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Increase of insular exotic arthropod diversity is a neglected aspect of the current biodiversity crisis

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27 Abstract:

28	1.	A dramatic insect decline has been documented on the grasslands and forests of
29		European or North American mainland. However, other parts of the world and
30		other ecosystems remain much less studied with unknown patterns.
31	2.	Using a unique time-series dataset, we investigate recent trends on abundance
32		and richness of arthropods sampled in Azorean native forest over six years
33		(2013-2018).
34	3.	We test the hypothesis that biodiversity erosion drivers are changing the
35		diversity and relative species abundance structure (Species Abundance
36		Distribution, SAD) of endemics, native non-endemics and exotic species over
37		time. We also examine temporal trends in abundance for each individual species.
38	4.	In contrast with mainland studies, we observed no decline in overall arthropod
39		diversity, but a clear increase on the diversity of exotic arthropods and some
40		evidence of a tendency for decreasing abundance for some endemic species. We
41		also document stronger species turnover for exotic species, but no specific
42		changes in the SAD.
43	5.	We argue that many changes, particularly on unique systems such as islands,
44		will be noticed not at the richness but mostly at compositional level. Special
45		attention has to be given to exotic species which are known to be one of the
46		major drivers of biodiversity erosion on islands.
47		
48	Keywo	ords: arthropods, diversity, islands, long-term monitoring, sampling
49	standa	rdization, exotic species
50		
51	Introd	luction
52	Biodiv	versity loss is well recognized as a key challenge for this century (Sala <i>et al.</i> ,

53 2000; Cardinale et al., 2012). Although insect biodiversity in particular is an essential

54 component for ecosystem functioning (Allan *et al.*, 2015; Bennett *et al.*, 2015) and

55 biodiversity loss being a risk to both ecosystem sustainability and Human health and

56 well-being (Sandifer *et al.*, 2015), insect biodiversity loss or just plain changes in

57 population abundances tended to be relatively ignored by the public, policy-makers and

local and national authorities (Cardoso et al., 2011). Yet, recently, insect population 58 59 declines have made the news, with multiple reports describing what appear to be 60 dramatic losses in richness, abundance and biomass (Halmann et al., 2017; 2019, 2020; 61 Habel et al.; 2019; Homburg et al., 2019; Seibold et al., 2019; Wagner, 2020). There is 62 a recent call for urgent measures to be taken to avoid massive insect declines (e.g. 63 Cardoso et al., 2020; Harvey et al., 2020; Samways et al., 2020) and obtain more long-64 term standardized robust data (Cardoso & Leather, 2019, Thomas et al., 2019). The 65 many insect population reports that are arriving from across the world do however 66 present a strong geographical bias, focusing on the European or North American 67 mainland. The rest of the world remains much less studied and to what point the current 68 findings are general is unknown.

69 The present biodiversity crisis is hitting islands disproportionately (Kier *et al.*, 70 2009), with impacts at all levels of biodiversity but also affecting Human populations 71 and economies (Chapin *et al.*, 2000; Weiss, 2015). This biodiversity crisis on islands 72 and elsewhere is a consequence of several biodiversity erosion drivers including land-73 use changes, habitat degradation, pollution, invasive species and climatic changes 74 (Borges et al., 2019a). In fact, historical human colonization of most isolated oceanic 75 archipelagos promoted whole island ecosystem extirpation, and at best, native habitats 76 fragmentation. Despite the evidences of historical losses in species diversity on islands 77 after Human occupation (e.g., Goodfriend et al., 1994, Blackburn et al., 2004; Triantis et 78 al., 2010; Alcover et al., 2015; Terzopoulou et al., 2015; Kirch, 2015) there is no study 79 that investigates the recent temporal trends on species diversity and composition on 80 island native faunas.

81 In this contribution, we use a unique time-series dataset of arthropods sampled in 82 Azorean native forest over six years (2013-2018) (see Borges et al., 2017; Matthews et 83 al., 2019b) to investigate recent trends on arthropod diversity and composition. The Azores is one of the world's most isolated archipelagos made of nine main islands 84 85 aligned on a WNW-ESE axis in the Atlantic Ocean. At the time of human colonization, 86 around AD 1440, the Azorean archipelago was almost entirely forest-covered. In less 87 than 600 years, 95% of the original native forest has been destroyed (Gaspar et al., 88 2008) due to the development of an economy based on dairy and the plantation of 89 forests of exotic species. The protection of the remaining native forest fragments 90 became recently a priority for local authorities, since those fragments play a

91 fundamental role as refuges and source habitats for the endemic fauna and flora (Gaspar
92 *et al.*, 2011).

93 Several negative biodiversity erosion drivers are currently impacting Azorean 94 biota (Borges et al., 2019b). For instance, Triantis et al. (2010) investigated the 95 possibility of an extinction debt attributable to the forest destruction in Azorean 96 arthropod fauna and have estimated that more than half of the extant native forest-97 dependent arthropod species might eventually be driven to extinction. The current lack 98 of connectivity between forest patches (Aparício et al., 2018) and potential enhanced 99 habitat fragmentation due to climatic changes (Ferreira et al., 2016; Aparício et al., 100 2018) is reducing the habitat quality for many arthropod species. Based on this previous 101 work and despite recent studies showing that there is a dominance of endemics (Ribeiro 102 et al., 2005; Rego et al., 2019) and possible resistance to invasions (Florencio et al., 103 2016), we expect a visible decrease in endemics diversity over time most markedly in 104 abundance. Moreover, since exotic arthropod species are not in equilibrium and 105 consequently are more dynamic in space (Cardoso et al., 2009; Rigal et al., 2018) and 106 time (Matthews et al., 2019b) than indigenous species, we also expect a temporal 107 positive signal for this group of species. Given the expected loss of endemics but gain 108 of exotics, overall richness and abundance would remain similar across time. We test 109 these predictions using the diversity metrics (Hill numbers), change in species 110 composition over time and Species Abundance Distribution (SAD) for all arthropod 111 species, endemics, native non-endemics and exotic species.

112

113 Material and Methods

114 Study sites and sampling methods

The Azorean archipelago is located in the North Atlantic, roughly between 37° to 40° N latitude and 25° to 3° W longitude. Terceira Island (Fig. 1), a roughly circular island with an area of 402 km², contains the largest area of native pristine forests in the Azores (Triantis *et al.*, 2010), with five main fragments of native forest distributed across four main volcanic polygenetic complexes. The study was initiated in 2012 as part of the EU-NETBIOME –ISLANDBIODIV (Cicconardi *et al.*; 2017; Borges *et al.*, 2018a) (Fig. 1). SLAM (Sea, Land, and Air Malaise) traps were setup in 10 plots for

122 long-term monitoring, maximizing the distance between plots within the continuous 123 forest patch. These traps are passive flight interception traps with approximately 110 x 124 110 x 110 cm, similar to Malaise traps, but allowing the interception of insects from all 125 directions (arthropods hit an area of black mesh and are funneled into a sampling 126 bottle). The collecting bottles, containing Propylene Glycol as preservative, operated 127 continually for six years, being collected and changed every three months; thus, each 128 sample covers one season of the year. Two of the original ISLANDBIODIV plots were 129 not considered due to the fact that some samples were missing in some of the years. In 130 total, 192 (8 plots x 4 seasons x 6 years) samples were considered for the study. A more 131 comprehensive outline of the study is provided in Borges et al. (2017) and Matthews et 132 al. (2019b).

133 Species identification

134 Arthropods were sorted to order level and to morphospecies by students working 135 as parataxonomists. One of the authors (PAVB) identified to species level the 136 morphospecies of the following arthropod classes: Diplopoda (Chordeumatida, Julida), 137 Chilopoda (Geophilomorpha, Lithobiomorpha, Scolopendromorpha), Arachnida 138 (Araneae, Opiliones, Pseudoscorpiones) and Insecta (Blattaria, Coleoptera, Hemiptera, 139 Microcoryphia, Neuroptera, Psocoptera, Thysanoptera, Trichoptera). All material is 140 stored at EDTP—Entomoteca Dalberto Teixeira Pombo, University of Azores, Angra 141 do Heroísmo, Portugal.

142 Arthropods were grouped into three colonization categories: endemic (i.e. 143 restricted to the Azores); native non-endemic, i.e. species that arrived naturally to the 144 archipelago but are present both in the Azorean Islands and elsewhere; and exotic non-145 native species, i.e., species whose original distribution range did not include the Azores 146 and that are believed to have been introduced in the Macaronesian region after human 147 settlement in the 15th century. The exotic status was inferred either from historical records of detected species introductions or from their current distribution being closely 148 149 associated with human activity. For unidentified species, if other species in the same 150 genus, subfamily or family were present in the archipelago and all belonged to the same 151 colonization category (according to Borges et al., 2010), the unknown species were 152 classified similarly. Otherwise, we assumed the species to be unclassified.

153 Data Analysis

154 For the current study, we used data sampled over the years 2013 –2018 (inclusive) and 155 pooled the data from the four seasons of each year to create yearly datasets for each of 156 the eight plots considered (temporal α diversity). We further pooled the eight plot trap 157 data to have yearly datasets at the regional scale (temporal γ diversity). Unless 158 otherwise stated, all the following analysis were performed with temporal γ diversity 159 (one value per year). A sensitivity analysis was performed previously by Matthews et 160 al. (2019b) to ensure our results were robust, namely sampling completeness estimates 161 for each year in each plot and an evaluation if a single SLAM trap was sufficient to 162 capture the relevant community properties, evaluating the results of three SLAM traps 163 setup in one of the plots during one year. In both cases the data was considered robust.

164 Our first set of analyses aimed to test whether species diversity of arthropod 165 assemblages show temporal trends over the six years period of sampling. We calculated 166 the Hill numbers at three different orders (q) of diversity with a q value of 0 for species 167 richness with all species having the same weight, q = 1 for the exponential of Shannon's 168 index with species being weighted exactly for their abundance in the community and 169 whereas q = 2 for the inverse of Simpson's index which favors abundant species. We 170 used a sample-size-based rarefaction approach to estimate the rate of increase in Hill 171 number with increasing number of individuals sampled, and then extrapolated the 172 observed accumulation curve using the rarefaction-extrapolation approach (Chao & 173 Jost, 2012). Second, we estimated accumulation rates in relation to the degree of 174 completeness of sampling effort, rather than just sample size, as recommended by Chao 175 & Jost (2012). Degree of completeness for each year was evaluated using the coverage estimator (\hat{C}_n , Chao & Jost, 2012) which estimates the proportion of the total number of 176 177 individuals in an assemblage that belong to the species represented in the sample. 178 Sample coverage is considered to be an objective measure of completeness (Chao & 179 Jost, 2012). Hill numbers were subsequently calculated for endemic, native non-180 endemic and exotic species separately. Generalized linear models with Quasi-Poisson 181 error and linear regression models with log-transformed data were used to examine the 182 relationships between diversity and years for species richness and the exponential of 183 Shannon's index and the inverse of Simpson's index respectively. This was carried out 184 for all species and for endemic, native non-endemic and exotic species. All 185 aforementioned analyses were also performed by averaging diversity across the eight

186 plots (mean temporal α diversity) to test whether trends found at regional scale were 187 congruent or not with patterns found at plot scales.

Our second set of analyses was to evaluate temporal trends in abundance per individual species across the six years. We only selected species occurring in a minimum of 4 years out of the six years and with a minimum of 5 individuals per year of occurrence. We used this cut off because temporal changes of very rare species could be caused by minor, chance events. Generalized linear models with Quasi-Poisson error were run to test for the relation between the abundance and years.

194 Our third analysis aimed to examine β diversity patterns over time considering all 195 species together but also for endemic, native non-endemic and exotic species separately. 196 We used the Bray-Curtis index as a β diversity measure with square-root transformed 197 abundance. Relationships between β diversity and distance in time were tested with Mantel permutation tests, based on 9,999 permutations and using Spearman's 198 199 correlation coefficient. We also tested for differences in ß diversity values between 200 endemic, native non-endemic and exotic species using Kruskal-Wallis tests followed by post-hoc pairwise Wilcoxon tests. Our fourth set of analyses was to evaluate temporal 201 202 changes in species abundance distribution (SAD) to further quantify the contribution of 203 endemic, native non-endemic and exotic species abundance patterns over time. We used 204 the Gambin model (Ugland et al., 2007, Matthews et al., 2014) to characterize the shape 205 of the SAD (Ugland et al., 2007). The unimodal gambin model has a single free 206 parameter (α), which characterizes the distribution shape with low values indicating 207 logseries-distribution and higher values indicating more lognormal- distribution. 208 Gambin has been shown to provide good fits to a wide variety of empirical datasets 209 (Matthews et al., 2014, 2019a). Recent developments (Matthews et al., 2019a) have 210 derived the likelihood functions for multimodal gambin models (i.e. with one α per 211 mode) providing a means of easily assessing multimodality in SAD datasets. Therefore, 212 for each year, we fitted both unimodal and bimodal gambin models and used the 213 Bayesian information criterion (BIC) values to compare both models (Burnham & 214 Anderson, 2002). The bimodal model was considered to better fit the SAD if its BIC 215 value was lower than the unimodal model. We also recorded the χ^2 goodness-of-fit 216 statistic and its associated p-value for both one and bimodal models. Given that SAD 217 model parameters are sensitive to variations in sample size (McGill, 2011) and that we

218 were also interested in comparing parameter values across years, we used a procedure 219 where, for each sample, we subsampled 3000 individuals (the least abundant sample 220 having 3944 individuals), fitted the best gambin model (either uni- or bimodal) to this 221 subsample and stored the α parameter value(s). Given that this subsampling procedure is 222 stochastic, we repeated the process 100 times for each sample and took the mean α 223 value. Mean α values were regressed against years using linear regressions. Finally, we 224 calculated the mean weighted octaves (i.e. weighted with species number) for endemic, 225 native non-endemic and exotic species per year and (1) we used weighted t-tests to 226 examine whether mean weighted octaves differ between groups in each year and (2) run 227 linear regressions to test whether, for a given group, mean weighted octaves increase or 228 decrease over time. Statistical analyses were implemented within the R programming 229 environment (R Development Core Team, 2014) using the packages vegan (Oksanen et 230 al., 2013), iNEXT (Chao et al., 2014), BAT (Cardoso et al., 2015) and gambin 231 (Matthews et al., 2014).

232

233 Results

234 A total of 30,875 arthropod specimens were collected and 159 (morpho) species were identified, representing 17 orders. Of the 159 species, 32 were considered to be 235 236 endemic to Azores, 63 to be native (non-endemics) and 57 to be exotics while seven (7) species were not assigned to any group. About 10% of the taxa were identified to 237 238 morphospecies rather than species. The number of species and total abundance per year 239 for all species and for the three species groups are presented in Table 1. Overall, we 240 found marginal significant differences in species richness over time between the three 241 groups (Friedman's test, P=0.04) with exotics representing a larger fraction of diversity 242 over time (Paired Wilcoxon post hoc test P=0.036).

Sample-size-based species accumulation curves (Fig. S1) indicated that the arthropod
fauna was well sampled for each year, but did not represent a complete census of
species. The majority of these unsampled species are likely to be rare (and potentially
vagrants) as coverage-based rarefaction revealed a sample completeness of almost
100% for the six years, suggesting that very few individuals of the community belonged
to species not represented in our samples. Therefore, we conclude that our sampling was
satisfactory for characterization of arthropod communities for each year (See Figure S1

and Table 1). Overall, we only detected a significant increase of gamma diversity with time for exotic species, for both the exponential of Shannon's index ($R^2 = 0.81$, P=0.01) and the inverse of Simpson's index ($R^2 = 0.84$, P = 0.009) (Figure 2; see detailed results in Table S1). Similar results were obtained with mean α diversity (exotic species: exponential of Shannon's index; $R^2 = 0.86$, P=0.007 and inverse of Simpson's index; R^2 = 0.86, P = 0.007) (See detailed results in Table S2).

Only 48 species were retained for the individual abundance analysis, representing
31% of the total species recorded in our study but 96% of the individuals (Figure 3).
Overall, average effect size was -0.064±0.41, -0.066±0.417 and -0.066±0.249 for
endemic, native non-endemic and exotic species respectively. However, 11 species
showed a significant decline in abundance, while only 3 species showed a significant
increase (Table S3).

262 We found significant and positive relationships between β diversity with distance in time for overall, endemic and exotic species ($r_s = 0.85$; P=0.002; $r_s = 0.71$; P= 0.016 263 264 and $r_s = 0.60$; P=0.011 respectively, Figure 4) but not for native non-endemic species (r_s = 0.20; P= 0.247). On average, β diversity values were strongly and significantly 265 266 different between the three species groups (Kruskal-Wallis; H=36.25; P<0.001) with 267 exotic species having the higest β diversity over time and endemics the lowest (Post-hoc 268 Pairwise Wilcoxon test: all pairs being significantly different, P<0.001, Figure 4).For 269 each of the six years, SADs was best represented by a bimodal gambin model according to the χ^2 goodness-of-fit test and BIC (Figure 5 and see Table S4). Non-significant 270 271 relationships were detected between the mean α parameter values and time for both 272 modes ($R^2 = 0.15$, P=0.44 and $R^2 = 0.04$, P=0.68). Our weighted t-tests showed that, 273 regardless of the years, exotic species were always significantly associated to smaller 274 octaves (rare species, Table S5) than endemic species that were mostly represented in 275 higher octaves (dominant species). We did not detect any significant temporal trends in 276 the weighted mean octaves for endemic, native non-endemic or exotic species ($R^2 =$ 0.04, P=0.68, $R^2 = 0.01$, P=0.85 and $R^2 = 0.003$, P=0.91 respectively). 277

278

279 Discussion

280 Contrasting with recent studies on the European and North American mainland, 281 our study shows no evidence of a decline of overall species diversity for endemic and 282 native non-endemic species, although the data are limited to six years of sampling. 283 However, our study clearly identified three important patterns: i) an increasing diversity 284 of exotic species over time; ii) the high temporal dynamism of exotic species (see also 285 Matthews *et al.*, 2019b) and iii) some evidence of a tendency for decreasing abundance 286 for some endemic species.

287 Therefore, all our predictions were generally confirmed, and here we clearly 288 identify exotic species as a potential driver of future biodiversity erosion on Azorean 289 native forests. This is partly similar to the pattern found by Seibold et al. (2019) in 290 German forests, where few initially abundant invasive (and potential pest) species 291 increased in abundance. In previous studies we observed that exotic species are already 292 permeating Azorean indigenous arthropod communities (Gaston et al., 2006; Rigal et 293 al., 2013), being however only abundant in anthropogenic habitats (Cardoso et al., 294 2009). Rapid demographic fluctuations (Matthews et al., 2019b) and contingent spatial 295 factors related with native forest fragmentation and land-use changes (Cardoso et al., 296 2009; Florencio et al., 2016) are surely involved on the increased diversity through time 297 of exotic species in the Azores. It is worth noting that the increasing diversity of exotic 298 species in six years is mostly due to juveniles. This suggests the increasing importance 299 of a source-sink dynamics between natural forests as sinks and other habitat types as 300 sources. The dispersion of juveniles from the surrounding matrix of semi-natural 301 grasslands and exotic plantations of *Cryptomeria japonica* towards native forests seems 302 to be more significant from year to year (see also Borges et al., 2008). We have no data 303 yet to know what is causing this change, but it probably is only a matter of time before 304 many of the exotic species can establish and multiply healthy populations in native 305 forests, which might cause displacement or local extinctions of endemic and native non-306 endemic species. Despite previous observations suggesting that Azorean canopies may 307 act as physical barriers to the colonization of exotic spiders (Florencio et al., 2016), the 308 results obtained in this long-term study are less optimistic. If this process continues, we 309 may expect that in addition to the ongoing invasion of soil communities (see Cicconardi 310 et al.; 2017), the Azorean arthropod canopy communities are also under and a potential 311 process of ecological meltdown and homogenization.

312 The observation that there is a tendency for a decreasing abundance of some 313 endemic species is also of some concern. A recent assessment of the IUCN red list 314 status of Azorean endemic forest arthropods (Borges et al., 2017, 2018c; see also 315 http://www.maiisg.com/), concluded that most species are threatened. There is no 316 current easy explanation for the observed trend in the endemic arthropod species, but it 317 can be associated with the current spread of invasive plants that are changing 318 dramatically the cover and structure of forest understory, namely the cover of ferns and 319 bryophytes in the forest floor (Borges et al., 2017, 2018c). In addition, António Frias 320 Martins (pers. comm.) observed a tendency for a decrease in the cover of bryophytes on 321 the canopy of some endemic Azorean trees at high elevations in the last twenty years 322 with a consequent decrease in the abundance of endemic micro land snails. This 323 observation indicates an ongoing impact of climatic changes on Azorean native forest 324 and a tendency to change on habitat structure with impact on endemic invertebrates. 325 Continuing monitoring of island forest ecosystems is badly needed (Borges et al.,

2018b), on the Azores as well as other regions to avoid unexpected declines and
extinctions of native, often endemic, species.

328

329 Conclusions

In this study no major insect diversity decline was observed in the native forests of a small Atlantic volcanic island in Azores (Portugal). In contrast, in addition to some evidence of decreasing abundances of endemic species, the increase through time of the diversity of exotic arthropods was the stronger pattern.

We can consider that our results are representative of the current situation on Azorean native forests since we included most of arthropod orders encompassing several trophic levels, even if excluding Acari, Collembola, Lepidoptera, Diptera and Hymenoptera from our diversity measurements. The impact of exotic species on islands is well known (Sax & Gaines, 2008), and as a result of this six-year study on Azores, important management actions should be taken to tackle this problem (see also Harvey *et al.*, 2020; Samways *et al.*, 2020).

This is therefore a different, complementary view of many studies showing insect
 population declines. On islands, as studied extensively in the past, invasive species are

- 343 particularly relevant in a conservation context. This signal would have been missed if
- 344 species were not identified and classified according to their origin, masking a
- 345 worrisome pattern.
- 346
- 347

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364 **Conflict of Interest**

365 The authors declare no conflict of interest

366

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578	Figure legends
579	
580	Figure 1. A map of the eight out of the ten originally sampled 50m x 50m plots and
581	areas of native forest on the island of Terceira, Azores.
582	
583	Figure 2. Relationships between species diversity and years. Analyses were performed
584	with first three Hill numbers namely species richness, the exponential of Shannon and
585	the inverse Simpson and for all species and endemic, native (non-endemic) and exotic
586	species separately. Generalized linear model with Quasi-Poisson error and linear
587	regression models with log-transformed data were used to examine the relationships

588 between diversity and years for species richness and the exponential of Shannon's index

and the inverse of Simpson's index respectively. Dotted red lines indicate non-

590 significant relationships while solid red lines indicate significant ones.

591

592 Figure 3. Effect sizes of the relationships between individual species abundance with 593 years. Effect size refers to the standardized slope of the relationship extracted from the 594 Generalized linear models with Quasi-Poisson error fitted to the data. Analyses were 595 performed only for the species occurring in a minimum of 4 years out of the six years 596 and with a minimum of 5 individuals per year of occurrence. In total, 48 species were 597 considered representing 31% of the species sampled across the six years but 96% of all 598 individuals. Horizontal lines indicate the confidence interval at 95% calculated for each 599 effect size. Negative effect size indicates decline in abundance over the six years while 600 positive effect size indicates an increase in abundance. Endemic, native (non-endemic) 601 and exotic species per octave are indicated with different colors. Species for which the effect size was significant are labelled. 602

603

604 **Figure 4.** Results of the β diversity analyses over time for all species, endemic, native 605 (non-endemic) and exotic species. β diversity was computed with the Bray-Curtis index. 606 (A) Relationship between β diversity and distance in years. Relationships were tested 607 using Mantel test with Spearman correlation. Dotted red lines indicate non-significant 608 relationships while solid red lines indicate significant ones. (B) Distribution of the β 609 diversity values between endemic, native and exotic species. Differences were tested 610 with Kruskal-Wallis test. The test was significant and post-hoc pairwise Wilcoxon test 611 showed that all groups differed between each other.

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613 Figure 5. Species abundance distribution (SADs) histograms for arthropods, with

614 predicted values of the bimodal gambin model (black dots), for each year. The

following binning system was used: bin 1 corresponds to the number of species with 1

616 individual per species, bin 2 corresponds to the number of species with 2–3 individuals

617 per species, bin 3 corresponds to the number of species with 4–7 individuals per

618 species, etc. Number of endemic, native (non-endemic) and exotic and unclassified

619 species per octave are indicated with color code.

621

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Insect Conservation and Diversity

- 1 **Table 1.** Degree of completeness estimated with coverage (\hat{C}_n) and number of species and individuals for all species (ALL) and for the endemic
- 2 (END), native (non-endemic) (NAT) and exotic (EXO) species separately. The coverage estimator estimates the proportion of the total number of
- 3 individuals in an assemblage that belong to the species represented in the sample.

Years	\hat{C}_n	S_{ALL}	S_{END}	S_{NAT}	S_{EXO}	N_{ALL}	N_{END}	N_{NAT}	N _{EXO}
2013	0.9944	83	24	32	24	5894	3858	1646	217
2014	0.9969	87	29	30	27	7026	4469	2357	199
2015	0.9949	75	26	29	19	3944	2479	1336	128
2016	0.9964	76	22	30	23	4120	2683	1274	160
2017	0.9947	80	20	29	29	3933	2358	1430	140
2018	0.9960	86	24	30	31	5958	3042	2729	186
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Figure 1. A map of the eight out of the ten originally sampled 50m x 50m plots and areas of native forest on the island of Terceira, Azores.



Figure 2. Relationships between species diversity and years. Analyses were performed with first three Hill numbers namely species richness, the exponential of Shannon and the inverse Simpson and for all species and endemic, native (non-endemic) and exotic species separately. Generalized linear model with Quasi-Poisson error and linear regression models with log-transformed data were used to examine the relationships between diversity and years for species richness and the exponential of Shannon's index and the inverse of Simpson's index respectively. Dotted red lines indicate non-significant relationships while solid red lines indicate significant ones.

355x304mm (300 x 300 DPI)



Figure 3. Effect sizes of the relationships between individual species abundance with years. Effect size refers to the standardized slope of the relationship extracted from the Generalized linear models with Quasi-Poisson error fitted to the data. Analyses were performed only for the species occurring in a minimum of 4 years out of the six years and with a minimum of 5 individuals per year of occurrence. In total, 48 species were considered representing 31% of the species sampled across the six years but 96% of all individuals. Horizontal lines indicate the confidence interval at 95% calculated for each effect size. Negative effect size indicates decline in abundance over the six years while positive effect size indicates an increase in abundance. Endemic, native (non-endemic) and exotic species per octave are indicated with different colors. Species for which the effect size was significant are labelled.

152x177mm (300 x 300 DPI)



Figure 4. Results of the □□ diversity analyses over time for all species, endemic, native (non-endemic) and exotic species. □ diversity was computed with the Bray-Curtis index. (A) Relationship between □ diversity and distance in years. Relationships were tested using Mantel test with Spearman correlation. Dotted red lines indicate non-significant relationships while solid red lines indicate significant ones. (B) Distribution of the □ diversity values between endemic, native and exotic species. Differences were tested with Kruskal-Wallis test. The test was significant and post-hoc pairwise Wilcoxon test showed that all groups differed between each other.

152x101mm (300 x 300 DPI)



Figure 5. Species abundance distribution (SADs) histograms for arthropods, with predicted values of the bimodal gambin model (black dots), for each year. The following binning system was used: bin 1 corresponds to the number of species with 1 individual per species, bin 2 corresponds to the number of species with 2–3 individuals per species, bin 3 corresponds to the number of species with 4–7 individuals per species, etc. Number of endemic, native (non-endemic) and exotic and unclassified species per octave are indicated with color code.

406x254mm (300 x 300 DPI)

Supplementary Material

Increase of insular exotic arthropod diversity is a neglected aspect of the current biodiversity crisis

Paulo A.V. Borges François Rigal Alejandra Ros-Prieto & Pedro Cardoso

for Review Only



Figure S1. (A) Sample-size-based rarefaction (solid lines) and extrapolation (dotted lines, up to twice the sample size actually taken) of arthropod species richness per year of sampling, along with 95% unconditional confidence intervals (color shading). The symbols indicate the full sampling extent for each year (See Table 1 for the total abundance per year). (B) The sample-completeness plot with 95% confidence interval for rarefied samples (solid line) and extrapolated samples (dashed line) as a function of the number of individuals (See Table 1 for coverage value per year). (C) Coverage-based rarefaction (solid line) and extrapolation

(dashed line) with 95% unconditional confidence intervals. All 95% confidence intervals in three panels were obtained by a bootstrap method based on 100 replications.

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Table S1. Relationships between species diversity of arthropods and years. Species diversity was calculated using Hill numbers at three different orders (q) of diversity with a q value of 0 for species richness, q = 1 for the exponential of Shannon's index and q = 2 for the inverse of Simpson's index. Generalized linear models (GLM) with Quasi-Poisson error were used to examine the relationships between species richness and years while linear regression (LM) models with log-transformed data were used for the exponential of Shannon's index and the inverse of Simpson's index. The effect size (standardized coefficient of the effect of year) with it associated standard error (SE) is given as well as the R² and the P-value of the χ^2 and F-test for GLM and LM respectively. For GLM, R² was calculated as one minus ratio between residuals deviance and null deviance.

Metrics Groups		Effect sizes	SE	R ²	Р
q = 0	All species	-0.003	0.029	0.003	0.920
	Endemics	-0.064	0.051	0.283	0.278
	Natives	-0.020	0.014	0.347	0.219
	Exotics	0.088	0.066	0.297	0.256
<i>q</i> = 1	All species	-0.028	0.022	0.297	0.264
	Endemics	-0.027	0.020	0.299	0.261
	Natives	-0.056	0.030	0.470	0.133
	Exotics	0.142	0.035	0.809	0.015
<i>q</i> = 2	All species	-0.035	0.034	0.214	0.356
	Endemics	-0.034	0.029	0.259	0.303
	Natives	-0.063	0.046	0.325	0.238
	Exotics	0.161	0.034	0.848	0.009

Table S2. Relationships between mean plot species diversity of arthropods and years. Species diversity was calculated using Hill numbers at three different orders (q) of diversity with a q value of 0 for species richness, q = 1 for the exponential of Shannon's index and q = 2 for the inverse of Simpson's index. Generalized linear models (GLM) with Quasi-Poisson error were used to examine the relationships between species richness and years while linear regression (LM) models with log-transformed data were used for the exponential of Shannon's index and the inverse of Simpson's index. The effect size (standardized coefficient of the effect of year) with it associated standard error (SE) is given as well as the R² and the P-value of the χ^2 test of deviance and F-test for GLM and LM respectively. For GLM, R² was calculated as one minus ratio between residuals deviance and null deviance.

Metrics	Groups Effect sizes		SE	R ²	Р
q = 0	All species	All species -0.009		0.020	0.789
	Endemics	-0.042	0.030	0.340	0.226
	Natives	-0.022	0.031	0.116	0.508
	Exotics	0.097	0.045	0.531	0.098
<i>q</i> = 1	All species	-0.017	0.031	0.071	0.609
	Endemics	-0.026	0.033	0.134	0.475
	Natives	-0.079	0.046	0.430	0.158
	Exotics	0.149	0.036	0.810	0.014
<i>q</i> = 2	All species	-0.017	0.052	0.025	0.763
	Endemics	-0.021	0.043	0.058	0.645
	Natives	-0.106	0.061	0.430	0.157
	Exotics	0.157	0.032	0.858	0.008

Table S3. Relationships between abundance and years for the 48 individual species selected (See main text). Relationships were examine using generalized linear models (GLM) with Quasi-Poisson error. For each of the 48 species, the order, the name, the colonization group, the effect size (standardized coefficient of the effect of year) with it associated standard error (SE) is given as well as the R² and the P-value of χ^2 test of deviance. R² was calculated as one minus ratio between residuals deviance and null deviance.

Order	Species names	Group	Effect sizes	SE	R ²	P-value
Coleoptera	Drouetius borgesi borgesi	Endemics	-0.525	0.222	0.595	0.014
Coleoptera	Calacallessubcarinatus	Endemics	-0.425	0.141	0.688	0.002
Neuroptera	Hemerobiusazoricus	Endemics	-0.393	0.154	0.601	0.009
Microcoryphia	Trigoniophthalmusborgesi	Endemics	-0.358	0.248	0.378	0.143
Araneae	Savigniorrhipisacoreensis	Endemics	-0.306	0.103	0.681	0.003
Psocoptera	Elipsocusbrincki	Endemics	-0.297	0.096	0.711	0.002
Araneae	Acorigoneacoreensis	Endemics	-0.223	0.081	0.667	0.005
Hemiptera	Strophingiaharteni	Endemics	-0.216	0.289	0.118	0.453
Araneae	Pisauraacoreensis	Endemics	-0.191	0.194	0.192	0.320
Hemiptera	Pinalitusoromii	Endemics	-0.172	0.111	0.374	0.121
Araneae	Sancusacoreensis	Endemics	-0.167	0.125	0.283	0.181
Araneae	Rugathodesacoreensis	Endemics	-0.166	0.093	0.431	0.074
Araneae	Gibbaraneaoccidentalis	Endemics	-0.159	0.085	0.468	0.060
Hemiptera	Cixiusazoterceirae	Endemics	-0.148	0.153	0.192	0.333
Psocoptera	Elipsocusazoricus	Endemics	-0.127	0.256	0.058	0.620
Araneae	Canariphantesacoreensis	Endemics	0.182	0.806	0.015	0.820
Araneae	Walckenaeriagrandis	Endemics	0.318	0.150	0.522	0.032
Coleoptera	Athetadryochares	Endemics	0.320	0.251	0.242	0.196
Hemiptera	Eupteryxazorica	Endemics	0.411	0.450	0.135	0.351
Hemiptera	Gen.sp.	Endemics	1.350	0.455	0.755	0.000
Blattaria	Zethavestita	Natives	-0.482	0.207	0.597	0.016
Lithobiomorpha	Lithobiuspilicornis pilicornis	Natives	-0.437	0.158	0.668	0.005
Coleoptera	Anaspisproteus	Natives	-0.402	0.208	0.501	0.048
Araneae	Microlinyphiajohnsoni	Natives	-0.389	0.174	0.580	0.023
Psocoptera	Bertkauialucifuga	Natives	-0.291	0.655	0.046	0.653
Hemiptera	Kleidocerysericae	Natives	-0.283	0.227	0.245	0.208
Psocoptera	Valenzuelaflavidus	Natives	-0.253	0.366	0.106	0.487
Hemiptera	Monalocorisfilicis	Natives	-0.148	0.327	0.052	0.650

Thysanoptera	Hoplothripscorticis	Natives	-0.085	0.217	0.036	0.697
Coleoptera	Catopscoracinus	Natives	-0.004	0.234	0.000	0.987
Coleoptera	Pseudophloeophagustenax	Natives	0.039	0.110	0.031	0.725
Araneae	Tenuiphantesmiguelensis	Natives	0.060	0.298	0.010	0.840
Araneae	Lathysdentichelis	Natives	0.062	0.080	0.132	0.435
Araneae	Xysticuscor	Natives	0.116	0.313	0.023	0.711
Hemiptera	Triozalaurisilvae	Natives	0.127	0.196	0.094	0.516
Hemiptera	Cinarajuniperi	Natives	0.129	0.100	0.287	0.199
Araneae	Macaroeriscata	Natives	0.164	0.094	0.434	0.078
Opiliones	Leiobunumblackwalli	Natives	0.203	0.280	0.116	0.466
Hemiptera	Cyphopterumadcendens	Natives	0.217	0.176	0.273	0.214
Psocoptera	Trichopsocusclarus	Natives	0.321	0.411	0.136	0.429
Psocoptera	Ectopsocusbriggsi	Exotics	-0.609	0.371	0.374	0.085
Araneae	Cheiracanthiumerraticum	Exotics	-0.447	0.257	0.348	0.074
Araneae	Erofurcata	Exotics	-0.367	0.094	0.798	0.000
Julida	Ommatoiulusmoreletii	Exotics	-0.238	0.249	0.186	0.337
Araneae	Tenuiphantestenuis	Exotics	0.025	0.314	0.001	0.937
Araneae	Dysderacrocata	Exotics	0.164	0.077	0.528	0.033
Coleoptera	Tachyporusnitidulus	Exotics	0.381	0.385	0.205	0.312
Coleoptera	Athetaaeneicollis	Exotics	0.564	0.329	0.408	0.075

Table S4. Comparison between the performance of the unimodal and bimodal gambin model in fitting species abundance distribution (SAD) of arthropods species per year. Comparison was performed using its BIC value as well as χ^2 goodness-of-fit statistic and its associated p-value. The α parameter of each mode is also given. For each of the six years, SADs was best represented by a bimodal gambin model.

	Unimodal gambin model			Bimodal gambin model						
Years	χ^2	Р	BIC	α		χ^2	Р	BIC	α1	α2
2013	56.325	0.000	372.475	0.95		11.147	0.346	344.536	0.11	7.35
2014	22.490	0.013	399.620	1.53		3.606	0.963	391.415	1.04	10.55
2015	29.487	0.001	334.209	1.48		7.571	0.578	323.496	3.07	15.62
2016	8.207	0.513	335.067	1.86		1.058	0.999	334.934	6.26	5.68
2017	15.144	0.087	353.441	1.61		1.128	0.999	348.076	0.70	11.53
2018	16.893	0.077	378.642	1.25		4.106	0.942	372.887	2.96	5.59

Table S5. Mean weighted octaves for endemic, native non-endemic and exotic species and P-values for the weighted t-tests testing pairwise differences in mean weighted octaves between species groups. For a given species group, the mean weighted octave is calculated by averaging octave values, each being weighted by it associated species number.

	Mea	n weighted octav	P-values of the weighted <i>t</i> -tests			
	Endemics	Natives	Exotics	End-Nat	End-Exo	Nat-Exo
2013	4.708	2.812	1.042	0.126	< 0.001	0.096
2014	4.345	3.567	1.370	0.500	0.002	0.010
2015	3.846	2.966	1.368	0.440	0.020	0.072
2016	4.591	2.833	1.435	0.106	< 0.001	0.130
2017	5.150	3.138	1.034	0.054	< 0.001	0.031
2018	4.417	3.200	1.194	0.299	0.003	0.050