Whittaker et al. – Functional diversity of an oceanic archipelago, Supporting Information R.J. Whittaker et al – **Functional biogeography of oceanic islands and the scaling of functional diversity in the Azores**

Supporting Information

SI Materials and methods

Study area. The Azores is one of the world's most isolated archipelagos. Located in the North Atlantic (37–40° N, 25–31° W), the archipelago comprises nine islands aligned on a west/northwest to east/south-east axis (Flores and Corvo to the west, Faial, Pico, São Jorge, Terceira and Graciosa in the centre and São Miguel and Santa Maria to the east). The islands range in date of origin from 0.25 Ma for Pico to 8.12 Ma for Santa Maria. Azorean native forest (*laurisilva*) comprises an impoverished association of evergreen shrub and tree species, which almost entirely covered the islands before human settlement (*c.*AD 1440) (1). By 300 yr ago (*c.*AD 1700) anthropogenic clearance had restricted the native forest in most islands to areas above 300 m a.s.l. and by *c.*AD 1850 to areas above 500 m a.s.l. (2). Extensive dairy farming in the latter part of the $20th$ century led to widespread clearing at mid- and high-elevations for pasture, further decreasing the native forest to its current extent of about 5% of the total area of the archipelago \approx 58 km² in total), mostly in high and steep areas (2). Currently, four major habitats dominate: (i) native forests; (ii) exotic forests (*Cryptomeria japonica* and *Eucalyptus* monoculture plantations, monocultures and mixed forest of the invasive *Pittosporum undulatum*); (iii) semi-natural pastures (mid- and high- elevation pastures that maintain some indigenous plants); and (iv) intensively managed pastures mainly used for milk production (3–5). There are also small

patches of high elevation natural grassland and bogs (*Sphagnum* spp.), and low elevation agricultural fields, vines and orchards. Urban areas are mostly coastal in location.

Being remote oceanic islands, the Azores support a significant number of endemic species but the current biota is dominated by introduced exotic species, representing 80% of the flora (6) and 60% of the arthropods (7). Their introduction started during land-use changes commencing almost 600 hundred years ago, as the Portuguese settlers brought plants from all parts of the world and especially from mainland Portugal, South America and Africa.

Species distributions in the nine islands and in native and exotic habitats. The recently updated lists of Azorean arthropods derive from an unprecedented collaboration of more than 100 taxonomists (7), involving the update of taxonomic information, listing of synonyms, and quantification of the numbers of endemic, native and exotic species (available online at http:/[/www.azoresbioportal.angra.uac.pt/](http://www.azoresbioportal.angra.uac.pt/) (see also 8). Sources included an exhaustive literature review of taxonomical and distributional data, in addition to data from museum collections (e.g. the University of Azores entomological collections), BA, MSc and PhD theses and expert field reports. Our data also include information derived from extensive standardized sampling (4, 5) of: native forest (100 sites in 7 islands), high elevation natural grasslands (20 sites, 5 islands), peat bogs (4 sites, 1 island), exotic forests (37 sites, 4 islands), semi-natural pastures (29 sites, 4 islands), and intensively managed pastures (38 sites, 4 islands). This distributional data set was used to attribute species as occurring in native forest (SONF) for the purposes of specific tests reported below.

Selection of taxa and functional traits. A recent study of the extinction debt attributable to the extensive destruction of the native forest of Azorean Islands, estimated that more than half of the extant native forest-dependent arthropod species might eventually be driven to extinction (2). Among the three taxa considered in that analysis, spiders and beetles exhibited very high percentages of species 'committed' to future extinction and, consequently, we regard them as of particular ecological interest.

Spiders. Spiders (order Araneae) are one of the most diverse and abundant arthropod orders. They include more than 40,000 known species (9) and their relative abundance compared with other arthropod orders is particularly high in Macaronesia (e.g. 4, 5). Due to the almost complete absence of ants in native forests, spiders are the most important arthropod predators in the Azores (4). Theory predicts that higher trophic levels are more prone to extinction due to habitat change as, besides intrinsic factors, such species suffer from cascade effects from lower trophic levels (e.g. 10). Spiders in the Azores are relatively intolerant of the destruction and disturbance of mature forests on these islands because the replacement of native forest with intensively managed pastures, or with exotic forest of lower vegetation architecture, is restricting the availability of suitable sites for web-building (11, 12). Cardoso et al. (13) suggested that spider diversity patterns in the archipelago could best be explained by incorporating forest destruction as an explanatory factor, with past extinctions of endemic species playing a part in shaping these patterns at the island level. Additionally, exotic species may have caused past extinctions due to competition with indigenous species (13).

Beetles. Beetles (order Coleoptera) are the largest order of insects (constituting about 40% of all described insect species) and occupy a vast array of environments: the same is true of the Azores, where they constitute around 35% of the fauna (7). Beetles influence local communities by various roles in food webs, litter decomposition, and nutrient flow. The functional significance of

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beetles is reflected in their diversity of foraging behaviors, and they may act as detritivores, herbivores, fungivores or predators (e.g. 14, 15, Table 1). In the Azores at least nine species became extinct during the last century (e.g. 2, 7).

Traits. Spider trait data were collected from a number of sources. When species-level information was not available we used the general characteristics of families or genera, acknowledging that some misattributions may thus be involved (16). Body length was collated from the literature, separately for males and females to address the possible effects of sexual dimorphism (e.g. 17). As females and males body lengths were highly correlated (Pearson correlation = 0.96; *P*<0.001), we used the mean value between females and males. For beetles, feeding guild and wing morphology traits data were obtained based on personal knowledge of many colleagues contacted due to their expertise in the life history of each beetle family and from monographs. To estimate mean body size, whenever possible, ten specimens were measured per species per island. When no specimens were available in the *Dalberto Pombo Insect Collection* of the University of Azores, we used body size data available from the literature and in a few cases we asked colleagues to measure specimens in their private collections. A description of the biological meaning of each trait is given in Table S1.

Table S1. Functional traits for spiders and beetles used in the study

The above traits for beetles were listed for all but six (1.2%) species of the 524 currently known from the archipelago (7): the six species lacking data were excluded from the analysis. We measured the correlations for each pair of traits for both spiders and beetles in order to estimate the level of redundancy in our functional information. We first computed the distance matrices for each trait and then we calculated the Spearman rank correlations between every possible pair of distance matrices (see *Supplementary Results,* Table S4, below). Here we used Gower's distance, a metric that accommodates continuous and nominal variables (18, 19), following the general formula:

$$
D_{ij} = \sqrt{1 - \frac{\sum_{k=1}^{n} S_{ijk} \delta_{ijk} w_k}{\sum_{k=1}^{n} \delta_{ijk} w_k}}
$$

where D_{ij} is the Gower's dissimilarity between species *i* and *j*, *n* is the number of variables (traits), s_{ijk} is the similarity between species *i* and *j* for the trait *k*, $\delta_{ijk} = 0$ if information is missing for at least one species and 1 if the information is available for the two species (here fixed at 1) w_k is the variable weights (here fixed at 1).

Functional diversity assessment. Functional diversity (FD) was assessed by a multidimensional continuous measure based on a distance matrix summarizing pair-wise difference between species computed using Gower's distance. To estimate the independent contributions of each trait to the global Gower's distance, we applied the method proposed by Pavoine et al. (20), in which squared distance matrices for each trait are correlated with the global squared distance. Independent contributions are as follows: for spiders, body size: 26%; the use of the web: 84%;

architecture of the web: 70%; foraging strategy: 80%; prey range: 11%; and vertical stratification: 36%. For beetles, body size: 46%; wing morphology: 66% and feeding guild: 61%.

Although there are several options for calculating continuous measurement of FD none is optimal for all cases (see 21). As species abundance data are lacking at the island level, we used a metric that mostly captures the notion of richness, i.e. amount of functions contained in a given community, based on presence/absence data. There are several such indices, each with limitations. For example, the Functional Attribute Diversity index (FAD2) and its modified version (MFAD), are extremely sensitive to species splitting and then increase exponentially with species richness, meaning that they do not correctly translate the degree of redundancy among species (e.g. 21, 22). Petchey and Gaston's dendrogram-based index (23) has similarly attracted criticisms (e.g. 24). Herein we use the FRic index of functional richness (25), which has been shown to be efficient at detecting assembly rules in simulation tests (21). FRic estimates the multidimensional trait space within the convex hull volume. For instance, in a two dimensional space, the convex hull volume represents the smallest polygon that encloses all species. As our functional information is summarized in the Gower distance matrix, we first analyzed this distance matrix through a principal coordinates analysis (PCoA) and used the resulting PCoA axes as the new traits to compute FRic (26). To avoid negative eigenvalues being returned by the PCoA, Gower distance matrices were primary square-root transformed (27).

One constraint of using FRic is that the number of species must always exceed the number of traits (herein PCoA axes scores). As there are only three endemic spiders and four endemic beetles on Corvo Island, we could only use two and three PCoA axes respectively, to estimate FRic for Corvo. Hence, we excluded Corvo from the analyses for endemics presented in the text, but include subsidiary analyses below including Corvo, based on two (55% inertia) and three (69% inertia) axes, respectively, for spiders and beetles. By removing Corvo, the second lowest

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species richness values in the dataset were for Graciosa for spiders and beetles, with seven and eight endemic species, respectively. We therefore used the first six PCoA axes for spiders and the first seven axes for beetles in the main island-by-island analyses, capturing respectively 81% and 92% of total inertia.

Sensitivity to number of traits for spiders. Identifying functionally important traits and excluding functionally unimportant traits is always subject to uncertainty (28). To test the robustness of our results to the particular selection of traits included in the analyses for spiders (for which the seven traits listed in Table S1 were used), we conducted a sensitivity analysis by calculating FD and the SR–FD relationship based on all possible combinations of three, four, five and six traits. For each distributional category we first investigated the Pearson's correlation between the observed FD values (i.e. computed with the seven traits) for the nine islands (expect for endemic species, for which Corvo was excluded) with the averaged FD values arising from all possible combinations for a given number of traits (i.e. for three, four, five and six traits). Second, we re-fitted the SR–FD relationship for each distributional category and determined the best fit between linear and polynomial forms using ΔAIC_c and R^2 (as described in the main text). The results showed FD values and the outcome of subsequent analytical steps to be robust (*Supplementary Results, Table S5*) and so for all further analyses the full seven-trait data set was used. For beetles, since we only used three traits in the analyses, no such sensitivity analysis was performed.

Supplementary Results

Functional diversity of endemics. In the main results we were obliged to exclude Corvo Island from analysis of the FD–SR relationship for endemics because of low species number. Here we report the results including Corvo Island and based on two PCoA axes for spiders and three for beetles, respectively. In contrast to the results reported in Fig. 2, both linear and polynomial models provide significant fits, with polynomial models having higher R^2 values but being indistinguishable in fit from the linear model based on ΔAIC_c values (Fig. S1). This result shows that the pattern for endemics is unstable and is dependent on the amount of trait space and/or the inclusion of the least rich island.

Body length. Many life-history traits of animals, such as growth rate, clutch size, or life span, are strongly correlated with body size. Thus, body size represents an important surrogate for other ecological attributes across species and environments, and is considered a synthetic functional trait (29, 30). Moreover, dispersal range for small species of spiders may be far greater than for larger ones owing to their increased ballooning ability (e.g. 31, 32) and thus we expected indigenous species (endemics and natives), which arrived by their own means on this isolated archipelago, to be smaller (on average) than exotics. For both spiders and beetles, we compared the body sizes of endemic, native and exotic species using Kruskal-Wallis one-way analysis of variance. For spiders, we used the mean body size of males and females. For spiders, the average body size for exotic species was 5.02 ± 3.24 (range: 1.4–15 mm), for natives 3.91 ± 2.20 (range: 1.45–9.88 mm) and for endemics 3.14 ± 2.49 (range: $1-10.5$ mm). For beetles, the average body length for exotic species was 4.12 ± 3.30 (range: 0.50–23.88 mm), for natives 3.70 ± 3.48 (range: 0.58–18.63 mm) and for endemics 3.96 ± 2.58 (range: 0.98–12.92 mm). Body size of endemic,

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native and exotic spider species were significantly different (Kruskal-Wallis: χ^2 =13.43; df=2, P =0.001), with endemics being significantly smaller than the other two similar groups (*a posteriori* test). For beetle species, no significant differences between the three categories (Kruskal-Wallis: χ^2 =5.60; df=2, *P*=0.061) were found. When only species occurring in native habitats were considered, difference in body size for spiders and beetles between the three categories were consistent, with a significant difference found for spiders (Kruskal-Wallis: χ^2 =10.52; df=2, *P* =0.006, with only endemics being different from natives and exotics) and an absence of difference for beetles (Kruskal-Wallis: χ^2 =0.98; df=2, *P* =0.616).

Other Supplementary Results. Additional results follow below in Tables S2–S7 and in Figures S1–S3, as described in the relevant legends and cited in the main text.

Table S2. Area, species richness (SR) and functional diversity (FD) per island for each distributional category for Azorean

	spiders and beetles.		
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Natives are indigenous species excluding those that are endemic to the Azores. For beetles, from a total of 524 species recorded in Azores, we were able to obtain trait data for 518 of them. The remaining six (four native and two exotic species) were thus excluded from all trait calculations. Therefore, in the row "all islands", we give the species richness corresponding to the number of species used

to compute FD and also give in the row denoted "real total" the total number of species recorded in the Azores, providing the values used in the species–area computation for all species. FD was computed by using the index of functional richness FRic (25). Respectively, 6 PCoA axes (81% total inertia) and 7 PCoA axes (92 % inertia) were used to estimate FRic for spiders and beetles. For FD, Corvo was excluded from the computation for endemics (See SI Material and methods and main text for further details). All FRic values are standardized by the global FRic, which includes all species, such that FRic is constrained between 0 and 1. FD* refers to FRic computed for endemic species with Corvo included, but based on only 2 (55% inertia) and 3 (69%) PCoA axes for spiders and beetles, respectively.

Table S3. Model details and comparisons for the island species–area relationships (ISARs) and for the island functional diversity–area relationships (IFDARs) for spiders and beetles using the log–log model, for the five distributional categories, for the Azorean archipelago.

a) Model parameters and fits

Where, C is the intercept, z the slope, SE Standard errors, df the degree of freedom, *F* the *F* statistic, R^2 the fit, and *P* indicates the significance level; n = 9 islands, except for the endemics category, wherein Corvo island was excluded; species numbers are as given in Table S2.

	Categories tested		Intercept			Slopes	
Spiders	ISAR	df	F	\boldsymbol{P}	df	\boldsymbol{F}	\boldsymbol{P}
	Endemics–Natives–Exotics	2,21	114.031	< 0.001	2,21	7.081	< 0.001
	Indigenous–Exotics	1,14	57.315	< 0.001	1,14	0.449	0.514
	IFDAR	df	\boldsymbol{F}	\boldsymbol{P}	df	\boldsymbol{F}	\boldsymbol{P}
	Endemics-Natives-Exotics	2, 20	24.361	< 0.001	2,20	1.671	0.213
	Indigenous–Exotics	1, 14	32.980	< 0.001	1, 14	0.031	0.863
Beetles	ISAR	df	\boldsymbol{F}	\boldsymbol{P}	df	\bm{F}	\boldsymbol{P}
	Endemics–Natives–Exotics	2,21	59.739	< 0.001	2,21	0.123	0.885
	Indigenous–Exotics	1,14	7.354	0.017	1,14	0.058	0.813
	IFDAR	df	$\cal F$	\boldsymbol{P}	df	\boldsymbol{F}	\boldsymbol{P}
	Endemics-Natives-Exotics	2, 20	9.844	0.001	2, 20	2.275	0.128
	Indigenous–Exotics	1, 14	1.324	0.269	1, 14	6.561	0.023

(a) using two ways of grouping species into distributional categories.

The degrees of freedom (df), *F* statistic and corresponding *P* value are given for both intercept and slope. For the spider ISARs, the slopes do not differ when natives and endemics are aggregated into indigenous species and compared with exotics, but do when the three separate categories are compared. This reflects differences in the form of the ISAR for natives and endemics (Fig. 1). For the spiders IFDARs, the intercepts differ for both comparisons but the slopes do not. For the beetle ISARs, the intercept differs for both the endemics–natives–exotics and indigenous-exotics comparison but the slopes do not. For the beetles IFDARs, the intercepts differ for the endemics–natives–exotics comparison and the slopes differ for the indigenous– exotics comparison.

Table S4. Spearman rank correlations between Gower's distance matrices implemented for each trait, where the traits and their various states (modalities) are as given in Table S1. For spiders $n = 124$, and for beetles $n = 518$.

Table S5. Summary of sensitivity analyses of all possible number and combination from three to six traits for spiders in the estimation of the functional diversity index FRic and the relationship between FRic and species richness.

Distributional groups	3 traits (35; 81%)	4 traits (35; 82%)	5 traits (21; 83%)	6 traits (7; 82%)	
Endemics					
\boldsymbol{r}	$0.925**$	$0.931**$	$0.971***$	$0.989***$	
$\triangle AIC_c$ linear	0.000	0.000	0.000	0.000	
$\triangle AIC_c$ polynomial	8.655	8.650	9.196	9.318	
R^2 linear	$0.568*$	$0.570*$	0.472	0.414	
R^2 polynomial	$0.603*$	$0.605*$	0.481	0.416	
Natives					
r	0.667	$0.771*$	$0.800*$	$0.921***$	
$\triangle AIC_c$ linear	0.000	0.000	0.000	0.000	
ΔAIC_c polynomial	7.198	7.063	6.948	3.476	
R^2 linear	$0.641*$	$0.742**$	$0.767**$	$0.840**$	
R^2 polynomial	$0.641*$	$0.745**$	$0.773**$	$0.894***$	
Indigenous					
\boldsymbol{r}	$0.947***$	$0.979***$	$0.969***$	$0.995***$	
$\triangle AIC_c$ linear	0.000	0.000	0.000	0.000	
ΔAIC_c polynomial	6.987	5.976	7.037	6.768	
R^2 linear	$0.449*$	$0.606*$	$0.508*$	$0.627*$	
R^2 polynomial	0.462	$0.656*$	$0.517*$	$0.644*$	
Exotics					
r	$0.928***$	$0.944***$	$0.974***$	$0.992***$	
$\triangle AIC_c$ linear	0.000	0.000	0.000	0.000	
ΔAIC_c polynomial	4.119	4.742	6.742	7.197	
R^2 linear	$0.786**$	$0.816**$	$0.846***$	$0.879***$	
R^2 polynomial	$0.848**$	$0.860**$	$0.853**$	$0.879**$	
All species					
r	$0.948***$	$0.956***$	$0.980***$	$0.995***$	
$\triangle AIC_c$ linear	0.000	0.000	0.000	0.000	
ΔAIC_c polynomial	5.636	6.576	7.169	7.137	
R^2 linear	$0.770**$	$0.748**$	$0.781**$	$0.842***$	
R^2 polynomial	$0.806**$	$0.765**$	$0.781**$	$0.844**$	

Results are for nine islands, except for the endemic grouping (eight Azorean islands, as Corvo was excluded). Bold values indicate significance, where * indicates $0.01 < P < 0.05$; ** $0.001 < P$ ≤ 0.01 , *** *P* ≤ 0.001 while in all other cases, *P* > 0.05 . For a given number of traits, the mean of the FD values was calculated with all the combinations of those traits. The number of PCoA axes used to measure FRic was selected to ensure around 80% trait inertia in each case (in line with our main analyses), resulting in the use of varying numbers of PCoA axes within this sensitivity analysis. The number of combinations as well as the average inertia retained is given in parentheses in the column headers. Pearson correlations (*r*) were calculated between mean FD values and the observed FD (i.e. computed with the seven traits) for each distributional category. The mean FD from all the combinations was used to re-fit the SR–FD relationship and the preferred model between linear and polynomial models was assessed by using $\triangle AIC_c$ and R^2 (see details in Materials and methods). FD is shown to be robust to the number of traits used and in all cases, the linear model is preferred according to the ΔAIC_c values, although this does not necessarily mean they are all significant. These analyses indicate that patterns obtained do not show any evidence of saturation and appear generally robust to the number of traits used in the analysis of spiders: elsewhere we report only the full results using 7 traits.

Table S6. Results of the null model tests exploring deviations in functional richness (FRic) from the null expectation for each island given observed SR, for spiders and beetles on the Azorean islands. Deviations, expressed as standardized effect sizes (SES) and *P* **values are given for five distributional groups under two distinct null models (below).**

Null model 'All' is for all habitats and all species. In null model 'SONF' only species occurring in native forest (whether indigenous or exotic) were considered. Which species qualify as SONF was determined from systematic field data (above $(4, 5)$). Except for endemic species for Corvo, FD was calculated by using FRic index based on 6 and 7 PCoA axes for spiders and beetles, respectively. Null simulations for Corvo were run by retaining only 2 and 3 PCoA axes for spiders and beetles, respectively. SES values are calculated as (O-M)/S where O is the observed value and M and S are the mean and standard deviation respectively of 999 randomizations of the traits distribution. Negative SESs indicate that FRic is lower than expected by chance while positive SESs mean the opposite. *P* values are calculated as a two tailed-test. We applied the false discovery rate correction (FDR, (33)) to correct for multiple comparisons. Bold values indicate significance, where * indicates $0.01 < P < 0.05$; ** $0.001 < P < 0.01$, *** $P < 0.001$ while in all other cases, $P > 0.05$.

Table S7. Pearson correlations between body size and the position of each species within the first six and seven axes of the principal coordinates analysis (PCoA) of the Azorean traits data for spiders and beetles, respectively.

Percentages of inertia explained by each PCoA axis are presented in parentheses. Where islandlevel calculations are undertaken we used six axes for spiders and seven for beetles, but for archipelago-level analysis using the whole species pool, computational restrictions meant we could use only the first four axes for each taxon. Further analyses demonstrating the loadings of other traits in the PCoA space are presented in Fig. S2 (below).

Supporting Figures

Figure S1. The relationship between FD (using FRic (25)) and species richness (SR) for endemic Azorean spiders (left panel) and beetles (right panel). In contrast to Fig. 2, the island of Corvo was included in the analysis (i.e. $n = 9$ islands, although only 7 points can be seen for spiders because of over-plotting). FRic was therefore computed based on only the first two PCoA axes for spiders and the first three axes for beetles, representing 55 and 69% of total inertia for spiders and beetles, respectively (See *Materials and methods* for further details). Linear (full lines) and polynomial (dotted lines) fits are given, with their respective ΔAIC_c and R^2 . Both linear and polynomial models provide significant fits (F statistic test $P \le 0.05$). The models with the lowest ΔAIC_c values are given in bold, but as they differ from the alternative model by <2.0, we are unable to distinguish a single best model in either case. The outcome of this analysis is thus equivocal for both taxa.

Figure S2. Trait loadings on the PCoA axes, showing how the derived traits relate to the underlying functional traits: (a) Trait loadings for spiders for the first six axes of the principal coordinates analysis (PCoA) based on the global distance matrix, for the 124 species of Azorean spiders**.** The different modalities (character states) of each trait are placed on each PCoA axis at the center of gravity of their associated species, with the lines representing the standard deviation around the center of gravity. The values in parentheses indicate the inertia represented in each axis.

Figure S2 continued: (b) Trait loadings for beetles for the first seven axes of the principal coordinates analysis (PCoA) based on the global distance matrix, for 518 species of Azorean beetles. These diagrams provide ecological insight into the trait space described by the PCoA analyses for the interested reader.

Figure S3. Projections of the convex hull functional space of endemics (blue), natives (green) and exotics (red) estimated by the first six PCoA axes for spiders (left) and by the first seven PCoA axes for beetles. Percentages of inertia summarized per axis are given in parentheses alongside the x and y axes. Crosses represent the center of gravity of the volume occupied while colored dots indicate species.

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