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PHYLOGENETIC SUPERTREE FOR FALCONIDAE (AVES): SPECIES-LEVEL METAPHYLOGENY WITH MORPHOLOGICAL AND MOLECULAR DATA

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A large and well-supported phylogeny represents an important tool for taxonomic and systematic classifications and to infer hypotheses on a large scale in nature. Usually, due insufficient data resulting from the inequality of research efforts throughout taxa, is not possible the construction of large trees completely comprehensive. Falconidae is one of four families of Falconiformes with 63 species in 11 genera and 2 subfamilies according to the systematic classification most recently accepted. Several types of data has been analyzed to infer the phylogenetic relationships of the family, like osteological, morphological and molecular data. The Supertree Construction approach represents one method to generate more comprehensive phylogenies, through the combination of existing phylogenetic information using data already published or incorporated into databases. Studies have shown that supertrees built with numerous and large enough source trees can represent the information provided by the phylogenetic trees with source precision. In the Matrix Representation using Parsimony (MRP) method the matrix representations of different source trees are combined into a single matrix that can be analyzed using a criterion of parsimony. The aim of this work is collected different source trees inferred for Falconidae, apply the Supertree Construction method by MRP criterion and analyze the phylogenetic and systematic relationships within the family, for this were researched papers that contain potential source trees inferred for Falconidae. Several source trees were collected and their topologies were reproduced in software of dendrogram edition. A digital file in NEXUS format was obtained for each cladogram considered, which were contained the sequences of characters in Newick format. Due to the variance in the methodology of source trees, discrepancies were found in the number of taxa considered among the different trees, but they have no conflict in the overlap analysis all 63 taxa corresponding to the species of the Falconidae were included in all trees reproduced, as well as the taxon Accipitridae, added as outgroup. A total of 23 trees were edited at the end of the review and editing of publications considered. Sequences of characters in Newick format were combined and run in the program CLANN and the criterion for MRP was performed. It was obtained at the end of analysis 544 most-parsimonious trees, the strict-consensus was performed, resulting in one Supertree to Falconidae. The bootstrap analysis was run in PAUP* with 100 replications. The Supertree is in agreement with the most recently systematic classification where they are considered two subfamilies, the Subfamily *Herpetotherinae* and Subfamily *Falconinae*. The pattern of biogeographical distribution of Falconidae taxa around the World are compatible with the topological distribution of taxa on the Phylogenetic SuperTree obtained. The basal branches appear exclusive in the Neotropics (America). This pattern of distribution indicates, parsimoniously, that origin of family Falconidae occurred in the Neotropics, more specifically in South America. The Supertree Construction approach show satisfactorily results to generate a large, holistic and comprehensive phylogeny of Falconidae.