

ISLAND BIOGEOGRAPHY USING MULTIPLE TAXA ON THE SAME SET OF ISLANDS

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Studies on island biogeography are usually based on distributional data for one taxon in an island group. Cross-taxon comparisons are scarce and usually different sets of islands for each taxon are used due to availability of data. Several island biogeography patterns are sensitive to the effects of the values of a few data points, e.g. island size, so the use of the same islands for comparisons among taxa is a much-needed addition to respective analyses. Aegean islands have been under intensive biogeographical study during the past three decades, resulting to the substantial knowledge of a quite variable set of taxa from a large number of islands. From a scrutiny of the respective literature, we were able to collect distributional data from the same 26 islands for 5 groups of organisms (isopods, snails, orthopterans, birds and reptiles, from 22 and 21 islands for 6 groups (adding either butterflies or plants), and from 19 islands for all these 7 groups together. We compared species-area relationships (SAR) among these taxa in order to test certain predictions of island biogeography theory. In particular, we checked for the best SAR model for each taxon, compared slopes and intercepts of the logarithmic power model, checked for correlations of slopes and intercepts with mean species richness, explored effects of habitat diversity, and compared species richness among taxa. Our results provide useful insights to the behavior of SAR and the biological significance of the constant parameters of its most common and widely applicable model.