

Phylogeny of major lineages of galliform birds (Aves: Galliformes) based on complete mitochondrial genomes

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ABSTRACT. Complete mitochondrial DNA sequences have been used successfully to estimate phylogenetic relationships among animal taxa, and for studies of population genetics and molecular evolution. We made phylogenetic analyses of 22 species of Galliformes, with two species of Anseriformes as outgroups, using maximum likelihood (ML), maximum parsimony (MP) and Bayesian inference (BI) methods based on the nucleotide dataset and the corresponding amino acid dataset of 13 concatenated protein-coding genes. The consensus phylogenetic trees supported monophyly of Galliformes, Phasianidae (nucleotide and amino acid: posterior probabilities 1.00 in BI, bootstrap value >99% in ML and MP), Coturnicinae, and Gallininae (nucleotide and amino acid: posterior probabilities 1.00 in BI, bootstrap value >85% in ML and MP), but failed to demonstrate monophyly of Pavoninae and Phasianinae. Our

results also support a sister-group relationship between megapodes and all other galliforms. We found that Arborophilinae is basal to the balance of the Phasianidae. Moreover, we suggest that the turkey should be classified in the Phasianinae of Phasianidae. Although the relationships among the various lineages of the Galliformes remain controversial, these results should be useful for further study.

Key words: Galliformes; Phylogeny; Mitochondrial genome; Maximum likelihood; Maximum parsimony; Bayesian inference