
Disharmony of the world's island floras

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Abstract

Disharmony is a key concept in island biology that describes the biased representation of higher taxa on islands compared to their mainland source regions. Although differential colonization success of taxa is predicted by selective dispersal, environmental and biotic filtering, the empirical evidence for disharmony remains largely anecdotal. Here, we develop a novel method for delineating island source regions and present the first global quantitative assessment of island disharmony. We analyzed the overall compositional bias of 320 island floras and examined the over- or under-representation on islands for 450 plant families. We found that the compositional bias of island floras is strongly predicted by geographical and climatic island characteristics (isolation, area, geologic origin, temperature, precipitation), whereas the representation of individual families is only weakly related to family-specific characteristics (family size, family age, taxonomic group, functional traits), indicating that

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the taxonomic scope of the disharmony concept has historically limited its wider applicability. Our results provide a strong foundation for integrating disharmony with quantitative functional and phylogenetic approaches in order to gain a deeper understanding of assembly processes on islands.

Keywords: source regions, island syndromes, generalized dissimilarity modelling, assembly processes, ancestral area reconstruction