

MOLECULAR AND MORPHOLOGICAL ANALYSES CONFIRM THAT ALL LOONS (AVES: GAVIIFORMES) FORM A SINGLE HOLOBARAMIN

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ABSTRACT

Loons or divers (*Aves: Gaviiformes*), a group of waterbirds found primarily in the Northern Hemisphere, are comprised of several extinct taxa as well as an extant family (*Gaviidae*) with one genus (*Gavia*) and five species. Recent phylogenetic studies suggest that the *Sphenisciformes* (penguins) and *Procellariiformes* (petrels, albatrosses, and shearwaters) form a sister group to the loons. Our previous research, based on hybridization, morphological, and vocalization data, found that all extant loons form a single holobaramin (i.e., created kind). This previous study, however, was inconclusive as to the membership of fossil taxa within the kind. The goal of the present study is to verify the baraminic status of the extant loons using new molecular baraminology techniques and to further evaluate extinct loon morphology to determine whether they also belong to the loon holobaramin. DNA sequences from four mitochondrial genes (*CO1*, *CYTB*, *NADH1*, and *NADH2*) were gathered, for all extant loons and several outgroups, from the BOLD and GenBank databases and aligned with ClustalW in MEGA. Corrected distance matrices were created with the TN93 + Gamma model and analyzed using hierarchical clustering, classic multi-dimensional scaling, and medoid partitioning in R software. A newly published dataset of skeletal characters, from extinct and extant loons as well as several outgroups, was also analyzed using statistical baraminology clustering methods (BARCLAY: DCA, MDS, PAM, FANNY). Extant loons consistently formed significant/separate clusters across all genes and molecular analyses, confirming they share significant continuity with one another and significant discontinuity from the outgroups. Morphological analyses demonstrated that all loons, extant and extinct, were positively associated/correlated with one another, sharing significant continuity, and negatively associated/correlated, displaying significant discontinuity, with several key avian outgroups. Based on considerable evidence of both continuity among loon species and discontinuity from other avian groups (including the supposed sister groups, *Sphenisciformes* and *Procellariiformes*), we conclude that all loons (*Aves: Gaviiformes*), both extant and extinct species, form a single holobaramin. These results are consistent with our previous research and Answers in Genesis's brief analysis of loon hybridization for their Ark Encounter Project.

KEYWORDS

Loons, *gaviiformes*, statistical baraminology, molecular baraminology, holobaramin

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