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Biogeographic Congruence Analysis of Ten Species of Bats of the Family Emballonuridae (Chiroptera)

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Poster Presentation 28

**BIOGEOGRAPHIC CONGRUENCE ANALYSIS OF TEN SPECIES OF
BATS OF THE FAMILY EMBALLONURIDAE (CHIROPTERA)**

Jennifer Moyer and Thomas A. Griffiths*, Department of Biology, IWU

The biogeographical distribution of five bat species of the Family Emballonuridae, populating Africa, mainland Southeast Asia, Indonesia, the Solomon Islands, Fiji Islands, and smaller western Pacific islands were plotted. Data were combined with distributions of five additional emballonurid species from Mann (poster, this conference). The geographical distributions of the ten species were then used to test the validity of two rival phylogenies (a cladogram generated by Griffiths, Koopman, and Starrett, 1991 and a tree produced by Tate and Archbold, 1939). A congruence analysis was done to test which hypothesized phylogeny was better supported by the distributional data. The calculated congruency of the phylogenetic tree of Tate and Archbold (1939) is 0.75. The congruency of the cladogram of Griffiths et al. (1991) was 0.625. The Tate and Archbold phylogeny has a higher congruency value and we conclude that the Tate and Archbold phylogeny is slightly better supported by the data of this study.