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The flamingo–grebe clade: A response to Storer (2006).—In a recent letter, Storer (2006) criticized a study in which I presented morphological characters in support of a flamingo–grebe clade (Mayr 2004). Because many of his claims are incorrect, I would like to address some of his arguments.

A sister-group relationship between flamingos (Phoenicopteriformes) and grebes (Podicipediformes) was first proposed by van Tuinen et al. (2001), who analyzed mitochondrial and nuclear DNA sequences as well as DNA–DNA hybridization data. A clade (Phoenicopteridae and Podicipedidae) was supported by independent and combined analyses of these different kinds of molecular data. Although my study provided the first evidence of shared derived morphological similarities, additional morphological synapomorphies of flamingos and grebes were described by Manegold (2006).

In my 2004 study, I discussed 11 characters as potential apomorphies of a clade including Podicipedidae and Phoenicopteridae. Storer discussed only two of these, the presence of a notarium and the chalky covering of the eggshell. He noted that the presence of a notarium is likely to be convergent because this feature also occurs in several other avian groups. However, there is no way to recognize convergence *a priori*. If there were, there would be no controversies on the phylogeny of birds at all. To show that the notarium of flamingos and grebes evolved convergently, Storer would have had to present more convincing evidence for alternative phylogenetic hypotheses, which he did not.

Storer (2006) admitted that the eggshell character was unique to flamingos and grebes. However, he then (Storer 2006:1184) made the curious comment that an “analysis omitting this structure and the notarium would, *ipso facto*, diminish support for a sister-group relationship between the flamingos and grebes.” I completely concur with this statement, but see little reason why one should leave out potential synapomorphies from phylogenetic analyses. Anyway, in bootstrap analyses, which I also performed in my study, the robustness of the tree is evaluated by randomly omitting characters from the analysis.

I also listed other characters that were not mentioned by Storer, most notably that flamingos and grebes have 11 primaries, which are otherwise found only in storks (and, in fact, are one of the characters used to support a flamingo–stork alliance). Instead,

Storer (2006) discussed in detail the parasitological evidence for a flamingo–grebe clade, which I merely noted as further evidence but deliberately excluded from the phylogenetic analysis (Storer's note that this character was also mentioned by van Tuinen et al. [2001] is incorrect).

Storer further listed some purported technical inaccuracies in my manuscript. However, I do not understand what he intended to express with his comment that “in figure 3 [of Mayr 2004], the tubercle on the cnemial crest of the grebe is not clearly depicted, and the structure connected to the tubercles in the three species should be identified to confirm that it is the same in all groups” (Storer 2006:1184). Storer appears to have misinterpreted the figure that I used to illustrate the length of the cnemial crests in the figured species, and in which I did not indicate any particular tubercle. His notes on the hypotarsus structure (i.e., that I was “unaware that the hypotarsal canal for *M. flexor perforatus digiti* II is present in the primitive genera of grebes” [Storer 2006:1184]) are irrelevant, because this character was not included in my analysis. Storer (2006:1184) noted “other inaccurate representations of skeletal characters,” but in regard to the only example he provided, he was mistaken. In the illustration of the grebe's foot, the longest toe is indeed the fourth (in any case, this figure does not illustrate the relative length of the foretoes but that of the hallux, which is clearly visible).

Storer (2006:1183) dismissed my morphological analysis and noted my “failure to use the mass of basic natural-history information relevant to the subject.” He then noted my “inability to explain how the structure of the feet could change from webbed in flamingos to the far more complex structure of grebes, or vice versa” (Storer 2006:1184). Apart from the fact that his considerations on the evolution of the foot morphology of grebes are speculation, there is no reason to assume that the foot of any of these extant taxa evolved from a morphology that is represented by its extant sister group, and the foot morphologies of extant grebes and flamingos may represent autapomorphic specializations of these taxa.

In addition to van Tuinen et al.'s (2001) study, the sister-group relationship between flamingos and grebes resulted from analyses of various different gene sequences, such as the nuclear ZENK gene (Chubb 2004), RAG-2 exon (Cracraft et al. 2004), and RAG-1 exon and myoglobin intron 2 (Ericson et al. 2006; their figs. ESM-2 and ESM-3, respectively).

Recent comments to the contrary by Livezey and Zusi (2007) notwithstanding, the flamingo–grebe clade is one of the best-supported higher-level clades of birds.

Storer (2006:1183) introduced his note by remarking that information “on phylogeny is obtainable from at least two present sources: the whole-animal biology of the organisms and molecular biology. The most accurate phylogenies will result from those sets of data in which there is the closest agreement.” There is nothing to add to these statements, except that I find it difficult to understand why in this case he did not follow his own advice.—GERALD MAYR, *Forschungsinstitut Senckenberg, Sektion Ornithologie, Senckenberganlage 25, D-60325 Frankfurt a.M., Germany. E-mail: gerald.mayr@senckenberg.de*

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LITERATURE CITED

- CHUBB, A. L. 2004. New nuclear evidence for the oldest divergence among neognath birds: The phylogenetic utility of ZENK (i). *Molecular Phylogenetics and Evolution* 30:140–151.
- CRACRAFT, J., F. K. BARKER, M. J. BRAUN, J. HARSHMAN, G. J. DYKE, J. FEINSTEIN, S. STANLEY, A. CIBOIS, P. SCHIKLER, P. BERESFORD, AND OTHERS. 2004. Phylogenetic relationships among modern birds (Neornithes): Toward an avian tree of life. Pages 468–489 in *Assembling the Tree of Life* (J. Cracraft and M. Donoghue, Eds.). Oxford University Press, New York.
- ERICSON, P. G. P., C. L. ANDERSON, T. BRITTON, A. ELZANOWSKI, U. S. JOHANSSON, M. KÄLLERSJÖ, J. I. OHLSON, T. J. PARSONS, D. ZUCCON, AND G. MAYR. 2006. Diversification of Neoaves: Integration of molecular sequence data and fossils. *Biology Letters* 2:543–547.
- 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.
- MANEGOLD, A. 2006. Two additional synapomorphies of grebes Podicipedidae and flamingos Phoenicopteridae. *Acta Ornithologica* 41:79–82.
- MAYR, G. 2004. Morphological evidence for sister group relationship between flamingos (Aves: Phoenicopteridae) and grebes (Podicipedidae). *Zoological Journal of the Linnean Society* 140: 157–169.
- STORER, R. W. 2006. The grebe–flamingo connection: A rebuttal. *Auk* 123:1183–1184.
- VAN TUINEN, M., D. B. BUTVILL, J. A. W. KIRSCH, AND S. B. HEDGES. 2001. Convergence and divergence in the evolution of aquatic birds. *Proceedings of the Royal Society of London, Series B* 268:1345–1350.

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Moas and phylogenomics: How nomenclatural errors do a disservice to the understanding of moa taxonomy.

—Recently, Baker et al. (2005) published a Bayesian tree based on 658 base-pair control-region mitochondrial DNA sequences from 125 individual moas from widespread localities in New Zealand, a sample that included all then-accepted taxa (Worthy and Holdaway 2002, Bunce et al. 2003). They recognized 14 clades (interpreted as shown in Table 1) but avoided equating these clades with species by using only geographic identifiers. More recently, however, Baker (2007:18), in a paper whose title claims “advances in the study of geographic variation and speciation,” has equated each of the 14 clades with the status of species (Table 1). It is not my intention here to assess the validity of Baker’s conclusions, nor is it to assess their relevance to taxonomy, but rather to point out that he applied incorrect nomenclature to 5 of the 14 clades while overlooking an important paper on moa systematics. The result has only further confused the taxonomy and nomenclature of moas.

People often confuse the three components to “labeling” taxa. First, taxonomy is the science of circumscription of a taxon, for example, at the species, generic, familial, or other levels, by diagnosis. Such taxa are based on a type or type series and delimit a group of individuals and their relationships to other such groups. Second, nomenclature is a technique for the naming of such taxa, and it is governed by rules (e.g., International Code of Zoological Nomenclature). Nomenclatural activity includes formulating new names for taxa and determining the correct name to be applied to existing taxa. The issues discussed below involve the determination of lineages leading to either a suggested split of taxa and the attribution of names to those taxa or synonymy of taxa, and thus are of a nomenclatural nature. Thirdly, the assignment of a specimen to a given taxon, or its identification, employs a name but has no bearing on nomenclature or taxonomy.

Clades 1 and 2.—Baker et al. (2005) labeled these clades as *Pachyornis mappini* from eastern and western North Island, respectively. Baker (2007) modified this by calling clade 1 *P. mappini* and clade 2 *Pachyornis*, n. sp. A, which is erroneous in two regards. First, the type specimen of *P. mappini* is from the western North Island (Archey 1941), so that if only a single clade takes the name *P. mappini*, it would have to be the western population, not the eastern one. Secondly, as