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A Biogeographical Analysis of the Distribution of Bats of the Family Emballonuridae

Brandi Mann

Illinois Wesleyan University

Thomas A. Griffiths, Faculty Advisor

Illinois Wesleyan University

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**A BIOGEOGRAPHICAL ANALYSIS OF THE DISTRIBUTION OF
BATS OF THE FAMILY EMBALLONURIDAE**

Brandi Mann and Thomas A. Griffiths*, Department of Biology, IWU

This project examined the biogeographical distribution of the bat family Emballonuridae (Order Chiroptera). The distributions of five species populating Africa, Southeast Asia, and islands of the western Pacific were mapped and data were pooled with data of five species compiled by Moyer (poster in this conference). Data on the ten species were used in a congruence analysis to test the validity of two rival phylogenies. Such an analysis is done by looking at the general distributional patterns of the species, and then trying to reconstruct a possible biogeographic history to account for such a distribution (Crisp, Linder, and Weston, 1995). If the distribution can be explained scientifically by means such as continental drift or by an increase in sea level which submerged previously exposed land masses, or divided an original land mass into two (resulting in speciation via isolation), then the proposed evolutionary relationship being tested is thought valid. Alternatively, species may have actively dispersed via migration or been passively dispersed through human intervention or natural events (hurricanes etc.). The more incongruencies there are (or the more unusual events required to explain the biogeographic distribution observed) the greater the possibility that the evolutionary hypothesis being tested is invalid. A slightly higher congruence was found for the hypothesized phylogeny of Tate and Archbold, 1939 (0.75) over that of Griffiths et. al., 1991 (0.625), favoring very slightly the former phylogeny over the latter.