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# High evolutionary and functional distinctiveness of endemic monocots in world islands

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34 **Abstract**

35 Functionally and evolutionarily distinct species have traits or an evolutionary history that are  
36 shared by few others in a given set, which make them priority species for biodiversity conserva-  
37 tion. On islands, life in isolation has led to the evolution of many distinct forms and functions as  
38 well as to a high level of endemism. The aim of this study is to assess the evolutionary and func-  
39 tional distinctiveness of insular monocotyledons and their distribution across 126 islands world-  
40 wide. We show that evolutionary and functional distinctiveness are decoupled but that both are  
41 higher on islands than on continental areas. Anagenesis on islands followed by extinctions and/or  
42 diversification on the mainland may have led to highly evolutionarily distinct species while func-  
43 tionally distinct species may have arisen from ecological niche shift or niche expansion. Insular  
44 endemic species with high evolutionary distinctiveness but not with high functional distinctiveness  
45 are significantly range-restricted compared to less distinct species, possibly indicating dif-  
46 ferences in dispersal potential. By showing that distinctiveness is high on islands and that the  
47 most distinct species are range-restricted, our study has important conservation implications.  
48 Indeed, islands are among the most threatened systems of the world, and extinctions of the most  
49 distinct species could lead to significant loss of phylogenetic and functional diversity.

50

51 **Keywords:** functional distinctiveness, island biogeography, monocotyledons, evolutionary  
52 distinctiveness, range restriction.

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## 66 **Introduction**

67 The distinctiveness of a species is defined as the rarity of some of its characteristics compared to  
68 all other species in a given set (Pavoine et al. 2005). When those characteristics are related to  
69 ecological functions, distinctiveness is referred to as functional distinctiveness. Distinctiveness  
70 can also be related to species' evolutionary history, i.e. its isolated position on the tree of life.  
71 This is referred to as evolutionary distinctiveness (e.g; Pavoine et al. 2005; Redding et al. 2014 ;  
72 Kondratyeva et al. 2019). Distinctiveness has been poorly studied in community ecology or  
73 biogeography (see Grenié et al. 2018) even though it is used in conservation biology (Isaac et al.  
74 2007; Gumbs et al. 2020; Robuchon et al. 2021). By harbouring significant amounts of  
75 functional diversity, functionally distinct species may ensure key ecosystem processes and  
76 services to humanity (Mouillot et al. 2008; Kondratyeva et al. 2019). For example, Petchey,  
77 Hector, & Gaston (2004) studied 12 plant traits and showed that functionally distinct species  
78 may contribute to ecosystem functions by increasing plant biomass production. Loss of  
79 functionally distinct species may therefore directly impact ecosystem stability, resilience and  
80 multi-functionality (Fonseca and Ganade 2001; Oliver et al. 2015). On the other hand,  
81 phylogenetic isolation may lead to distinct ecological functions so that species with high  
82 evolutionary distinctiveness could contribute significantly to ecosystem functioning (Cadotte et  
83 al. 2008; Redding et al. 2008; Cadotte and Davies 2010). Most importantly, evolutionarily  
84 distinct species contribute greatly to the phylogenetic diversity of a set of species (Cadotte et al.  
85 2008; Redding et al. 2008). Phylogenetic diversity represents a reservoir of yet-to-be-discovered  
86 resources for humanity, also called option-values, and the most evolutionarily distinct species  
87 may capture a large proportion of these resources (Faith 1992; Faith 2018). Although debated,

88 evolutionarily distinct species may also contribute greatly to the evolutionary potential of a set of  
89 species (Faith 1992) and, beyond utilitarian values of biodiversity, preserving evolutionarily  
90 distinct species should preserve the evolutionary heritage of our planet (Faith 2016; Gumbs et al.  
91 2021). Based on this rationale, evolutionary distinctiveness is a well-recognised measure for  
92 biodiversity conservation (Redding and Mooers 2006; Isaac et al. 2007; Stein et al. 2018).

93 Insular systems are important biodiversity hotspots, as they harbour a very high proportion of  
94 species that are found nowhere else on Earth and that represent a unique evolutionary history as  
95 well as a multitude of forms and functions (Warren et al. 2015; Ottaviani et al. 2020). The island  
96 biota could thus be composed of many evolutionarily and functionally distinct species, but their  
97 role in shaping insular diversity has been only recently investigated (Veron et al. 2019a). In  
98 addition, very little is known about the rise and distribution of species distinctiveness. Examining  
99 patterns of species distinctiveness on islands may provide new insights of processes underlying  
100 species evolution and strengthen conservation strategies. Here, we focused on monocotyledon  
101 plant species (monocots), a morphologically and functionally diverse clade comprising a quarter  
102 of all flowering plants including orchids, palms and cereals.

103 In order to study both functional and evolutionary distinctiveness, it is necessary to assess how  
104 these aspects of biodiversity are related. However, functional and evolutionary distinctiveness  
105 have rarely been studied in conjunction (but see Cooke et al. 2020), particularly in insular  
106 communities. On islands, the relationship between evolutionary and functional distinctiveness  
107 may be weak, as early diversification and simultaneous cladogenesis may result in a lack of  
108 phylogenetic signals for some traits of insular species (Losos 2008). The radiation of *Bidens*  
109 (Asteraceae) on Hawaii is a classic example, where closely-related species display a greater  
110 diversity of traits (e.g. growth form, floral morphology) than all other representatives of this

111 genus worldwide (Knope et al. 2012). This is probably due to the diversity of habitat types found  
112 on the archipelago and to the loss of these species' dispersal potential (Knope et al. 2012). In  
113 addition, phenotypic changes in insular species do not necessarily involve speciation or a  
114 cladogenetic pattern, thus variation in evolutionary history does not necessarily reflect trait  
115 variation (Whittaker and Fernández-Palacios 2007). Moreover, the number of traits considered,  
116 convergences and/or models of trait evolution among other reasons can lead to the decoupling of  
117 functional and evolutionary distinctiveness (Veron et al. 2019b). Therefore, we first investigated  
118 to what extent functional and evolutionary distinctiveness of monocots are related.

119 Another unresolved question is whether species distinctiveness differs between insular and  
120 continental communities. On islands with long history in isolation, the availability of unfilled  
121 niches and the oceanic climate, along with extinctions that would have isolated species in both  
122 the Tree of Life and the functional trait space, may have given rise to many evolutionarily and  
123 functionally distinct species (Gillespie and Roderick 2002; Grandcolas et al. 2014). However,  
124 there have been few studies assessing whether insular species are more distinct than continental  
125 ones, and results may be taxon-specific (Jetz et al. 2014). We investigated this question in a large  
126 and important plant group and provided an additional line of evidence for preserving insular  
127 biodiversity.

128 Some distinct species are at high risk of extinction because they are range-restricted (Cadotte and  
129 Davies 2010; Harnik 2011). Range-restriction is a key factor associated with extinction risk, and  
130 is one of the main criteria used to assess the threat status of species by the International Union  
131 for Conservation of Nature (IUCN) (Rodrigues et al. 2006). As with distinct species, range-  
132 restricted species have been reported to provide unique functions within ecosystems as well as  
133 unique services to humanity (Mouillot et al. 2013; Leitão et al. 2016). Species that are both

134 range-restricted and distinct may therefore support highly vulnerable and unique functions and  
135 option-values (Rosauer et al. 2009; Violle et al. 2017). We expect that many of such species may  
136 be found on islands. Indeed, islands have a remarkably high level of endemism, which is around  
137 9 times higher than on continents (Kier et al. 2009). More specifically, many insular species are  
138 spatially range-restricted, occurring only on a few islands, and/or in very restricted areas (e.g.,  
139 Caesar et al. 2017). Beyond the practical implications for conservation, assessing the correlation  
140 between distinctiveness and range restriction may shed light on the mechanisms shaping both  
141 species distinctiveness and distribution in islands. For example, factors that have led to past  
142 extinctions may have led to the isolation of species on the phylogenetic tree and/or in functional  
143 space and shrunk their distribution range. However, the association between range-restriction  
144 and distinctiveness in insular species is unclear. Specifically, to the best of our knowledge, the  
145 relationship between range-size and functional distinctiveness has never been tested in plants  
146 (see Cooke et al. 2020 for birds and mammals). In an attempt to fill this gap, we explored the  
147 relationship between species distinctiveness and range restriction of monocots in world islands.  
148 As plant distribution patterns are driven by factors influencing colonization (e.g. Negoita et al.  
149 2016), such as the proximity of the island to a pool source during its geological history, we also  
150 studied how the characteristics of the islands where highly distinct monocots occur can account  
151 for their range restriction.

152 Overall, there is a growing consensus for a better representation of multiple dimensions of  
153 biodiversity in biogeography (Davies and Buckley 2011; Violle et al. 2014) especially on islands  
154 (Patiño et al. 2017). As far as we know, functional and evolutionary species distinctiveness on  
155 islands had never been studied before and our study brings a fresh contribution to this need.  
156 Through our analyses, we addressed four main questions that may lay the foundations for future

157 research on this topic and highlight the importance of islands to preserve evolutionary and  
158 functional distinctiveness: 1) To what extent are evolutionary and functional distinctiveness  
159 related?; 2) Are insular species more evolutionarily and functionally distinct than mainland  
160 endemics?; 3) Are evolutionarily and functionally distinct insular species range-restricted?; 4) Is  
161 the range restriction of distinct species associated with the geographical characteristics of the  
162 islands they occur on?

## 163 **Materials and methods**

### 164 *Geographical and occurrence data*

165 Occurrence data was obtained from the e-monocot database that is now part of the World  
166 Checklist of Selected Plant Families (WCSPF; [wmsp.science.kew.org](http://wmsp.science.kew.org)), and is regularly updated.  
167 It records presences and absences of monocot species across the world within geographic units as  
168 defined by the Biodiversity Information Standards (BIS; Vocabulary Maintenance Specification  
169 Task Group 2017). BIS help to “establish international collaboration among the creators,  
170 managers and users of biodiversity information and to promote the wider and more effective  
171 dissemination and sharing of knowledge about the world's heritage of biological organisms”  
172 (<https://www.tdwg.org/>). We extracted spatial distribution data for all native terrestrial monocot  
173 species in 126 island regions as delimited by the level 3 of the BIS. The number of species we  
174 used vary between 6,682 and 2,581 depending on the analysis performed and data availability  
175 (see ” see section Relationship between evolutionary and functional distinctiveness”). We used  
176 level 3 of BIS as it was the most appropriate to study islands at a global scale. This level of  
177 spatial resolution considers factors such as the distance of the disjunction of an island or group of  
178 islands with the mainland, its size, and its phytogeographical significance. Therefore, one main  
179 advantage of the spatial scale we used is to define regions based on their ecological boundaries



180 and associated communities, which can comprise a single island or a group of islands. In  
181 addition, analyses undertaken at broader scale, representing natural boundaries are key to  
182 advance our understanding of ecological and evolutionary processes in island biogeography  
183 (Triantis et al. 2015).

#### 184 *Species characteristics*

185 To estimate evolutionary distinctiveness (ED), a monocot phylogeny was extracted and pruned  
186 from an updated version of the megaphylogeny of land plants (Qian and Jin 2016). In total, 6,682  
187 species with occurrence data were also present in the phylogeny and were attributed an ED score.  
188 Regarding functional distinctiveness (FD), we used six quantitative traits: adult plant height,  
189 stem specific density, leaf size expressed as leaf area, leaf mass per area, leaf nitrogen content  
190 per unit mass, and diaspore mass (see Díaz et al. 2015 for details). These traits have been widely  
191 used and recognized as fundamental representatives of the ecological strategies of plants (Díaz et  
192 al. 2015). Our dataset comprised 2,581 species with at least one trait value and present in our  
193 phylogeny. Yet, not all these species had values for the 6 traits. Missing trait values were  
194 therefore imputed by running a Random Forest algorithm 1,000 times and then estimating the  
195 mean value of the 1,000 imputations. The Random Forest method imputes missing values for a  
196 species according to the non-missing values of other traits and of other species having similar  
197 functional features, therefore species without any trait values could not be considered. Although  
198 priority should be given to trait data collection, the random forest algorithm was shown to  
199 perform well to impute missing trait data (Penone et al. 2014). We performed a sensitivity  
200 analysis to 1) assess to what extent missing values may have influenced our results; 2) estimate  
201 the correlation between traits; 3) assess the contribution of each trait to FD scores 4) compare the  
202 obtained distinctiveness scores with other indices (Appendix 1). This sensitivity analysis showed

203 that trait imputation performs well to estimate functional distinctiveness values (e.g. high  
204 correlations between functional distinctiveness scores computed on a complete dataset and those  
205 obtained after artificial deletion and imputation of trait values; little influence of the number of  
206 missing data per species on scores of functional distinctiveness [see Appendix 1]). Furthermore,  
207 Díaz et al. (2015) already performed several tests and treatments on this dataset, e.g. “detecting  
208 erroneous entries (due to errors in sampling, measurement, unit conversion, etc.)”; “ensuring that  
209 extreme values that correspond to truly extreme values of traits in nature are not mistakenly  
210 identified as outliers”; test for robustness when missing values occur.

### 211 *Estimating evolutionary and functional distinctiveness*

212 As recommended by Pavoine et al. (2017), the distinctiveness of each monocot species was  
213 calculated with the distance-based metric *AV* (“average”) representing the average dissimilarity  
214 between a focal species and all others. It is thus sensitive to deep divergences but there is also a  
215 contribution of recent divergences (Pavoine et al. 2017). The *AV* metric works with a matrix of  
216 dissimilarity between species. Regarding ED, we computed phylogenetic pairwise distances  
217 (Paradis and Schliep 2019). Regarding FD, we computed pairwise functional distances with  
218 Gower’s metric (Gower 1971). Using phylogenetic and functional distances between species, we  
219 calculated species distinctiveness scores with the *distinctDis* function from the *adiv* package  
220 (Pavoine 2020b) in R (R Core Team 2020). ED is estimated in million years (Myr) of evolution.  
221 FD is a unitless index ranging from 0 (lowest distinctiveness possible) to 1 (highest  
222 distinctiveness possible). Distinctiveness scores per species are given in Appendix 2.

### 223 *Are species more distinct on continents or on islands?*

224 We sorted species into three non-overlapping categories a) insular endemics, i.e. present only on  
225 islands or group of islands; b) continental endemics, i.e. present only on continents; c) non-  
226 endemics, i.e. those found on at least one island or group of islands and in one location on the  
227 continent. We then estimated the distribution and average distinctiveness score for the three  
228 categories. We tested whether the average distinctiveness was significantly different between the  
229 three categories: we randomized species among categories without replacement 1,000 times,  
230 estimated the new average distinctiveness per category in the randomized sets, and compared the  
231 results to the observed distinctiveness in each category. Correcting the average ED scores under  
232 phylogenetic constraint did not affect the results and allowed us to perform pairwise correlations  
233 between categories (Appendix 3).

#### 234 *Relationship between evolutionary and functional distinctiveness*

235 For each endemism category, we tested the correlation between evolutionary and functional  
236 distinctiveness of monocot species. Because species distinctiveness scores depend on the  
237 reference set of species, we re-calculated a new ED score only for the 2,581 monocot species for  
238 which we previously calculated FD. Thus, the correlation between both ED and FD was assessed  
239 between similar sets of species. In addition, ED scores from this subset did not modify the  
240 relative ED rank of species compared to their rank within the larger set (significant Pearson  
241 correlation equals to 0.96). As a complementary analysis helping to understand the relationship  
242 between evolutionary and functional distinctiveness, we measured phylogenetic signal of each of  
243 the six traits individually (Appendix 1). We used the  $K^*$  test based on the core statistics of  
244 Blomberg et al. (2003), as suggested by Pavoine (2020).

#### 245 *Are the most distinct insular species also the most geographically range restricted?*

246 Focusing on endemic monocotyledons present on islands we tested the correlation (Pearson's  
247 test) between distinctiveness and geographical range restriction as measured by the number of  
248 islands or group of islands where each species occurs. The fewer the islands, the more range-  
249 restricted the species is. We also used linear regressions corrected for phylogenetic signal in  
250 model residuals to perform pairwise tests between categories and correct models by adding a  
251 phylogenetic constraint (Appendix 3). Other factors related to range-restriction such as distance  
252 to other landmasses will be considered in the next section analysis. We focused on endemic  
253 insular species because the number of islands where each species occurs can be considered as a  
254 measure of their full range-size but analyses for non-endemic insular species are presented in  
255 Appendix 4.

256 In line with conservation projects that gave priority to the most distinct species (e.g. Isaac et al.  
257 2007), we tested whether the species with the highest ED and FD occurred on fewer islands  
258 compared to species with lower distinctiveness values. We divided species into five classes  
259 according to their distinctiveness score: "top distinctiveness", "high distinctiveness", "moderate  
260 distinctiveness", "low distinctiveness", "very low distinctiveness" (ranked in the 5%, 25%, 50%,  
261 75% and >75% of the distribution, respectively). For each class, we calculated the mean number  
262 of islands or group of islands where each monocot species occurred. We randomized species  
263 among classes 1,000 times and estimated whether the observed mean number of islands where  
264 species occurred per distinctiveness class was lower than in the randomized set (see also  
265 Appendix 3). The main reason to bin species by distinctiveness class is to mainstream our results  
266 into actual biodiversity conservation. Generally, the aim to use distinctiveness for biodiversity  
267 conservation is to identify the most distinct species in order to protect them. Therefore, many  
268 papers studying distinctiveness identified "top distinct species" (Isaac et al. 2007, Huang 2012,

269 Forest et al. 2018, Robuchon et al. 2021). In particular, the EDGE of existence program funds  
270 conservation projects to preserve some of the most evolutionarily distinct and threatened species  
271 of the planet (<https://www.edgeofexistence.org/>). In our study, binning species by distinctiveness  
272 class allowed us to identify the most distinct species and to make a preliminary assessment of  
273 their extinction risks by investigating their range restriction.

#### 274 *Geographical characteristics of islands and species distinctiveness*

275 In this section, we aimed to understand how factors influencing species dispersal could explain  
276 the number of islands or group of islands in which distinct species are found. We first  
277 investigated the relationship between certain island features and the distribution of distinct  
278 species. We focused on geographical characteristics related to past, present and future dispersal  
279 events (Table 1). When information was not available at the BIS-level 3 scale, it was measured  
280 from single-island values (Table 1). However, we acknowledge that the relationship between  
281 these features and species dispersal involves a high level of complexity that we could not  
282 account for. For example, not only current distance to other landmasses and current area may  
283 explain the presence of a species on an island: long lasting environmental changes that may have  
284 modified archipelago configurations through time may also have a role in shaping island  
285 biodiversity (Norder et al. 2019). Other factors to consider are therefore plate tectonics, climate  
286 change, sea level change but also species dispersal vectors or modes and their interactions  
287 (Fajardo et al. 2019). .

#### 288 **Insert Table 1**

289 Our aim was to assess the characteristics of the islands where distinct monocot species occur,  
290 potentially revealing the factors that enabled or impeded colonization by dispersal (Table 1).

291 This approach is species-centred and not area-centred. It addresses the general features of the  
292 islands where each highly distinct species occurs, rather than investigating the features of islands  
293 with the highest average distinctiveness. We made this choice because distinctiveness  
294 characterizes each species in a set and not just the species set. Moreover, counting the number of  
295 distinct species or averaging distinctiveness scores in an area-centred approach may be  
296 inadequate as it will not consider phylogenetic and/or functional complementarity (Veron et al.  
297 2019b). For each species, we estimated the average value of each of the nine geographical  
298 characteristics of the islands or groups of islands where it occurred (Table 1). For qualitative  
299 variables, i.e. past connection to the mainland and glaciations, we attributed a quantitative value  
300 to each of their attributes (glaciated=1; non-glaciated=0; connected to the mainland=1; non-  
301 connected to the mainland=0). We then performed generalized linear models and multi-model  
302 selection with species distinctiveness as the response variable and island average features as the  
303 explanatory variables (see also Appendix 3). Multi-model selection was based on the generation  
304 of “best model sets” relying on Akaike's Information Criteria (AIC). The best models were those  
305 which had a cumulative AICc weight (a measure of relative statistical support) that reached 95%  
306 of the total AICc weights. Parameter estimates were then averaged across the selected models  
307 using the model averaging function (full average; Barton and Barton (2019)). We identified the  
308 strongest interactions using Boosted Regression Trees, which were added to the multi-model  
309 selection process.

## 310 **Results**

### 311 *Functional and evolutionary distinctiveness are not correlated*

312 Functional and evolutionary distinctiveness were weakly correlated, although the correlation  
313 coefficient was higher for insular endemic species (Pearson's correlation coefficients:  $r=0.16$ ,

314 0.13, 0.018 and 0.093, for insular endemics, insular non-endemics, continental endemics and all  
315 monocot species, respectively, with  $p$ -value  $\leq 0.05$ ). This result was congruent with the low  
316 phylogenetic signal of traits and was robust to our sensitivity tests (see Appendix 1).

### 317 *Insular endemics are more distinct*

318 The mean ED and FD per endemism category was respectively 236.7 Myr and 0.061 for insular  
319 endemics, 234.9 Myr and 0.043 for continental endemics, and finally 224.5 Myr and 0.047 for  
320 non-endemics (Fig. 1). Distribution maps of the most evolutionary and functionally distinct  
321 species are presented in Appendix 5. Average ED was significantly higher than expected by  
322 chance for insular endemics and continental endemics. Average FD was significantly higher than  
323 expected by chance for insular endemics, and for species occurring on both islands and  
324 continents. Using phylogenetic analysis of variance, we found that ED and FD were higher for  
325 insular endemic species compared to other categories (Appendix 3).

### 326 **Insert figure 1**

### 327 *Evolutionarily but not functionally distinct species have a restricted geographical range*

328 Geographical range was found to decrease slightly but not significantly with ED in insular non-  
329 endemic monocot species (Pearson's coefficient  $r=-0.043$ ,  $p=0.26$ ), but increased significantly  
330 with FD in insular endemic species ( $r=0.43$ ,  $p<0.001$ ).

331 Insular endemic monocot species in the top 5% for either ED or FD were present on average on  
332 1.7 and 3.2 islands, respectively (Table 2). The top 5% ED endemic species were found on fewer  
333 islands than expected by chance while the top 5% FD species occurred on more islands than  
334 expected by chance (Table 2, Appendix 3).

335 **Insert table 2**

336

337 *Spatial distribution of distinctiveness and its relationship with geographical features of islands*

338 Both functionally and evolutionarily distinct monocot species were located at low latitudes,  
339 indicating that there may be a possible latitudinal gradient for distinctiveness (Table 3). As for  
340 the longitudinal effect, it was generally greater for FD than ED. We observed a high number of  
341 differences between the effects of island features on FD and ED. Concerning evolutionary  
342 distinctiveness, we found a significant positive effect of age and of the continental origin of  
343 islands and a significant negative effect of glaciation, elevation and distance to the mainland (a  
344 similar result was found for non-endemic species, Appendix 4). The effect of the proportion of  
345 the surrounding landmass and area on evolutionary distinctiveness was weak to non-significant  
346 (Table 3, Appendix 4). Regarding high functional distinctiveness of endemic monocots, it was  
347 related to small area, high elevation, large distance from the mainland but not from other  
348 landmasses, the oceanic nature of island and the occurrence of past glaciations (Table 3).

349 **Insert table 3**

350 **Discussion**

351 *Decoupling functional and evolutionary distinctiveness*

352 The primary goal of our study was to perform the very first assessment of monocots  
353 distinctiveness on islands and to highlight its possible origins, contributions for conservation and  
354 research prospects. Distinct species contribute greatly to the diversity of island biota, to beta-  
355 diversity patterns with mainland communities, and to centres of endemism (Veron et al. 2019a).



356 Island regions that harbour both functionally and evolutionarily distinct monocots include the  
357 Indonesian islands, the Philippines, Taiwan, Hainan, New Guinea, Japan, Sumatra, and  
358 Madagascar. However, the most functionally and evolutionarily distinct species were not the  
359 same (appendices 2 and 5). One of the main reasons for lack of association between ED and FD  
360 is the evolutionary lability of species traits. This is supported here by the weak phylogenetic  
361 signal of traits representing the ecological strategies of monocots (Appendix 1). On islands,  
362 evolutionary lability of traits may occur in the case of an adaptive radiation, where  
363 representatives may have very similar ED but very distinct FD scores accentuated by vacant  
364 niche space and/or by competition (Gavrilets and Losos 2009). Another reason for trait lability is  
365 convergent evolution, which has been reported in multiple lineages on multiple islands  
366 (Whittaker et al. 2017). This is the process whereby evolutionarily unrelated organisms show  
367 similar features as a result of natural selection and adaptation under similar environmental  
368 constraints. Yet, there are many possible reasons why FD and ED of plants are not coupled and  
369 we also observed that ED and FD of species found on the mainland were not correlated. A recent  
370 debate about the extent to which phylogenetics captures trait diversity has put in evidence that  
371 the traits considered as well as their number, along with the model of evolution and the spatial  
372 and phylogenetic scale strongly influence the way one can infer the other (see discussions in  
373 Mazel et al. 2017 and Owen et al. 2019). Further eco-evolutionary studies and additional data  
374 would be necessary to better understand why traits fundamental to plant ecological strategies are  
375 not conserved in the phylogeny (Cássia-Silva et al. 2020). In particular, Cornwell et al. (2019)  
376 elucidated the genetic, trait and distribution data that are missing for plants. Their study defines  
377 targets for data collection and compilation, which could help increase the robustness of our  
378 findings.

379 *Species distinctiveness is higher on islands than on continents*

380 Our second important finding was that insular endemic monocots were, on average, more  
381 functionally and evolutionarily distinct than species occurring on continental areas. Highly  
382 evolutionarily distinct species endemic to islands may have arisen from deep divergences. Some  
383 endemic taxa belong to species poor families and are therefore distantly related to other species,  
384 such as *Japonolirion osense* (Petrosaviaceae) (Cameron et al. 2003). However, higher  
385 evolutionary distinctiveness on islands compared to the mainland was unexpected. Indeed, the  
386 initial insular species pool is generally a subset of the continental pool, and, therefore, one would  
387 expect that insular species would not be more ancient and more evolutionarily isolated than  
388 continental species (see Nattier et al. 2017 for an analysis of the age of island biota). Moreover,  
389 high speciation rates on islands may result in the diversification of many closely related species,  
390 which is expected to decrease the distinctiveness of insular species. Historical events on  
391 continents could explain this contradictory finding. One main process could be extinction of  
392 species populations on the continent and survival on islands leading to evolutionary isolation  
393 (Gillespie and Roderick 2002; Grandcolas et al. 2008). High climatic fluctuations and extreme  
394 events on the mainland, concomitant with a relatively stable climate on islands, promoted  
395 extinctions on the continent and allowed persistence on islands, especially for plants (Cronk  
396 1997; Whittaker and Fernández-Palacios 2007; Jetz et al. 2014). Climate change on the  
397 continents may not only have led to extinctions but also to diversification. Diversification on the  
398 mainland could result in the split of unique phylogenetic branches on the continent while species  
399 on islands remained evolutionarily isolated. For example, orchids and grasses represent large  
400 continental radiations contributing to relatively low average ED values of monocots on the  
401 mainland (e.g. Bouchenak-Khelladi et al. 2014; Pérez- Escobar et al. 2017). Furthermore, the

402 current high evolutionary distinctiveness on islands could be due to anagenetic speciation  
403 followed by extinctions or diversification on the mainland. Anagenesis refers to the sequential  
404 evolution of a branch over time (Rensch 1959) and leads to spatial segregation of a given insular  
405 endemic species and its sister species. It is a main model of evolution in islands that are flat,  
406 continental and located at intermediate distances from the mainland, which are also the  
407 characteristics of the islands where we observed the occurrence of highly distinct species  
408 (Stuessy et al. 2006; Rosindell and Phillimore 2011). We therefore suggest that, anagenesis,  
409 extinctions and recent radiations of continental populations may partly explain the evolutionary  
410 isolation of insular endemics at the global scale (Gillespie and Roderick 2002; Grandcolas et al.  
411 2014). It is worth noting that biogeographic considerations only give primary insights on the rise  
412 of evolutionarily distinct monocots and the story is sometimes very complex (Grandcolas et al.  
413 2014). Further research is therefore necessary on this topic: potential biases in phylogenetic tree  
414 topology and branch lengths due to missing data could be tested by building a larger  
415 phylogenetic tree, effects of extinctions could be better understood by investigating fossil  
416 records, and distinguishing clearly between models of evolution would require genetic studies  
417 focused on each highly distinct species.

418 We showed that the functional distinctiveness of monocots was higher on islands than on the  
419 mainland as well. This finding was reported in other taxonomic groups and particular traits, such  
420 as body size in mammals (Faurby and Svenning 2016), morphology, attack strategy and  
421 development in Hymenoptera and Braconidae (Santos et al. 2016). Here, we showed that it was  
422 also true in the monocots we studied regarding the multiple traits fundamental to their ecological  
423 strategies. Two main mechanisms may account for a higher functional distinctiveness of  
424 monocots on islands: niche expansion and niche shift. Niche expansion occurs when species

425 richness is low and disharmony is high, i.e. an imbalance in the taxonomic composition of  
426 species assemblages between islands and the mainland, thereby resulting in a diversity of vacant  
427 niches to be colonized (Whittaker et al. 2017). For example, Diamond (1970) reported that  
428 following the colonization of species-poor islands in the Pacific Ocean, insular birds occupied a  
429 wider altitudinal range and a greater diversity of habitats, and had a wider vertical foraging range  
430 than their continental counterparts. Supporting the niche expansion hypothesis, we found that  
431 functionally distinct species occurred on islands where species richness is assumed to be low, i.e.  
432 islands that were oceanic, small, far from the mainland, and which have been glaciated during  
433 the Last Glacial Maximum, possibly leading to the loss of its distinct biota. Niche shift relates to  
434 changes in the biological and ecological characteristics of insular species compared to their  
435 continental counterparts (MacArthur and Wilson 1967; Simberloff 1974). The persistence of  
436 insular species and especially plants may have been conditioned by adaptations to the oceanic  
437 climate of islands resulting in the evolution of specific ecological strategies.

#### 438 *Range-restriction of distinct species*

439 The few studies exploring the relationship between evolutionary distinctiveness and geographical  
440 range restriction showed that the most distinct species were not more range-restricted than other  
441 species (Jetz et al. 2014; Thuiller et al. 2015; Stein et al. 2018). Here, although the correlation  
442 between the range-restriction of a species (i.e. the number of islands or group of islands where it  
443 occurs) and its ED was generally low, we found that the most evolutionarily distinct monocot  
444 species were spatially range-restricted. Some factors that generate high distinctiveness within  
445 insular systems also generate endemism, such as the adaptation to particular environmental  
446 conditions and the fact that many islands act as a refuge. As stated above, extinctions could have  
447 isolated insular species in the Tree of life, but they could have also restricted species to very few

448 or to a single island and driven endemism through the loss of continental populations (Whittaker  
449 and Fernández-Palacios 2007). Extinctions may therefore be responsible for both higher  
450 distinctiveness and higher range-restriction on islands. On the opposite, we also found that  
451 species with very low distinctiveness had relatively small range sizes (although they tend to be  
452 larger than for the most evolutionarily distinct species). This possibly reflect in-situ speciation  
453 events leading to closely-related species restricted to few islands. Investigating rates of  
454 extinction, speciation and range evolution across the phylogeny of monocots could give further  
455 insights on the origin and distribution of ED on islands (Goldberg et al. 2011). Another potential  
456 mechanism explaining range-restriction of very distinct species is dispersal. While island  
457 features can provide insights on how high species distinctiveness arose, they are also related to  
458 colonization rates and could help understand how dispersal influenced the distribution of these  
459 highly distinct species. The most evolutionarily distinct monocots are often single-island  
460 endemics and rarely occur on islands where recent and/or long-distance dispersal would be  
461 needed to settle new populations. They are uncommon on remote, glaciated, young and oceanic  
462 islands. Future research is needed to understand whether this spatial distribution could be due, or  
463 not, to the dispersal potential of evolutionarily distinct species (Gillespie et al. 2012).

464 The patterns we found regarding the range-restriction of the most functionally distinct monocots  
465 are opposite to the patterns of the most evolutionarily distinct species. On average, highly  
466 functionally distinct monocots were found only on a small number of islands, which is congruent  
467 with studies showing that rare functions are usually supported by rare species (Mouillot et al.  
468 2013). Yet, using null models, we found that insular endemic monocots with the highest FD  
469 scores are not significantly more range-restricted than less distinct species. Violle et al. (2017)  
470 recently proposed a multifaceted framework for defining “functional rarity” by combining

471 characters pertaining to functional distinctiveness and range restriction. Within their framework,  
472 12 forms of functional rarity are possible, such as widespread species with distinct traits, as we  
473 found here. By contrast to the most evolutionarily distinct endemic monocots, functionally  
474 distinct endemic species occur on oceanic, remote and glaciated islands, which are patterns  
475 suggesting that functionally distinct species experience long-distance dispersal. The relationships  
476 between island features, plant distinctiveness and spatial range provide some insights into the  
477 role of species dispersal in range restrictions of the most evolutionarily and functionally distinct  
478 species. However, reconstructing dispersal events is complex and further research would be  
479 needed. In particular, investigating dispersal vectors and modes of distinct species as well as the  
480 influence of environmental and dispersal filtering could provide further insights on the  
481 distribution of species distinctiveness on islands (e.g. Heleno and Vargas 2015; Fajardo et al.  
482 2019).

### 483 ***Implications for conservation***

484 Highly evolutionarily distinct species capture large amounts of evolutionary history (or  
485 phylogenetic diversity [PD]) and highly functionally distinct species represent some rare  
486 functional trait values shared with few others. From a conservation perspective, this implies that  
487 the loss of highly distinct species will directly lead to the loss of some irreplaceable ecosystem  
488 functions and evolutionary branches (e.g. Leclerc et al. 2020). Preserving phylogenetic diversity  
489 is considered as a proxy for the conservation of the variety of species features (Faith 2018), and  
490 is associated with option values from benefits provided by biodiversity to people and nature  
491 (Faith 2016). The Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem  
492 Services adopted Phylogenetic Diversity as the indicator of the “maintenance of options”  
493 provided by feature diversity for future generations ("Nature’s Contributions to People" category

494 number 18; Díaz (2019)). This PD indicator was further developed by the IUCN Species  
495 Survival Commission Phylogenetic Diversity Task Force, now focusing on the conservation of  
496 evolutionary distinct species, in a formulation destined to be easily disaggregated into regional  
497 and national scales (Gumbs et al. 2021). It is presently being considered to be integrated as a  
498 Headline or Component Indicator in the Post-2020 biodiversity framework (sbstta-24-03-add1).  
499 However, feature diversity captured by evolutionary diversity should be distinguished from  
500 functional trait diversity, as phylogenetics does not “magically make inferences about every  
501 favourite character” (see above and the discussion in Faith (2018) and Owen et al. (2019)). In  
502 this study, we considered only six plant traits so that the functional distinctiveness scores  
503 estimated here are not fully representative of the plant feature diversity that is captured by  
504 evolutionary diversity and which is linked to the maintenance of option-values. However, these  
505 six traits are fundamental features pertaining to the ecological strategies of plants and it is  
506 expected that the loss of species with distinct ecological strategies may have very different  
507 consequences from the loss of species with common ecological strategies (Cooke et al. 2020).  
508 From a conservation perspective, the FD and ED scores we measured are therefore  
509 complementary.

510 An important consideration for conservation is that, among insular endemics, those with high  
511 distinctiveness could be threatened with extinction. Especially because the most evolutionarily  
512 distinct endemic species are found on a very low number of islands and their range-restriction  
513 may be the sign of a higher extinction probability (e.g. Harnik et al. 2012). Species occurring on  
514 islands are among the most vulnerable on Earth due to the combined effects of human-induced  
515 threats, species naiveté, short distribution ranges, unique species interactions, low functional  
516 redundancy and/or low population sizes (Caesar et al. 2017; Leclerc et al. 2018). In addition,

517 according to the age-dependent extinction hypothesis, whereby long-branches on the Tree of Life  
518 are more likely to be lost (Warren et al. 2018), the most evolutionarily distinct species may be at  
519 a higher risk of extinction depending on how ancient they are. The most functionally distinct  
520 monocots were not more geographically range-restricted than other species, although they were  
521 distributed across a small number of islands. A recent study showed that insular mammals and  
522 birds threatened by cultivation and wildlife exploitation support unique and extreme functions  
523 and are therefore functionally irreplaceable (Leclerc et al. 2020). In plants, although some studies  
524 investigated the impact of several threats on functional diversity (e.g. Flynn et al. 2009), we do  
525 not know studies that directly investigated the risks of loss of the most functionally distinct  
526 species (but see Grenié et al. (2018) for an example with corals and Loiseau et al. (2020) for  
527 birds and mammals). Further assessment of extinction risks, such as the ones performed by  
528 IUCN, would therefore be needed to understand the extent to which the most functionally  
529 distinct species are threatened. This would allow to explore the consequences on functional  
530 diversity in the event of their extinction.

531 Based on the IUCN threat status, conservation programs for the most evolutionarily distinct and  
532 threatened species do exist (the EDGE program of the Zoological Society of London; Isaac et al.  
533 2007), but not for functionally distinct species. Concerning plants, the EDGE program has  
534 recently added gymnosperms to their list, but not angiosperms as of yet (Forest et al. 2018). We  
535 would argue that insular endemic species with high ED and FD could contribute to a global list  
536 for the conservation of the evolutionary heritage and functional diversity of monocots.

537  
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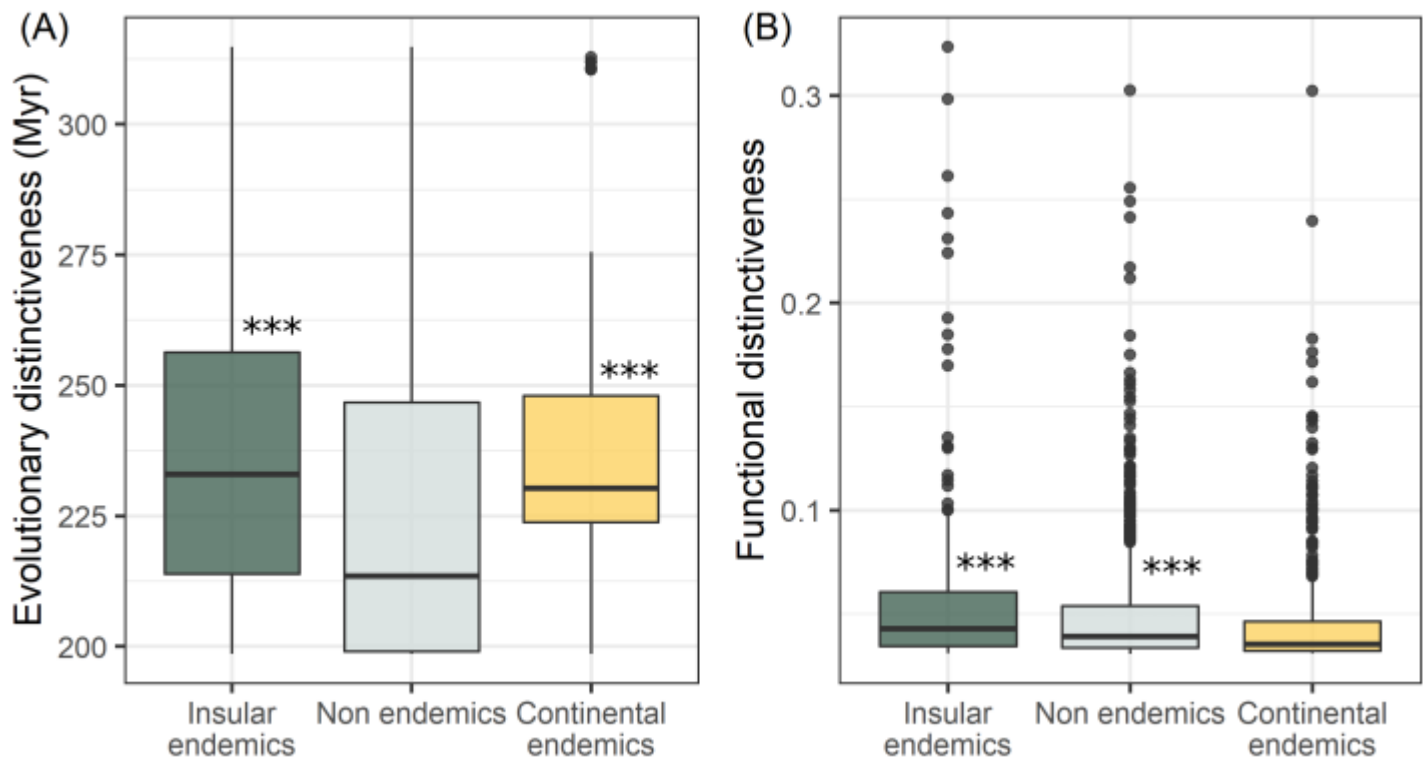
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## Fig. captions

**Fig. 1:** Box plots for (A) evolutionary and (B) functional distinctiveness of monocotyledons including insular endemic, non-endemic and continental species. Species evolutionary distinctiveness scores were calculated for each of 6,682 species from the phylogenetic tree (in millions of years) and functional distinctiveness scores were calculated for a subset comprising 2,581 species for which trait data was available (unitless). Average evolutionary distinctiveness was significantly higher than expected by chance for insular endemics and continental endemics; average functional distinctiveness was significantly higher than expected by chance for insular endemics and for species occurring on both islands and continents ( $P < 0.001$ , \*\*\*)

## Fig.1





## Tables

**Table 1:** Main assumptions regarding the influence of nine islands features on dispersal potential and geographical range restriction.

<i>Island characteristics</i>	<i>Assumption regarding its relation to dispersal</i>	<i>Data references</i>	<i>Measurement when a polygon is composed of several islands*</i>
<i>Distance from the continent (km)</i>	Colonization events may be less frequent toward/from distant islands (MacArthur and Wilson 1967)	Global Island Database (GID; UNEP-WCM 2013)	Minimum distance to the continent over all islands
<i>Proportion of surrounding landmass (SLMP)</i>	Colonization events may be less frequent toward/from isolated islands (MacArthur and Wilson 1967)	Weigelt et al. (2013)	Average SLMP
<i>Elevation (m)</i>	Elevation may provide a climatic refuge for ancient lineages that may presently rarely disperse (Steinbauer et al. 2016)	Weigelt et al. (2013)	Average elevation

<i>Area (m<sup>2</sup>)</i>	Successful colonization events may be more likely toward/from large islands (MacArthur and Wilson 1967)	GID (UNEP-WCM 2013)	Mean of areas over all islands
<i>Oceanic or Continental</i>	Oceanic islands were initially void of life and species settled through colonization whereas continental islands already harboured species assemblages when they fragmented.	Weigelt et al. (2013)	The most frequent type of island is retained
<i>Glaciated or non-Glaciated</i>	If glaciation led to local extinctions of most plant species on an island, then dispersal after glaciation may account for the current presence of ancient species on an island that underwent glaciation (e.g. Alsos et al. 2005)	Gillespie and Clague (2009); Will Iles pers. Comm (12/2018).	The most frequent feature is retained
<i>Age (millions of years)</i>	On young islands the occurrence of ancient endemics may be due to dispersal events (from continents, or inter- or intra-archipelago) (Emerson and Gillespie 2008) but see (Heads 2018))	Gillespie and Clague (2009); Will Iles pers. com.(12/2018)	Minimum age over all islands
<i>Latitude (decimal degrees)</i>	A variable used to account for a potential spatial effect	GID (UNEP-WCM 2013)	Latitude of the centroid
<i>Longitude (decimal degrees)</i>	A variable used to account for a potential spatial effect	GID (UNEP-WCM 2013)	Longitude of the centroid

\*Maximum elevation, average area and minimum age were not accounted for due to correlations with other variables

**Table 2:** Average number of islands per type (functional or evolutionary) and class (from very low to top distinct species) of distinctiveness for insular endemic species. In some cases, the average number of islands is significantly lower (red cells) or higher (blue cells) than expected by chance. Randomization procedure consisted in randomizing species among classes 1,000 times and estimated whether the observed mean number of islands where species occurred per distinctiveness class was lower than in the randomized set. Distinctiveness subsets “top distinctiveness”, “high distinctiveness”, “moderate distinctiveness”, “low distinctiveness”, “very low distinctiveness” correspond to the 5%, 25%, 50%, 75% and >75% of the distinctiveness score distribution, respectively. These scores were estimated over 6,682 monocot species for ED and 2,581 monocot species for FD.

	Top distinctiveness	High distinctiveness	Moderate distinctiveness	Low distinctiveness	Very Low distinctiveness
Evolutionary Distinctiveness	1.7	1.7	2.1	2.0	1.8
Functional Distinctiveness	3.2	2.4	1.7	1.8	1.8

**Table 3:** The effect and relative importance of selected island features estimated from multi-model selection on evolutionary and functional distinctiveness of endemic species. \*\*\*:  $P < 0.001$ ; \*\*:  $P < 0.01$  ; \*:  $P < 0.05$  ; •:  $P < 0.1$ . Summed AICc weights ( $\Sigma w_i$ ) indicate the relative importance of each variable. SLMP= Surrounding Landmass Proportion; GMMC= connection to the mainland during the last glacial maximum.

Evolutionary distinctiveness			Functional distinctiveness		
<i>Estimate</i>	<i>Pr(&gt;z)</i>	$\Sigma w_i$	<i>Estimate</i>	<i>Pr(&gt;z)</i>	$\Sigma w_i$

<b>SLMP</b>	-4.2	.	0.62	0.33	***	1
<b>Distance</b>	-2.6	*	0.89	0.049	**	0.98
<b>Area</b>	0.62		0.28	-0.083	***	1
<b>Elevation</b>	-6.3	***	1	0.029		0.42
<b>Age</b>	5.1	**	0.98	NA		
<b>GMMC</b>	7.07	***	1	-0.22	***	1
<b>Glaciated</b>	-5.9	***	1	0.081	***	1
<b>Latitude</b>	-6.79	***	1	-0.26	***	1
<b>Longitude</b>	-4.25	**	0.79	0.084	***	1
<b>Latitude:SLMP</b>	7.21	***	1	0.01		0.25
<b>Latitude:Age</b>	1.53		0.29	-0.14	***	1

## Electronic supplementary material

*Appendix 1: Sensitivity analysis*

*Appendix 2: ED and FD scores of each species*

*Appendix 3: Phylogenetic analyses of variance*

*Appendix 4: Range restriction and distinctiveness of non-endemic insular species.*

*Appendix 5: Spatial patterns of distinctiveness in islands*

## Declarations

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## Author’s contributions:

The authors’ interest is the multiple facets of biodiversity on islands. All authors work on projects investigating phylogenetic and functional diversity on a global scale. RP, TH, MM and SV conceived the project, and obtained the research funds. All authors contributed to the manuscript

and gave final approval for publication. SV, RG and TH collected the data. SV analysed the data. SV and AK prepared the figures. MM and RP are co-senior authors.

**Conflict of Interest/Competing interests:** The authors declare that they have no conflict of interest.

**Ethics approval:** Not applicable for that section

**Consent to participate:** Not applicable for that section

**Consent for publication:** Not applicable for that section

**Code availability:** Analyses were performed with R (R Core Team 2020)

**Availability of data and material:**

The datasets used and/or analysed during the current study are available from the corresponding author on reasonable request