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🌍 The relationship between naturalized and native plant species: insights from oceanic islands of the south-east Pacific after 200 years of records.

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ABSTRACT

We assembled the most comprehensive dataset of the flora of the OISEP from currently available island flora checklists and updated with recent publications. Each plant species was classified as being native or naturalized. We examined temporal changes by estimating species richness, naturalization rates and naturalized-to-native ratios over time based on the first collection year of each naturalized species. Then, we determined the best shape of naturalized species richness accumulation over time by contrasting the AIC of lineal, exponential, sigmoidal and Weibull regressions. Finally, we analyzed the relationships between native and naturalized species firstly at the inter-archipelagic scale by fitting island species-area relationship models and secondly at the island scale by performing ranged major axis regression analysis on residual values.

Data Assembly

1 Collecting previous flora works of the Desventuradas islands (Skottsberg, 1937; Sparre, 1949; Hoffmann and Marticorena, 1987; Hoffmann and Tellier, 1991; Muñoz-Schick, 1995; Mueller-Dombois and Fosberg, 1998; Cuvertino, 2001; Escobar et al., 2011), Juan Fernandez Archipelago (Danton et al., 2006; Danton and Perrier, 2016; Danton and Perrier, 2017; Stuessy et al., 2018) and for Rapa Nui (Zizka, 1991;, Matthei, 1995; Meyer, 2008; Finot et al., 2015). Species that have subsequently proved to be misidentified and those for whom there remains reasonable doubt over their identification were excluded (Danton and Perrier 2017).

2 Taxa standardization: according to the Global Biodiversity Information Facility (GBIF) taxonomic backbone using TAXADB package (Norman et al. 2020) of the statistical environment R (R Core Team 2020). Synonyms, heterotypic and homotypic synonyms were changed to the accepted names while the Catalog of the Vascular Plants of Chile (Rodriguez et al. 2018) was used as back-up source of information for more problematic taxa.

3 Classification of the assembled flora into native and naturalized species. Throughout this study, the term "naturalized species" refers to plant species deliberately or unintentionally introduced by humans that have gone on to form self-sustaining populations - or are in the process doing so - in an area outside their native range. We excluded cultivated or occasional species from the naturalized species richness (Tye 2006).

4 Determination of native and naturalized species richness for each island and the whole OISEP.

Data Analysis - Native and naturalized species relationship...

5 We obtained the year of the first record or reference of each alien plant that became naturalized on each island. If one naturalized species presented different years of first record throughout islands (because they have different arrival dates) the earlier one was selected as the first record for the entire study area. This allowed us to investigate the naturalized species richness accumulation and the naturalization rate over time at both island and inter-archipelagic scales.

6 We described how naturalized diversity changed over time by applying a regression model using the naturalized species richness from 1810 to 2021 for the entire OISEP. This was done by fitting three functions: linear ($y = a + bx$), exponential ($y = ae^{bx} + t$) and sigmoidal ($y = a\,(\,x^b/(x^b + c^b)\,)$). In addition, we fitted a Weibull function ($y = c+(d-c)\exp\{-\exp[b(\log(x)-\log(e))]\}$) to test for potential stabilization in the observed naturalized richness in recent years. Model fits were compared using Akaike's Information Criterion (AIC), whereby the lowest AIC value was considered to be the best.

7 To determine whether and when naturalized species richness could have surpassed native

species richness, we calculated the naturalized-to-native species ratio over time. This was achieved by examining the naturalized species richness at 20-year intervals over the past 200 years at two scales: the individual island level and the entire OISEP. Following that, we obtained the naturalized-to-native species ratio by dividing naturalized per native species richness by native species richness at both scales. Native species richness was assumed to be constant through time as it had not changed notably during the analyzed period (Castro et al. 2007; Sax and Gaines 2008).

Data Analysis - Current island native and naturalized specie..

8 To investigate native and naturalized species richness, we fitted two species-area relationship models for the 11 studied islands using the SARS package (Matthews et al. 2019). To describe the relationship between species richness and area, we employed the commonly-used Arrhenius power function (Arrhenius 1921) in a log-log transformed space:

$$\log_{10}(S) = c + z\log_{10}(A) \quad (1)$$

where S is species richness, A is island area and c and z are two fitted parameters that correspond to the intercept and the slope, respectively.

9 We tested for significant differences between native and naturalized ISAR intercepts and slopes using multiple linear regression. Here, the response variable was species richness (n = 22; 11 native and 11 naturalized) and the explanatory variables were area, a categorical variable (entitled status) describing if the response variable corresponds to native or naturalized species richness, and the interaction between area and status. Significant differences between intercepts and slopes were verified when the interaction (status*area) and the status variable were, respectively, significant (p-value < 0.05) (Gelman and Stern 2006).

10 To further analyze how species are responding to local island factors such as habitat heterogeneity, productivity, etc. (Stark et al. 2006; Hulme 2008), we extracted the ISAR model residuals, which denote deviations of predicted values from those that were observed. These residuals helped to assess the importance of island area, allowing a comparison of the influence of islands of varying size on species richness (Lonsdale 1999). For this purpose, we extracted naturalized and native ISAR residuals and carried out a regression analysis (naturalized ISAR residuals against native ISAR residuals) using type II regression (ranged major axis) (Sokal and Rohlf 1995; Lengendre and Legendre 2012). In this way, we tested if naturalized species richness is influenced by the same island factors that are promoting native species richness. If this is true, then ISAR residuals of both naturalized and native species will be strongly correlated with a positive slope of close to 1. The type II regression was run using the LMODEL2 package (Legendre 2018).