer. Version 8 (2009). A classification of the bird species of South America. American Ornithologists' Union. <u>http://www.museum.lsu.edu/~Remsen/SACCBaseline.html</u>

Sibley, C.G. and Ahlquist, J.E. 1990. Phylogeny and classification of birds. Yale. Univ. Press, New Haven, Connecticut

Name and affiliation of submitter: Shawn Billerman, Irby Lovette, Terry Chesser, NACC

Recognize six families arising from the breakup of the Sylviidae

Description of the problem:

The Sylviidae (Old World warblers) has traditionally been a taxonomic dumping ground for many "warbler-like" birds of the Old World. The traditional sylviids are quite similar, all being relatively small, insectivorous birds with straight thin bills, but it is now thought that many of these similarities are convergent (del Hoyo *et al.* 2006). The traditional Sylviidae, which comprises some 270+ species, has been divided into four subfamilies: 1) Megalurinae, consisting of 20 or so species of 'grassbirds,' 2) Acrocephalinae, consisting of roughly 130 species of the reed warblers and their allies (includes *Cettia* and *Bradypterus*, as well as *Hyliota*), 3) Phylloscopinae, composed of the leaf-warblers and their allies, and 4) Sylviinae, composed only of the genus *Sylvia* (del Hoyo *et al.* 2006).

Sibley and Ahlquist (1990) took a different approach to the division of the Sylviidae, recognizing 4 somewhat different subfamilies: the Acrocephalinae, the Megalurinae, the Sylviinae (which included all the babblers except laughing-thrushes) and the Garrulacinae (the laughing-thrushes).

Currently, the AOU treats the following species as part of the Sylviidae (AOU 2009):

Japanese Bush-Warbler Cettia diphone Middendorff's Grasshopper Warbler Locustella ochotensis Lanceolated Warbler Locustella lanceolata Millerbird Acrocephalus familiaris Sedge Warbler Acrocephalus schoenobaenus Willow Warbler Phylloscopus trochilus Wood Warbler Phylloscopus sibilatrix Dusky Warbler Phylloscopus fuscatus Pallas's Leaf-Warbler Phylloscopus proregulus Yellow-browed Warbler Phylloscopus inornatus Arctic Warbler Phylloscoupus borealis Lesser Whitethroat Sylvia curruca Tawny-faced Gnatwren *Microbates cinereiventris* Long-billed Gnatwren Ramphocaenus melanurus Blue-gray Gnatcatcher Polioptila caerulea Cuban Gnatcatcher Polioptila lembeyei California Gnatcatcher Polioptila californica Black-tailed Gnatcatcher Polioptila melanura Black-capped Gnatcatcher Polioptila nigriceps White-lored Gnatcatcher Polioptila albiloris Tropical Gnatcatcher Polioptila plumbea Slate-throated Gnatcatcher Polioptila schistaceigula

New information:

Recent molecular studies (Cibois 2003, Barker 2004, Barker *et al.* 2004, Alström *et al.* 2006, Johansson *et al.* 2008, Fregin *et al.* 2009, Gelang *et al.* 2009) have provided robust information on this phylogenetically challenging group. The study of Alström *et al.* (2006), based on ~2000 base pairs of nuclear and mitochondrial DNA sequence data, was the first to sample extensively within the traditional Sylviidae and other members of the superfamily Sylvioidea. They found the traditional Sylviidae to be paraphyletic, with many groups of "sylviids" more closedly related to other families. In this paper, Alström *et al.* called for the recognition of several new families:

Megaluridae: Grasshopper warblers (*Locustella*), bush-warblers (*Bradypterus*), and grassbirds (*Megalurus*). This family is sister to a clade that consists of the Bernieridae (a radiation of Malagasy warbler-like birds) (Johansson *et al.* 2008) and the Black-capped Donacobius (*Donacobius atricapilla*).

Acrocephalidae: Reed warblers (*Acrocephalus*) and similar birds, including the genera *Hippolais*, *Chloropeta*, and *Nesillas* (Fregin *et al.* 2009). This newly erected family is closely related to the Megaluridae, and is sister to the clade that contains the Megaluridae, Bernieridae, and the Donacobiidae (Johansson *et al.* 2008).

Phylloscopidae: Leaf-warblers (*Phylloscopus*) and similar warblers in the genus *Seicercus*. The Phylloscopidae appear to be sister to the bushtits (Aegithalidae), although this sister relationship did not receive high support (posterior probability of 0.84 in Alström *et al.* (2006) and 0.6 in Johansson *et al.* 2008). However, the family itself received very high support.

Cettiidae: Bush-warblers (*Cettia*) and several other genera, including *Tickellia* and *Tesia*. This clade of odd warblers received very high support in both Alström *et al.* (2006) and Johansson *et al.* (2008). This clade appears closely related to the Phylloscopidae, being sister to the clade that consists of the Phylloscopidae and the Aegithalidae.

The BOU has recently adopted these new family names for taxa that occur in their region (Sangster et al. 2010).

The *Sylvia* warblers (Sylviidae *sensu stricto*) were found by Alström *et al.* (2006) to be sister to the babblers (Timaliidae). This relationship was well supported and has also been recovered by other researchers (Cibois 2003, Johansson *et al.* 2008, Gelang *et al.* 2009; see Proposal 2009-C-09).

Other groups currently classified as sylviids were found to be only distantly related to the group. The gnatcatchers (*Polioptilus*), for example, were found to be part of the Muscicapoidea (outside the sylvioid radiation), where they appear to be sister to the Troglodytidae (Barker 2004, Barker *et al.* 2004, Alström *et al.* 2006, Johansson *et al.* 2008).

The Black-capped Donacobius (*Donacobius atricapillus*), as mentioned above, has been shown to be part of the sylvioid radiation, contrary to previous hypotheses (e.g., Kiltie and Fitzpatrick 1984). It is sister to a clade of exclusively Malagasy warbler-like birds, the Bernieridae. It is also closely related to the Megaluridae (Alström *et al.* 2006, Johansson *et al.* 2008, Gelang *et al.* 2009). The Donacobius may represent a relict species, unique not only in its biogeographic history, but also in its morphology and behavior, which differ substantially from those of its nearest relatives in the Megaluridae and Bernieridae.

Recommendation:

We recommend that the Sylviidae of the AOU area be split as follows:

- A. Elevate the gnatcatchers and gnatwrens to family status, as the Polioptilidae: The gnatcatchers and gnatwrens are not closely related to any of the former sylviids, and in fact belong to the Muscicapoidea. Numerous phylogenetic studies have shown that they are sister to the wrens (Troglodytidae) (Barker 2004, Barker *et al.* 2004, Alström *et al.* 2006, Johansson *et al.* 2008); therefore, we recommend that the Polioptilidae be placed before the Troglodytidae in the Check-list sequence.
- **B.** Recognize the family Cettiidae: The Cettiidae would include only a single species on the AOU check-list, the Japanese Bush-Warbler (*Cettia diphone*). Worldwide, this clade includes the bush-warblers (*Cettia*) and several other genera (including *Tickellia* and *Tesia*). This clade of odd warblers received very high support in the phylogenetic studies of both Alström *et al.* (2006) and Johansson *et al.* (2008). This clade is sister to the clade of the Phylloscopidae plus the Aegithalidae (Alström *et al.* 2006, Johansson *et al.* 2008).
- **C.** Recognize the family Megaluridae: This clade includes the *Locustella* warblers, two species of which have appeared as vagrants from Eurasia, mainly to Alaska. These species are part of a clade, found through much of the Old World, that includes the grassbirds (*Megalurus*) and bushwarblers (*Bradypterus*). This group is in turn sister to a clade that include a radiation of warbler-like birds from Madagascar, as well as the Black-capped Donacobius of Panama and South America (Alström *et al.* 2006, Johansson *et al.* 2008).
- **D.** Recognize the family Donacobiidae: There are several options available for the long-enigmatic Donacobius, currently placed *incertae sedis* in the check-list. In several studies, and depending on the taxa sampled, the Donacobius is sister to the Megaluridae, or to the Bernieridae (Malagasy Warblers), which is then in turn sister to the Megaluridae. Given that it is not embedded within either of these groups, and that it is unique biogeographically and biologically, it seems appropriate to assign family

status to the Donacobius, as have most other recent treatments (Aleixo and Pacheco 2006, Clements 2007, Gill *et al.* 2009, Remsen *et al.* 2009).

- E. Recognize the family Acrocephalidae: The AOU check-list includes two birds that are part of this clade, the Millerbird (*Acrocephalus familiaris*) of Hawaii and the Sedge Warbler (*Acrocephalus schoenobaenus*), a vagrant to Alaska. The Acrocephalidae includes the reed warblers (*Acrocephalus*) and several similar genera, including *Hippolais* and *Chloropeta* (Alström *et al.* 2006, Johansson *et al.* 2008, Fregin *et al.* 2009). The Acrocephalidae are sister to the clade that contains the Megaluridae, Bernieridae, and Donacobiidae (Alström *et al.* 2006, Johansson *et al.* 2006, Johansson *et al.* 2009)
- F. Recognize the family Phylloscopidae: The Phylloscopidae are represented in the AOU region by several species in the genus *Phylloscopus*; these species are vagrants from Eurasia, save for the Arctic Warbler (*Phylloscopus borealis*), which breeds widely in Alaska. The Phylloscopidae includes the genera *Phylloscopus* and *Seicercus*, and likely includes other Old World taxa that have not yet been included in molecular phylogenies. The Phylloscopidae represents a well supported clade that has been shown to be sister to the Aegithalidae (long-tailed tits and bushtits) (Alström *et al.* 2006, Johansson *et al.* 2008).

If these proposals are accepted, only a single representative of the Sylviidae (Lesser Whitethroat *Sylvia curruca*) will be listed for the AOU area, pending the vote on Proposal 2009-C-09.

The sequence of names should be rearranged as follows (families that fall within the sequence and have not been changed appear only as the family name). The Polioptilidae should be placed before the Troglodytidae. No changes to the sequence of species within the Polioptilidae are necessary.

Alaudidae (Larks) Pycnonotidae (Bulbuls) Hirundinidae (Swallows) Cettiidae (Bush-Warblers) Japanese Bush-Warbler *Cettia diphone* Aegithalidae (Long-tailed Tits) Phylloscopidae (Leaf-Warblers) Willow Warbler *Phylloscopus trochilus* Wood Warbler *Phylloscopus sibilatrix* Dusky Warbler *Phylloscopus fuscatus* Pallas's Leaf-Warbler *Phylloscopus proregulus* Yellow-browed Warbler *Phylloscopus inornatus* Arctic Warbler *Phylloscopus borealis* Sylviidae (Sylviid Warblers) [however, see Proposal 2009-C-09 below] Lesser Whitethroat *Sylvia curruca* Timaliidae (Babblers and White-eyes) [see Proposal 2009-C-09 below] Acrocephalidae (Reed Warblers) Millerbird Acrocephalus familiaris Sedge Warbler Acrocephalus schoenobaenus Donacobiidae (Donacobius) Black-capped Donacobius Donacobius atricapilla Megaluridae (Grassbirds) Middendorff's Grasshopper-Warbler Locustella ochotensis Lanceolated Warbler Locustella lanceolata

Literature cited:

Aleixo, A. and J. F. Pacheco. 2006. A family name for the monotypic oscine passerine genus *Donacobius. Rev. Bras. Orn.* 14 (2):172-173

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

American Ornithologists' Union. 2009. Check-list of North American birds (http://www.aou.org/checklist/north/full.php).

Barker, F.K., Cibois, A., Schikler, P., Feinstein, J., and Cracraft J. 2004. Phylogeny and diversification of the largest avian radiation. *Proc. Nat. Acad. Sci.* 101(30) 11040-11045

Barker, F.K. 2004. Monophyly and relationships of wrens (Aves: Troglodytidae): a congruence analysis of heterogeneous mitochondrial and nuclear DNA sequence data. *Molecular Phylogenetics and Evolution*. 31 486-504

Cibois, A. 2003. Mitochondrial DNA phylogeny of babblers (Timaliidae). *The Auk*. 120(1) 35-54

Clements, J.F. 2007. *The Clements Checklist of Birds of the World*. Cornell University Press, Ithaca, NY.

Del Hoyo, J., Elliott, A. and Sargatal, J. eds. 2006. *Handbook of the Birds of the World*. Vol. 11. Lynx Edicions, Barcelona

Fregin, S., Haase, M., Olsson, U., and Alström, P. 2009. Phylogeny of the family Acrocephalidae (Aves: Passeriformes) – the traditional taxonomy overthrown. *Molecular Phylogenetics and Evolution*. 52 866-878

Gelang, M., Cibois, A., Pasquet, E., Olsson, U., Alström, P., and Ericson, P.G.P. 2009. Phylogeny of babblers (Aves, Passeriformes): major lineages, family limits, and classification. *Zoologica Scripta* 38 225-236

Gill, F., M. Wright, and D. Donsker, D. 2009. IOC World Bird Names (version 2.0)

Johansson, U.S., Fjeldså, J., and Bowie, R.C.K. 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

Kiltie, R. A. and J. W. Fitzpatrick. 1984. Reproduction and social organization of the Black-capped Donacobius (*Donacobius atricapillus*) in southeastern Peru. *Auk* 101 804-811.

Remsen, J. V., Jr., C. D. Cadena, A. Jaramillo, M. Nores, J. F. Pacheco, M. B. Robbins, T. S. Schulenberg, F. G. Stiles, D. F. Stotz, and K. J. Zimmer. Version 8 (2009). A classification of the bird species of South America. American Ornithologists' Union. <u>http://www.museum.lsu.edu/~Remsen/SACCBaseline.html</u>

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

Sibley, C.G. and Ahlquist, J.E. 1990. Phylogeny and classification of birds. Yale. Univ. Press, New Haven, Connecticut

Name and affiliation of submitter: Shawn Billerman, Irby Lovette, Terry Chesser, NACC

Alter the composition of the Timaliidae by merging *Zosterops* and moving the Wrentit *Chamaea fasciata* to the Sylviidae

Description of the problem:

The babblers (Timaliidae) have traditionally been a "trash-bin" family where taxa of uncertain affinity have been placed (del Hoyo *et al.* 2007). Within the AOU area, the only taxa placed in the Timaliidae are the Wrentit (*Chamaea fasciata*) of western North America and three species introduced to Hawaii (AOU 2009).

New information:

The Timaliidae is part of the sylvioid radiation of oscine passerines. The babblers are sister to the "new" Sylviidae (sylviid babblers and parrotbills – see proposal 2009-C-08) (Cibois 2003, Gelang *et al.* 2009). Owing to the substantial genetic divergence and phenotypic differences between the Sylviidae and Timaliidae, we recommend treating them as separate families (Gelang *et al.* 2009), although other authors have suggested placing them in a single family (Cibois 2003, del Hoyo *et al.* 2006, 2007).

The white-eyes (*Zosterops*), a distinctive group of warbler-like birds generally placed in their own family (Zosteropidae), have now been shown to be nested within the Timaliidae (Cibois 2003, Gelang *et al.* 2009). Based on sequences of mitochondrial DNA, three nuclear introns, and the nuclear exon RAG-1, robust support was found for this result (Cibois 2003, Gelang *et al.* 2009). In Gelang *et al.* (2009), bootstrap values of 100 and posterior probabilities of 100 were obtained both for inclusion of the white-eyes in the Timaliidae and for monophyly of a Zosteropidae+ *Yuhina+Stachyris whiteheadi* clade sister to the other babblers.

Within the Timaliidae, Gelang *et al.* (2009) recognized four subfamilies: the Zosteropinae (including the white-eyes, *Yuhina*, and *Stachyris whiteheadi*), the Timaliinae (including the scimitar-babblers and other "typical" babblers), the Pellorneinae (another group of "typical" babblers, including many African genera), and the Leiothrichinae (including the laughing-thrushes and *Leiothrix*). Thus, they recommended that the white-eyes be merged into the Timaliidae.

To my knowledge, the sinking of the Zosteropidae has not yet been adopted in other classifications. Indeed, a viable alternative has been suggested – transferring *Yuhina* and *Stachyris whiteheadi* to the Zosteropidae and continuing to recognize both Timaliidae and Zosteropidae.

These groups are marginal to our area. Only four representatives of the Zosteropidae (1 species) and Timaliidae (3 species) are found within the Checklist area, in all cases as introductions to Hawaii. A fourth species of timaliid, the Wrentit *Chamaea fasciata,* has now been shown to belong to the Sylviidae rather than to the Timaliidae (Cibois 2003, Gelang *et al.* 2009). Support for this result is strong (95% bootstrap in Cibois, 98% posterior probability in Gelang *et al.*).

Recommendation:

General AOU policy is to follow the lead of others for major changes in the classification of groups distributed largely or exclusively in the Old World. We believe that shifting *Yuhina* and *Stachyris whiteheadi* to the Zosteropidae while retaining Timaliidae and Zosteropidae as families is less disruptive than merging the Zosteropidae into the Timaliidae. Therefore, pending action by committees tasked with the classification and nomenclature of Old World birds, we recommend transferring *Chamaea fasciata* from the Timaliidae to the Sylviidae, changing the English group name of Zosteropidae to "White-eyes and Yuhinas", reversing the current order of the Timaliidae and the Zosteropidae, and placing these two families after the Sylviidae and before the Acrocephalidae in the AOU Check-list (see Proposal 2009-C-08):

Sylviidae (Sylviid Warblers)

Lesser Whitethroat Sylvia curruca Wrentit Chamaea fasciata

Zosteropidae (White-eyes and Yuhinas) Japanese White-eye *Zosterops japonicus*

Timaliidae (Babblers)

Greater Necklaced Laughingthrush *Garrulax pectoralis* Hwamei *Garrulax canorus* Red-billed Leiothrix *Leiothrix lutea*

Literature cited:

American Ornithologists' Union. 2009. Check-list of North American birds (http://www.aou.org/checklist/north/full.php).

Cibois, A. 2003. Mitochondrial DNA phylogeny of babblers (Timaliidae). *The Auk*. 120(1) 35-54

Del Hoyo, J., Elliott, A. and Sargatal, J. eds. 2006. *Handbook of the Birds of the World*. Vol. 11. Lynx Edicions, Barcelona

Del Hoyo, J., Elliott, A. and Sargatal, J. eds. 2007. *Handbook of the Birds of the World*. Vol. 12. Lynx Edicions, Barcelona

Gelang, M., Cibois, A., Pasquet, E., Olsson, U., Alstöm, P., and Ericson, P.G.P. 2009. Phylogeny of babblers (Aves, Passeriformes): major lineages, family limits, and classification. *Zoologica Scripta* 38 225-236

Name and affiliation of submitter: Shawn Billerman, Irby Lovette, Terry Chesser, NACC

Date of proposal: 28 Dec 2009 (modified 11 Apr 2010 by Terry Chesser)

2009-C-10 N&MA Check-list Committee

Remove the longspurs (*Calcarius*) and snow buntings (*Plectrophenax*) from the Emberizidae and elevate them to the new family Calcariidae

Description of the problem:

The longspurs (*Calcarius*) and the *Plectrophenax* buntings (Snow Bunting and McKay's Bunting) are usually placed near the end of the Emberizidae along with the *Emberiza* buntings (Dickinson 2003, Gill and Wright 2006, AOU 2009). The AOU currently treats *Calcarius* and *Plectrophenax* as *incertae sedis* within Emberizidae, where they are separated by the *Emberiza* buntings (AOU 2009).

New information:

Recent investigations of the group using DNA sequence data have shown convincingly that *Calcarius* and *Plectrophenax* are not in fact closely allied to the *Emberiza* buntings, nor to other members of the Emberizidae. The longspurs and *Plectrophenax* buntings have instead been found to form a well supported clade that separated early in the radiation of the New World nine-primaried oscines (Yuri and Mindell 2002, Klicka et al. 2003, Alström et al. 2008). These findings have been replicated using mitochondrial DNA sequence data (Yuri and Mindell 2002, Klicka *et al.* 2003) and nuclear loci (Alström *et al.* 2008). Within this group, Klicka *et al.* (2003) found McCown's Longspur (*Calcarius mccowni*) to be sister to the *Plectrophenax* buntings rather than grouping with the other *Calcarius* longspurs, which formed a clade.

Alström *et al.* (2008) recommended that the *Calcarius+Plectrophenax* clade be named, and they recommended the tribe name Calcariini. This treatment has been followed in some recent classifications, although Gill *et al.* (2009) placed these genera in their own family, Calcariidae.

Recommendation:

We recommend that *Calcarius* and *Plectrophenax* be removed from the Emberizidae and placed together in their own family, the Calcariidae. This new family should be placed in the linear sequence after the Peucedramidae, but before the Parulidae and the remaining New World nine-primaried oscines (Yuri and Mindell 2002, Alström *et al.* 2008). To reflect the possible close relationship between McCown's Longspur and the *Plectrophenax* buntings, the order of the longspurs should be reorganized as listed below.

Proposed revision to the order of Checklist to accommodate Calcariidae:

Fringillidae

Calcariidae

Lapland Longspur (*Calcarius lapponicus*) Chestnut-collared Longspur (*Calcarius ornatus*) Smith's Longspur (*Calcarius pictus*) McCown's Longspur (*Calcarius mccownii*) Snow Bunting (*Plectrophenax nivalis*) McKay's Bunting (*Plectrophenax hyperboreus*)

The rest of New World 9-Primaried Oscines

Literature cited:

Alström, P., Olsson, U., Lei, F., Wang, H., Gao, W., and Sundberg, P. 2008. Phylogeny and classification of the Old World emberizinae (Aves, Passeriformes). *Molecular Phylogenetics and Evolution*. 47 960-973

Dickinson, E.C. ed. 2003. *The Howard and Moore Complete Checklist of the Birds of the World*. 3rd Edition. Christopher Helm, London

Gill, F. and Wright, M. 2006. *Birds of the World: Recommended English Names*. Princeton University Press, New Jersey

Gill, F., M. Wright, and D. Donsker, D. 2009. IOC World Bird Names (version 2.0)

Klicka, J., Zink, R.M., and Winker, K. 2003. Longspurs and snow buntings: phylogeny and biogeography of a high-latitude clade (*Calcarius*). *Molecular Phylogenetics and Evolution*. 26 165-175

Yuri, T. and Mindell D. 2002. Molecular phylogenetic analysis of Fringillidae, "New World nine-primaried oscines (Aves: Passeriformes). *Molecular Phylogenetics and Evolution*. 23 229-243

Name and affiliation of submitter: Shawn Billerman, Irby Lovette, Terry Chesser, NACC

Date of proposal: 28 Dec 2009 (revised 11 Apr 2010 by Terry Chesser)

2009-C-11 N&MA Check-list Committee p. 684

Create a new family, Viduidae, for the indigobirds and whydas

Description of the problem:

The waxbills, indigobirds, and whydas form an Old World group with its core diversity in Africa, Asia, and Australia; one species, *Vidua macroura*, occurs in the AOU area, as an established introduction in Puerto Rico. Although similar in morphology, the waxbills and the indigobirds/whydas differ substantially in some behavioral and ecological traits, especially relative to their breeding biology. The indigobirds and whydas form a clade, and the 20 or so species in this group are nest parasites that use only waxbills as hosts.

The indigobirds and whydas are all placed in the genus *Vidua*, save for the monotypic Cuckoo Weaver in *Anomalospiza* (Dickinson 2003, Clements 2007, Gill *et al.* 2009).

New information:

Phylogenetic analyses of mitochondrial DNA (ND2 and small ribosomal subunit RNA) place *Vidua* and *Anomalospiza* together in a clade that is in turn sister to a clade that includes the remaining Estrildid finches (Sorensen *et al.* 2004). Support for the reciprocal monophyly of these two groups is high, with 100% bootstrap value for each respective clade, in a maximum parsimony tree. Collectively, the clade of *Vidua*+ *Anomalospiza*+all estrildid finches is sister to the weavers (Ploceidae), which are then in turn sister to the accentors (Prunellidae), although these nodes did not receive high support.

Recommendation:

This proposal is not mandated by the need to create monophyletic higher taxa – the Viduinae and Estrildinae are sister taxa. Additionally, the genetic data supporting this proposal are based solely on a single study using mitochondrial DNA. Nevertheless, mtDNA has proven useful at this phylogenetic level. Based on their unique biology and their phylogenetic distinctness, we recommend placing the *Vidua* finches (indigobirds and whydas) in their own family, the Viduidae, which will be sister to the waxbills (Estrildidae), following a classification that has been recently adopted elsewhere (e.g., Dickinson 2003, Clements 2007, Gill *et al.* 2009). (These taxa do not occur in the BOU area.) The ordering of the taxa within these families remains unchanged.

Literature cited:

Clements, J.F. 2007. *The Clements Checklist of Birds of the World*. Cornell University Press, Ithaca, NY.

Dickinson, E.C. ed. 2003. *The Howard and Moore Complete Checklist of the Birds of the World*. 3rd Edition. Christopher Helm, London

Gill, F., M. Wright, and D. Donsker, D. 2009. IOC World Bird Names (version 2.0)

Sorensen, M.D, Balakrishnan, C.N., and Payne, R.B. 2004. Clade-limited colonization in brood parasitic finches (*Vidua* spp.). *Systematic Biology*. 53 140-153

Name and affiliation of submitter: Shawn Billerman, Irby Lovette, Terry Chesser, NACC