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*Ecology/Ecological Monographs/Ecological Applications*

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1 Mammalian phylogenetic diversity-area relationships at a continental scale

2

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27

28    Running title: **Phylogenetic diversity-area relationship of mammal diversity**

29

30    Number of words:

31              Abstract: 292

32              Main body: 3000

33

34    Number of references: 48

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36 **Abstract**

37

38 In analogy to the species-area relationship (SAR), one of the few laws in Ecology, the  
39 phylogenetic diversity-area relationship (PDAR) describes the tendency of phylogenetic  
40 diversity (PD) to increase with area. Although investigating PDAR has the potential to  
41 unravel the underlying processes shaping assemblages across spatial scales and to predict PD  
42 loss through habitat reduction, it has been little investigated so far. Focusing on PD has  
43 noticeable advantages compared to species richness (SR) since PD also gives insights on  
44 processes such as speciation/extinction, assembly rules and ecosystem functioning. Here we  
45 investigate the universality and pervasiveness of the PDAR at continental scale using  
46 terrestrial mammals as study case. We define the relative robustness of PD (compared to SR)  
47 to habitat loss as the area between the standardized PDAR and standardized SAR (i.e.  
48 standardized by the diversity of the largest spatial window) divided by the area under the  
49 standardized SAR only. This metric quantifies the relative increase of PD robustness  
50 compared to SR robustness. We show that PD robustness is higher than SR robustness but  
51 that it varies among continents. We further use a null model approach to disentangle the  
52 relative effect of phylogenetic tree shape and non random spatial distribution of evolutionary  
53 history on the PDAR. We find that for most spatial scales and for all continents except  
54 Eurasia, PDARs are not different from expected by a model using only the observed SAR and  
55 the shape of the phylogenetic tree at continental scale. Interestingly, we detect a strong  
56 phylogenetic structure of the Eurasian PDAR that can be predicted by a model that  
57 specifically account for a finer biogeographical delineation of this continent. In conclusion,  
58 the relative robustness of PD to habitat loss compared to species richness is determined by  
59 the phylogenetic tree shape but also depends on the spatial structure of PD.

60

61    **Keywords:** species area-relationship, strict nested design, null models, phylogenetic

62    **diversity**



63 **Introduction**

64

65 The species area relationship (SAR) describes the tendency of species richness (SR) to  
66 increase with area (Rosenzweig 1995). This relationship is documented for a wide range of  
67 taxonomic groups and ecosystems (Guilhaumon et al. 2008, Triantis et al. 2012) and its  
68 understanding is central to ecology and conservation biogeography (Rosenzweig 1995,  
69 Whittaker et al. 2005). For instance, the SAR is a key tool to estimate species extinctions  
70 from habitat destruction and climate change (Pimm and Raven 2000, Thomas et al. 2004,  
71 Pereira et al. 2010, Matias et al. 2014). Nevertheless a SAR approach reduces biological  
72 diversity to species richness only and fails to include the amount of evolutionary history in  
73 species assemblages (Mouquet et al. 2012). To fill this gap, the Phylogenetic Diversity Area  
74 Relationship (PDAR hereafter; Morlon et al. 2011) can help unravel the processes assembling  
75 communities across spatio-temporal scales and provides complementary tools for conserving  
76 the Tree of Life (Mazel et al. 2014). For instance, translating SAR into PDAR allows to  
77 predict the loss of PD through habitat destruction. This prediction is essential since the loss of  
78 a given amount of PD or the loss of an entire lineage could have strong negative ecological  
79 consequences since distinct lineages are likely to perform different functions (Cadotte et al.  
80 2008, Mouquet et al. 2012).

81

82 Several mechanisms have been proposed to explain the SAR, such as sampling effects  
83 (Rosenzweig 1995), the effect of habitat size on extinction rates (MacArthur and Wilson  
84 1967), the scaling of environmental heterogeneity with area (Kadmon and Allouche 2007) or  
85 dispersal limitation (Hubbell 2001). In complement to the SAR, the PDAR brings unique  
86 information about the different processes structuring biodiversity at different spatial scales,  
87 helping, for example, to quantify the effects of biotic interactions at small scales versus

88 biogeographical processes at large scale. A particular feature of the PDAR is that the shape of  
89 the phylogenetic tree ultimately drives its relative position to the SAR. A star phylogeny  
90 would produce a PDAR proportional to the SAR, while a complete and recent polytomy at  
91 the tips of the tree would produce an extreme PDAR that would reach its maximum from the  
92 smallest area (see Figure 1.A). In addition to those mechanisms, biogeographic history  
93 together with ecological processes should also influence the PDAR (see Fig. 1.B). Allopatric  
94 speciation and/or competition between close relative species would result in a relatively  
95 higher PD than expected for a given SR ('overdispersion'; Webb et al. 2002, O'Dwyer et al.  
96 2012). Coexistence theory indeed predicts that similar species will compete more strongly  
97 than dissimilar species, leading to the exclusion of one of the similar species  
98 (HilleRisLambers et al. 2012). If we assume that niche differences are properly portrayed by  
99 phylogenetic differences, we predict a phylogenetic overdispersion (i.e. distantly related  
100 species co-occur) under competitive interactions (Webb et al. 2002, but see Mayfield and  
101 Levine 2010). Reciprocally, low PD may be expected if close relative species tend to co-  
102 occur because of shared environmental niches and/or geographic isolation of land mass  
103 (phylogenetic clustering; Webb et al. 2002, O'Dwyer et al. 2012, see Fig. 1.B). Overall the  
104 difference between SAR and PDAR curves is thus very informative on the way the  
105 phylogenetic structure of assemblages varies across spatial scales.

106 In summary the PDAR is ultimately influenced by (1) the shape of the SAR that depends on  
107 species range placement over space (e.g. either 'clumped' or random), (2) the structure of the  
108 phylogenetic tree and (3) the species range placement in regards to the phylogeny (that  
109 ultimately depends on eco-evolutionary processes). Since the pioneering work by Morlon et  
110 al. (2011), that first introduced PDAR, no study has tried to explain large scale PDARs and to  
111 disentangle the relative influence of these three factors.

In this paper we report the first large-scale analysis of PDAR over the globe for mammal assemblages. We used the calibrated and dated ultrametric phylogenetic tree updated by Fritz et al. (2009) from Bininda-Emonds et al. (2007). We extracted the distribution maps provided by the Mammal Red List Assessment (<http://www.iucnredlist.org/>) for 4616 terrestrial species to obtain occurrence data on worldwide grid cells of approximately 110\*110 km and used a strictly nested design recently published (SNQ; Storch et al. 2012) to produce median SAR and PDAR at a continental scale (i.e. we computed median SR and PD over each spatial scale to produce median SAR and PDAR respectively). First we ask whether PDAR differs from the SAR at a continental scale and how this difference may affect the robustness of PD to habitat loss. To do so we define the relative robustness of PD (compared to SR) to habitat loss as the area between the standardized PDAR and standardized SAR (i.e. standardized by the diversity of the largest spatial window) divided by the area under the standardized SAR only (named ‘relative Area Under the Curve’,  $AUC_r$ ). This metric quantifies the relative increase of PD robustness compared to SR robustness (Fig. 2). Second, we ask whether PDARs is a simple consequence of the observed SAR and a random sampling of species on the phylogenetic tree or if it also depends on eco-evolutionary processes. Assuming that the continental SAR for mammals can be adequately modelled by a random placement model of species ranges (Storch et al. 2012), we derive PDAR expectations that only rely on the phylogenetic tree shape. To do so we use a tip-shuffling null model that keeps the observed species range distribution, SAR and phylogenetic tree shape while shuffling the phylogenetic relationships among species. Third we ask whether  $AUC_r$  depends on the phylogenetic tree shape only (see Fig. 1.A) or if it is also an outcome of eco-evolutionary processes (see Fig. 1.B). To do so we take advantage of our null model approach to produce null  $AUC_r$  expectations. More specifically we estimate the effect of tree structure (see Fig. 1.A) on the relative robustness of PD to habitat loss across continents. Our analyses confirm that PD

137 might be more robust than SR to habitat loss but that this higher robustness differs across  
138 continents for different reasons.

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140 **Methods**

141 **1. Datasets and diversity metrics**

142 We used the distribution maps provided by the Mammal Red List Assessment  
143 (<http://www.iucnredlist.org/>) for 4616 terrestrial species to obtain occurrence data on  
144 worldwide grid cells of approximately 110\*110 km. The best resolution to use the IUCN  
145 maps is still under discussion in the literature (Storch et al. 2012, Jenkins et al. 2013). We  
146 here used the resolution commonly used at global scale (Belmaker and Jetz 2011, Storch et  
147 al. 2012). This was our basic unit to construct SAR and PDAR. Domestic, aquatic and semi  
148 aquatic mammals were excluded from the analysis.

149 We used the calibrated and dated ultrametric phylogenetic tree updated by Fritz et al. (2009)  
150 from Bininda-Emonds et al. (2007) .

151 To characterize the PD of an assemblage we used the Faith's measure (Faith 1992). This  
152 metric represents a 'richness' or 'volume' of diversity (Pavoine and Bonsall 2011) and  
153 simply sums up branch lengths of the given species assemblage phylogeny (Rodrigues and  
154 Gaston 2002). Faith's measure is an intuitive and relatively simple measure of PD. It is also,  
155 by construction, generally highly correlated with SR (Huang et al. 2012, Tucker and Cadotte  
156 2013). The use of any PD metric theoretically linked with SR in the description of PDAR has  
157 been criticized because PDAR would be biased by "spurious artefacts of a statistical  
158 relationship between species richness and area "(Helmus and Ives 2012). Here the  
159 comparison of the SAR and the PDAR we propose, i.e. with the standardisation and the null  
160 model that removes the effect of SR on PD (see section describing our null model approach)  
161 avoid this artefact while it allows a simple interpretation of the results.

162

163 **2. Constructing SAR & PDAR**

164 Median and Median absolute deviance (MAD) of SR/PD were reported for each spatial scale  
165 (from 110\*110 km up to 2200\*2200 km) by using the framework proposed by Storch et al.  
166 (2012). We do not use mean SR and PD as the data was highly non-normal (see Appendix A  
167 for examples of distributions of diversity). It uses a strictly nested quadrat design where a  
168 moving window (Leitner and Rosenzweig 1997, Lennon et al. 2001) reports the SR/PD of all  
169 possible windows of a given size within a continent. The median and MAD of SR/PD are  
170 then computed for each spatial scale. This procedure implies that some cells are counted  
171 several time for a given spatial windows and thus some pseudo-replication is inevitably  
172 introduced. Nevertheless all designs have their own drawbacks and SNQ have several  
173 important advantages (Storch et al. 2012). We implemented the algorithm within a reduced  
174 subset of the five continents (see Appendix B for further details) to avoid some border effect:  
175 i.e. for each scale (whatever its size) all pixels of the selected area of the continent will be  
176 sampled at least one time. The spectrum of spatial scale analysed was set between 1\*1 to  
177 14\*14 cells for Australia (i.e. from approximately 110\*110 km to 1540\*1540 km) and from  
178 1\*1 to 20\*20 cells for North and South America, Africa and Eurasia (i.e. from approximately  
179 110\*110 km to 2200\*2200 km) following Storch et al. (2012). Note that the resulting curve  
180 corresponds to a type I curve in the terminology proposed by Scheiner (2003).

181

### 182 **3. Analysing SAR & PDAR**

#### 183 *3.1. Comparing the relative shape of SAR & PDAR*

184 We compared the shape of PDAR and SAR using two complementary approaches. First we  
185 fitted a power model (Rosenzweig 1995) to each SAR and PDAR. We then reported the slope  
186 (z) value of the linear model in a log-log space. These values were then used to depict in a  
187 simple way the relative shape of PDAR and SAR. Because PDAR and SAR are not  
188 necessarily best modelled by a power function (Guilhaumon et al. 2008, Mazel et al. 2014)

189 we also (1) fitted alternative statistical models (see Appendix C) and (2) directly compared  
190 PDAR and SAR without an a-priori function. As PD is expressed in units of times while SR  
191 in number of species, they are not directly comparable. Therefore we used a basic  
192 standardization procedure by rescaling each sampling windows PD/SR value by the value  
193 reached at the maximum sample size (Mazel et al. 2014). This gives a relative diversity value  
194 for each sampling windows, compared to the largest one (that thus represents 100%). We  
195 define the relative robustness of PD (compared to SR) to habitat loss as the area between the  
196 standardized PDAR and standardized SAR divided by the area under the standardized SAR  
197 only (eq. 1 and Fig. 2).

$$198 AUCr = \frac{AUC_{PDAR} - AUC_{SAR}}{AUC_{SAR}} \quad \text{Eq. 1}$$

199 If we define the absolute robustness of PD/SR as the AUC under the PDAR/SAR, our metric  
200 quantifies the relative increase of absolute PD robustness compared to absolute SR robustness  
201 (Fig. 1). To study the relative increase of PD and SR with area we simply computed the local  
202 slope (or derivative) of PDAR & SAR on the standardized coordinates assuming a first point  
203 of null diversity and area. Indeed when area tends to zero, diversity also necessarily tends to  
204 zero (as sampled area becomes smaller than a single individual).

### 205 3.2. Understanding the absolute value of PDAR

206 Second we used a null model approach to describe and investigate the absolute value of  
207 PDAR. This approach allows to compare null expectations with the observed PDAR and  
208 avoids the bias caused by the correlation between PD and SR.  
209 We chose to use the observed SAR as a starting point because it has already been shown to be  
210 modelled by a simple null model where species ranges are randomly distributed within the  
211 continent (Storch *et al.* 2012). Assuming the SAR, we computed a null PDAR expectation by  
212 randomly shuffling the tips of the phylogeny within a given pool of species. This procedure  
213 breaks the link between species range size/position and phylogenetic relationships but keep

unchanged the distribution of range size and the local species richness (Hardy 2008). By repeating this procedure  $n$  times (see below), we were able to assess the significance of the observed PDAR relative to our null expectation (using a two-sided test).

In other words, for each randomization, we (1) shuffled the tips of the phylogeny within a given species pool (see below). The resulting randomized phylogeny was used to (2) compute null PD values for each basic grid cells (approximately 110\*110 km) and we (3) applied the methodology described above to compute the resulting null median and MAD PDARs. Such null model may help unravel the determinants of the PDAR. For example we may expect competition (Pigot and Tobias 2013) or environmental filtering to occur at smaller scale, potentially leading to phylogenetic overdispersion or clustering respectively (Webb et al., 2002; but note that competition may also lead to clustering, see Mayfield & Levine, 2010). Also, phylogenetic clustering could be detected at larger scales because of biogeographical effect (Rosenzweig 1995). We used two null models that use either a (1) continental or a (2) biogeographic pool of species. We restricted the analysis of the biogeographic pool of species for Eurasia only because it is the only continent in our design that is a mix of distantly related zoogeographic regions (Wallace 1876, Holt et al. 2013).

### 230 **(1) Continental pool of species**

231 This null model simply shuffles the tips within the entire continental phylogeny. The  
232 significance of the observed values of PDAR was assessed by comparing observed values  
233 with 1000 randomized PDARs. We further confirmed this simulation approach by using  
234 analytical expectations of PD based on the framework of Nipperess and Matsen (2013,

235 Appendix D)

### 236 **(2) Biogeographical pool of species**

237 First we defined zoogeographic regions following the methodology of Holt et al. (2013). To  
238 do so we computed phylogenetic beta diversity values between each pair of grid cells from

239 the Eurasian continent by using an index independent of species richness (Lennon et al. 2001,  
240 Holt et al. 2013):

$$241 \quad \beta = 1 - \frac{a}{\min(b, c) + a} \quad (\text{Eq. 1})$$

242 where  $a$  = the branch lengths shared by the two grid cells and  $b$  and  $c$  represent the branch  
243 lengths unique to each grid cell.

244 Then we identified group of grid cells (=zoogeographic regions) using the unweighted pair  
245 group method with arithmetic mean (UPGMA, function *hclust* in R; R Development Core  
246 Team 2014). We varied the number of delimited zoogeographic regions from 1 to 30 (see  
247 Appendix E for examples). We then used these regions to construct a biogeographical null  
248 model of the PDAR. While we were shuffling species within the entire continental pool of  
249 species in the previous null model, we shuffled here species within the pool of species  
250 belonging to a specific zoogeographic region. Because all species are not restricted to one  
251 unique zoogeographic region, we adopted a probabilistic approach where, for each  
252 randomization independently, a zoogeographic region  $k$  is assigned to a species  $i$  with a  
253 probability of  $P_{i,k}$  depending on its coverage  $C_{i,k}$  in this region with respect to its total  
254 coverage across all regions:

$$255 \quad P_{i,k} = \frac{C_{i,k}}{\sum_k C_{i,k}} \quad (\text{Eq. 2})$$

256 where  $K$  represents the entire set of regions (from 2 to 30). For each randomization, we  
257 computed a null PDAR and tested significance by comparing the observed PDAR and 100  
258 null PDAR for each number of zoogeographic regions defined.

259

260 **Results & Discussion**

261 To visually compare the PDAR and the SAR of mammals we standardized the two curves by  
262 the maximal diversity reached in the data set. The two resulting curves are thus expressed in  
263 % of maximal diversity and are directly comparable (Fig. 3). We show that PDARs approach  
264 their maximum faster than SARs for all continents (Fig. 3). To describe the rate of PD and  
265 SR accumulation as a function of area, we estimated local derivatives and show that PDARs  
266 accelerate much faster than SARs for small areas and that this tendency reverses for large  
267 areas (see subplots of Fig. 3). We show that the power model is among the best model to fit  
268 the dataset (Appendix F) but fails to model the upward acceleration of PD on a log-log scale  
269 (e.g. Fig. 4). The slope of the power model is lower for the PDARs than for the SAR ( $z_{PDAR} <$   
270  $z_{SAR}$ , see Appendix G). The last point has been previously reported at this scale (Mazel et al.  
271 2014) but with a different PDAR/SAR reconstruction based on non-overlapping ecoregions  
272 (Olson et al. 2001). This result is thus independent of the sampling procedure and  
273 approaches, and is, overall, not surprising. Indeed the SAR fully represents the PDAR in the  
274 case of a star phylogeny (in this case the PD is proportional to SR). As the phylogenetic tree  
275 departs from a star phylogeny (i.e. as some branches start to be shared between species), the  
276 relationship between PD and SR becomes concave and the PDAR deviates from the SAR  
277 (because redundancies between species are introduced, see Fig. 1.A).

278 As a consequence,  $AUC_r$  values are positives but we find that they differ across continents  
279 (see Fig. 2-3). The use of the SAR to predict species extinction from habitat loss (Pimm and  
280 Raven 2000, Thomas et al. 2004, Halley et al. 2014) has been questioned (He and Hubbell  
281 2011) but remains useful (e.g. Axelsen, Roll, Stone, & Solow, 2013; Hanski & Zurita, 2013;  
282 Matias et al., 2014), especially when species ranges are randomly distributed (He and  
283 Hubbell 2011). If we assume that the SAR and the PDAR can be used to predict the loss of  
284 species and PD, respectively, through habitat loss (Mazel et al. 2014), the  $AUC_r$  (Fig. 2) then

285 represents the relative robustness of PD (compared to SR) to habitat destruction. In this case,  
286 we show, for example, that the Australian PD will be relatively more robust –at the  
287 continental scale- than the Eurasian PD to habitat loss (note that at the global scale, the  
288 evolutionary history of Australia is particularly unique; Holt et al., 2013). This difference  
289 could be explained by the different structure of the two trees (see Fig. 1.A) and/or by  
290 different eco-evolutionary processes leading to a different spatial pattern of PD (e.g. either  
291 clustered, random or overdispersed; see Fig. 1.B). Teasing apart these two mechanisms called  
292 for using appropriate null models.

293 For all continents except Eurasia and for most of the spatial scales, we find that PD values are  
294 not significantly different from those obtained with the null model randomizing the  
295 phylogenetic relationships among species (Fig. 4 and Appendix H). This means that the only  
296 significant phylogenetic effect that influences the PDAR is the shape of the observed  
297 continental tree. Several non-mutually exclusive hypotheses can be proposed to explain this  
298 result. First, we use here an averaged phylogenetic structure across a whole continent and  
299 different assembly processes may have been mixed. In North America for example we could  
300 expect a phylogenetic clustering at high elevation in the Rocky Mountains (e.g. due to  
301 environmental filtering) while overdispersion could be found in the lowland forest (e.g. due  
302 to competition, Graham and Parra 2009), resulting in higher MAD of PD than expected by  
303 chance (see Appendix I). Such distribution may likely compensate each other during the  
304 sampling process, resulting in a null random distribution when averaged across assemblages.  
305 Second, the spatial and phylogenetic scale of our analysis is perhaps too large to detect any  
306 effect of repulsion/attraction of species. Indeed, at the smallest resolution we have used  
307 (110\*110 km), co-occurring species do not necessarily interact with each other (probably  
308 because this scale is still very large) and may, for example, use different habitats (Araújo and  
309 Rozenfeld 2014, but see Cardillo 2011). Also, specific group of mammals may show

repulsion or attraction while others not, blurring the overall pattern (see e.g. Pedersen et al. 2014). The Eurasian PDARs is however much lower than expected by chance at all spatial scales, indicating phylogenetic clustering (Fig. 4 and Appendix H). This continent is a mosaic of biogeographic realms with diverging biogeographic history (Wallace 1876, Holt et al. 2013) and thus mixes very different faunas: there are many strict Palearctic species (e.g. the wolverine, *Gulo gulo*) and strict oriental species (e.g. the asiatic elephant, *Elephas maximus*). The continental null model mixes all these faunas and thus tends to overestimate the expected median PD of assemblages. For example *Elephas maximus* represents the only afrotherian species present in our data set so it has a very high distinctiveness at the continental scale and will considerably increase relative local PD. We consequently develop a biogeographical null model that takes into account the historical origin of taxa. We show that this null model progressively decreases the random PD expectations (Fig 5) and that 15 realms were sufficient to correctly predict most of the spatial scale median PD and observed  $c$  value (Fig. 5 and Appendix J-K). Our approach may sound circular at first glance because we use spatial and phylogenetic data (to define zoogeographic regions) to explain spatial and phylogenetic data (the PDAR). Nevertheless the aim of any null models is rather to ask how much synthetic information we need from the initial data to parsimoniously explain this data. The null model is necessarily constrained by the initial data but if this constrain is too high (i.e. a lot of the initial data is used) the null model will necessarily be plausible (the “narcissus effect”; Gotelli 2001). Here our aim is to quantify how much synthetic information is needed to parsimoniously explain the Eurasian PDAR. Finally it is not directly possible to conclude from the biogeographic null model that the effect we detected is purely ‘historic’, i.e. that it derives from the mix of fauna due to continental drift. Indeed Eurasia has also a steep North-South gradient in term of climate (and SR) and we cannot reject the hypothesis of a

335 phylogenetic clustering due to environmental filtering (Webb et al. 2002). One potential  
336 future avenue could be to contrast the relative predictive power of biogeographic null model  
337 versus a climate based null model.

338 We also find that PD at small scale tends to be higher than expected by chance for South  
339 America (phylogenetic overdispersion, Fig. 4), leading to a significantly low  $z$  value for the  
340 PDAR ( $p < 0.005$ , Appendix H). This observation may result from allopatric speciation events  
341 and/or competition at the smallest scale (Pigot and Tobias 2013) but more work is needed to  
342 test these hypotheses. For Eurasia, on the contrary, we observe that small scale PD tends to  
343 be relatively lower than expected by chance (phylogenetic clustering, Fig. 4) leading to a  
344 significant high  $z$  value ( $p < 0.01$ , Appendix H). This could be a possible product of  
345 environmental filtering occurring only at small scale.

346 These last two results shed light on the discrepancy between observed and null  $AUC_r$   
347 (Appendix L). Indeed the robustness of PD to habitat loss depends on the structure of the  
348 phylogenetic tree (represented here by the null model mean expectation) and also on the  
349 spatial pattern of phylogenetic structure (represented by the departure of the observed PDAR  
350 from the mean null model, see subplots in Fig. 4). We indeed find that Australian observed  
351  $AUC_r$  is higher than predicted by the continental tree structure because small scale Australian  
352 PD tends to be relatively higher than expected by chance (see Appendix L), providing a  
353 buffer against the loss of PD. In contrast, observed Eurasia  $AUC_r$  is lower than expected by  
354 the tree shape (see Appendix L). This is because Eurasian PD is disproportionately low at  
355 small scale, reducing the area between the PDAR and the SAR compared to random  
356 expectations and thus being more vulnerable to habitat reduction. Overall, we demonstrate  
357 that the additional robustness of PD to habitat loss compared to species richness is  
358 determined by the phylogenetic tree shape but also depends on the spatial structure of PD.

359

360 **Acknowledgements**

361 FM would like to thank Loïc Chalmandrier for helpful discussions on null models and Petr  
362 Keil for discussions on the PDARs. The research leading to these results had received  
363 funding from the European Research Council under the European Community's Seven  
364 Framework Programme FP7/2007-2013 Grant Agreement no. 281422 (TEEMBIO). FM, WT  
365 & JR belong to the Laboratoire d'Écologie Alpine, which is part of Labex OSUG@2020  
366 (ANR10 LABX56).

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501

**Supplemental materials**

502

503 Appendix A. Distribution of species richness and phylogenetic diversity values.

504 Appendix B. Details on the grain and extant of the study

505 Appendix C. Alternative statistical models list and fitting procedure

506 Appendix D. Congruence between analytical and null model approach

507 Appendix E. The biogeographic species pool model: illustration of the clusters

508 Appendix F. Results from the multi-model fits

509 Appendix G. Power model parameters for observed median SARs and PDARs

510 Appendix H. Null C and Z values under the continental null model

511 Appendix I. Null and observed Median absolute deviation (MAD) of PDARs

512 Appendix J. Detailed results of the biogeographical null models

513 Appendix K. Null C and Z values under the biogeographical null

514 Appendix L. Null and observed AUC<sub>r</sub> for median PDAR/SAR

515 **FIGURES LEGENDS**

516 **Figure 1. Expected variation of the standardized PDAR given (1.A) different tree shapes**  
517 **and (1.B) different eco-evolutionary processes.** (A) The three standardized PDARs  
518 correspond to the three trees depicted above the graph. Note that the red PDAR also  
519 corresponds to the observed SAR as the red tree is a star phylogeny. (B) Different eco-  
520 evolutionary processes may change the PDAR if they act differently among spatial scales.  
521 We expect that competition and/or allopatric speciation may relatively increase the PD at  
522 small scale while environmental filtering and/or geographic isolation of biotas may relatively  
523 decrease the PD at small scale.

524

525 **Figure 2. Hypothetical example to quantify the relative robustness of PD (compared to**  
526 **SR) to habitat loss ( $AUC_r$ ) using PDAR and SAR.** The example shows how to quantify the  
527 relative PDAR shape by measuring the Area between the two curves (SR, PD and Area are  
528 expressed in %) and computing  $AUC_r$ .

529

530 **Figure 3. Observed rescaled median SARs and median PDARs.** For each continent, we  
531 report the SAR & the PDAR rescaled by the value of the maximum SR and PD respectively.  
532 The two curves are both expressed in percentage of maximum diversity and thus directly  
533 comparable. We also report the corresponding  $AUC_r$  values (see Fig. 2). In the lower-right  
534 corner subplots we show the corresponding local derivatives.

535

536 **Figure 4. Median PDARs obtained from the continental null model.** For each continent,  
537 the envelope corresponding to 1000 null continental PDARs is shown in black while the  
538 observed PDAR is in red. In the corner of each panel, we plot the relative rank of observed  
539 PD value within the null PD distribution as a function of log Area. For each spatial scale, it is

540 computed as the percentage of null PD values that are lower than the observed value (a value  
541 of 0.5 indicates that observed PD equals the median of the null distribution). The dashed lines  
542 correspond to a relative rank of 2.5% and 97.5%. When the computed relative ranks fall out  
543 of this 95% envelope, a \* is reported in the main panel (see Appendix 8 for the relative ranks  
544 associated with power model parameters).

545

546 **Figure 5. Median PDARs obtained from the Eurasian biogeographical null models.** The  
547 biogeographical null models shuffle the tips of the phylogeny according to biogeographical  
548 origin (see methods). We present the results from null models containing different numbers  
549 of biogeographical regions. The top panel presents the median PDAR obtained for different  
550 number of biogeographic regions (see legend). The four other panels represent the details of  
551 four biogeographic null models that used 1 (=continental null model), 2, 15 or 30  
552 biogeographic regions, respectively. The \* indicates if the relative rank of observed PD value  
553 within the null PD distribution is lower (or higher) than 0.025 (or 0.975) for a given area.

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