
Distribution and relative age of endemism across islands worldwide

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Abstract

Islands are recognized by their remarkable rates of endemism so highly contributing to global diversity. One point remaining to be explored is the age of island endemics as it may provide new insights on the processes at the origin of island biota. We studied this issue by investigating the relative age of Monocots in islands worldwide, employing a measure of phylogenetic endemism and a method based on null models. We used the most comprehensive dataset on species occurrences in 4,306 islands, and identified 142 sites with neo-, paleo-, mixed and super-endemism. They were distributed all over the world, but more common at low latitudes. Mixed and super-endemism were the more frequent, putting in evidence the commonness of processes at all time scales at shaping present island biodiversity. Especially, we showed the importance of latitude, habitat availability and climate stability on the persistence of ancient taxa and on recent diversification events. These findings represent a great contribution to guide biodiversity conservation at global scale. These islands are irreplaceable both for the uniqueness and evolutionary history of their flora, so highly contributing to preserve "option values" and evolutionary potential.

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Keywords: Global scale, paleo endemism, neo endemism, mixed super endemism, phylogenetic endemism, evolutionary potential