S20-1 Supra-generic cladistics of landfowl (Order Galliformes)

Timothy M. CROWE1,2*, Paulette BLOOMER1,3, Ettore RANDI4, Vittorio LUCCHINI4, Rebecca KIMBALL5, Edward BRAUN6, Jeffrey G. GROTH2
1. Percy FitzPatrick Institute, University of Cape Town, Rondebosch 7701, South Africa; * tmcrowe@botzoo.uct.ac.za
2. Dept. of Ornithology, American Museum of Natural History, Central Park West at 79th Street, New York, NY 10024-5192, USA
3. Dept. of Genetics, University of Pretoria, Pretoria 0001, South Africa
4. Istituto Nazionale per la Fauna Selvatica (INFS), via Cà Fornacetta 9, 40064 Ozzano dell’Emilia (BO), Italy
5. Dept. of Zoology, University of Florida, Gainesville, FL 32611, USA
6. Dept. of Biology, University of New Mexico, Albuquerque, New Mexico 87131, USA

Abstract Molecular and organismal evidence bearing on the evolutionary relationships of gamebirds within the order Galliformes is reviewed. The monophyly of most traditionally recognized supra-generic taxa is supported, but the Phasianini (pheasants) and Perdicini (partridges and quails) are shown to be polyphyletic. Contrary to DNA-DNA hybridization data, New World quails (Odontophoridae) did not branch off the galliform evolutionary tree before the guineafowl (Numididae), but rather immediately after; and the cracids (Cracidae) and megapodes (Megapodiidae) are not sister groups of one another. Evidence is presented to support the notion of very early divergence among species currently confined to the New World, Africa and southeast Asia. Evidence from mtDNA sequences (cytochrome \textit{b} and D-loop), proteins (ovomucoids), life history, behavior, and bones and feathers is analyzed phylogenetically in three ways: separately, combined and combined but differentially weighted. Separate analysis always produces less well-resolved trees than those suggested by combined data; and deweighting putatively less informative evidence undermines rather than enhances phylogenetic signal. Furthermore, analysis of combined data produces a tree with a novel, but biogeographically meaningful, topology, with organismal and molecular information more useful at respective more basal and more terminal branches of the tree.

Key words Galliformes, Phylogeny, Combined vs separate vs deweighted evidence

1 Introduction The phylogeny of the pheasant, quail and turkey order Galliformes is reconstructed for 102 in-group taxa listed in Crowe et al. (1992, Appendix 3) and rooted on two representatives of the Anseriformes, a duck (\textit{Cairina moschata}) and a screamer (\textit{Chauna torquata}). Exemplars represent all putative supra-generic taxa and 55 traditionally recognized genera (after del Hoyo et al., 1994). Character data include a combination of 949 phylogenetical informants, from morphology and behavior (n = 47), ovomucoid amino acids (n = 47), and gene sequences in mitochondrial cytochrome \textit{b} and D-loop (n = 522, 333 respectively). Raw data matrices for these three sources of character variation are available from the senior author or from the web site of the Percy FitzPatrick Institute.

2 Methods Phylogenetic analyses were conducted using WinClada ver. 0.9.99m8.1 BETA (Nixon, 2000). The searching strategy employed was the Ratchet Island Hopper (1 000 iterations; 2 trees to hold; ±10% characters to sample; and amb. poly. = option), with organismal characters as additive and all molecular characters nonadditive. Bootstrap analyses were conducted with 1 000 replicates.

3 Results and discussion Analysis of the combined dataset of characters yielded two equally parsimonious trees (CI = 0.21, 7 296 steps), of which a strict consensus application required the collapsing of five nodes, all within the tetraonine grouse (Fig. 1). Traditionally recognized supra-generic taxa supported by this consensus tree with ≥ 50% bootstrap support are: (1) the Superfamily Phasianioidea, including all galliforms except the megapodes and cracids; (2) the megapodes (Megapodiidae); (3) the cracids (Cracidae); (4) the guineafowls (Numididae); and (4) the New World quails (Odontophoridae). Resolution within the Phasianidae is not well supported. Within the phasianids, the grous (Tetraoninae), the gallo-phasian subset of the pheasants (Phasianinae, including \textit{Syrmaticus}, \textit{Phasianus}, \textit{Chrysolophus}, \textit{Lophura} and \textit{Catreus} and \textit{Crossoptilion}), and the pavoine peafowl (Pavonini, including \textit{Rheinardia}, \textit{Argusianus}, \textit{Afropavo} and \textit{Pavo}) are supported. However, although grouping with the gallo-phasians, the basal pheasant assemblage of Johnsgard (1986), excluding the junglefowls (\textit{Gallus} spp.) and peacock-phasians (\textit{Polyplectron} spp.), does not have “significant” (≥ 50%)
Fig. 1 (page 355 and above)  Phylogenetic relationships of galliform birds
Tree based on maximum parsimony analysis of a combination of 949 phylogenetically informative morphological-behavioral, ovomucoid amino acid, and mitochondrial cytochrome b and D-loop characters. Numbers at nodes are bootstrap values (NS = not supported by bootstrap values of ≥50).

The monophyly of several traditionally recognized groupings is not supported. The megapodes and cracids which comprise the order Craciformes or superfamily Cracoidea are paraphyletic with respect to one another. Partridges (tribe Perdicini) are highly polyphyletic. The grey partridge (Perdix perdix) groups with the wild turkey (Meleagris gallopavo) or with the pheasants when the turkey is excluded. The sister taxon of the Madagascan partridge (Margaroperdix madagarensis) is the common quail (Coturnix coturnix), and that of the sand partridge (Ammoperdix heyi) is the bush quail (Perdicula argoondah). The francolins (Francolinus spp., sensu Hall, 1963) comprise at least two distantly related clades: (1) true francolins, including Dendroperdix, Peliperdix, Francolinus and Scleroptila, and (2) spurfowls, including Pternisits (also Crowe et al., 1992; Bloomer and Crowe, 1998).

Contrary to DNA-DNA hybridization results (Sibley and Ahlquist, 1985, 1990; Sibley, 1994) and those of “culled” DNA sequences of mitochondrial cytochrome b from a small set of exemplar taxa (Kornegay et al., 1993), the New World quails, although basal within the Phasianidea, are not basal relative to the guineafowls. Noteworthy among the other novelties is the placement of the red junglefowl (Gallus gallus) with bamboo partridges (Bambusicola spp.), within a clade dominated by “francolins” and “partridges” and outside of clades including pheasants (cf., Fumihito et al., 1995; Kimball et al., 1999). Other novel groupings include the association of the recently discovered African “partridge” Xenoperdix udzungwesis (Dinesen et al., 1994) with Asiatic “partridges” (Rollulus rouloul and Arborophila spp.), and the crimson-headed wood partridge (Haematortyx sanquineus) with the peacock-pleasants (Polyplectron).

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References


