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**SUPPORTING INFORMATION****Global patterns in the divergence between phylogenetic diversity and species richness in  
terrestrial birds**

Alke Voskamp, David J Baker, Philip A Stephens, Paul J Valdes, Stephen G Willis

**Appendix S1***S1a) Choice of environmental covariates to explain rPD (PD relative to that expected from Species  
Richness)*

We selected several potential correlates for phylogenetic diversity (PD) using literature. PD reflects the evolutionary history of communities and can be used to detect the signature of important historical processes (Losos & Glor, 2003). Macro-ecological changes such as mass migrations (e.g. Great American Biotic Interchange; (Webb, 2006)) and extinctions can leave their signature in PD (Mooers & Heard, 1997) and potentially lead to mismatches between PD and Species Richness (SR). Areas of long-term climate stability, for instance, can serve as climate refugia (Keppel *et al.*, 2012) that might allow species to persist during periods of rapid climate change. Such regions have been found to correlate with species endemism and sometimes contain very old species lineages (Fjeldså & Lovette, 1997). The presence of those ancient lineages can lead to an increased relative PD (rPD; PD relative to that expected from SR) in these areas. We therefore included climate stability for each grid cell over time as potential correlate for PD. We explored the mean climate stability since the last glacial maximum (LGM) and the last interglacial period (LIG). The climate data were available on two different timescales. Data since the LGM (present to 20,000 years ago) were available in steps of 2000 years. Data since the LIG period (present to 125,000 years ago) were available in intervals of 4000 years. To represent overall palaeo-climate stability in each cell, we used temperature and precipitation data. We determined mean values of z-transformed temperature and precipitation

27 data in each relevant year. For each consecutive temporal transition, we estimated the mean  
28 Euclidean distance between temperature and precipitation in bivariate space. The mean of these  
29 Euclidean distances was our measure of overall palaeo-climatic stability. Additionally, we repeated  
30 the above calculations for each cell but used the maximum Euclidean distance for the two variables,  
31 since extreme events may drive extinction (Crowley & North, 1988; Parmesan, 2006). To estimate  
32 stability in temperature and precipitation individually over time, we calculated the standard  
33 deviation within each cell for both variables for each of the LIG and LMG climatic datasets. We  
34 considered temperature and precipitation separately, as well as jointly, as their importance may  
35 differ regionally.

36 Mountain ranges have the potential to limit extinctions by providing a high diversity of  
37 climates in a local area and, thus, providing localised climatic refugia. SR is especially strongly related  
38 to altitudinal range in warmer climates, where it creates a steeper gradient on a small scale (Janzen,  
39 1967; Ruggiero & Hawkins, 2008). Unsurprisingly, mountains harbour half of the currently recognised  
40 biodiversity hotspots (Kohler & Maselli, 2009), although this might be partly an artefact, due to  
41 lower human impacts in remote mountain regions (Joppa & Pfaff, 2009). Areas such as the northern  
42 Andes still harbour ancient lineages of arctic species which have persisted since the late Pliocene or  
43 early Pleistocene (Hughes & Eastwood, 2006) and could therefore potentially harbour a high Relative  
44 PD. Species in mountain ranges at lower latitudes as the tropical Andes and the Afro and Sino  
45 Himalayan montane regions, by contrast, are suggested to have undergone high rates of speciation  
46 (Fjeldså *et al.*, 2012). Relatively young mountain areas, such as the Himalayas, which are still rising a  
47 centimetre per year (Bilham *et al.*, 1997), and the central Andes, could contain recent species  
48 radiations (McGuire *et al.*, 2014). This could be reflected in a low Relative PD due to the occurrence  
49 of a great variety of closely related species.

50 Ecological transitions between ecosystems can be important zones of differentiation and  
51 speciation caused by species adaptations (Smith *et al.*, 1997). Those transition zones are well known  
52 to harbour high species richness and biodiversity (Odum, 1971) and have been related to genetic

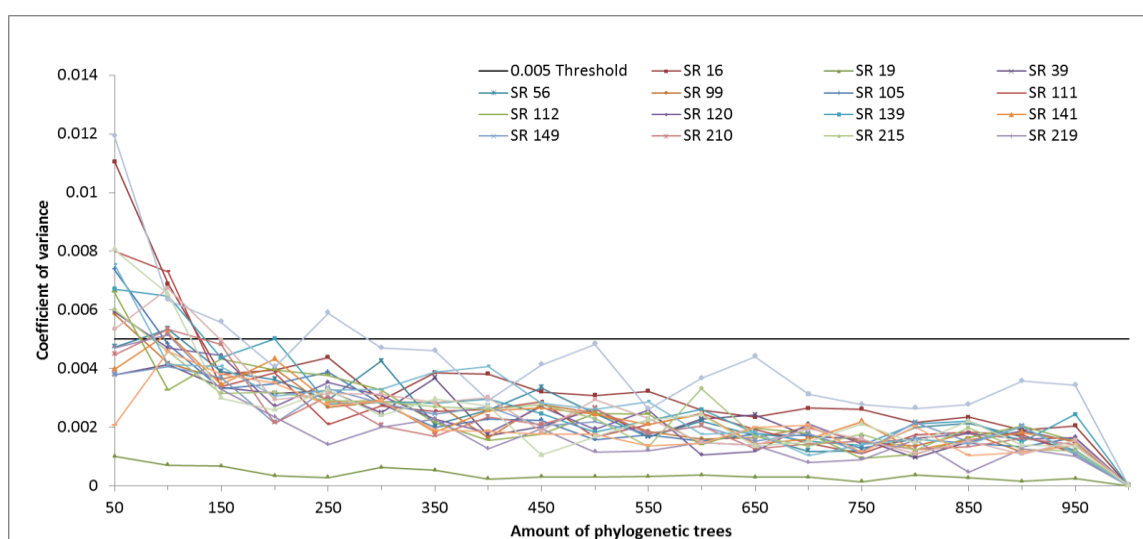
53 diversity within taxa (Petit *et al.*, 2003). They can accommodate species from two or more realms,  
54 each of which may have experienced very different evolutionary histories. Hence, such regions could  
55 potentially contain high Relative PD. However, high speciation rates have also been recorded in  
56 some ecological transition zones (Schilthuizen, 2000), which would result in a low Relative PD.

57 Habitat diversity was selected because SR has often been related to it. A study of South American  
58 breeding birds found that up to 51% percent of the variation in species richness could be explained  
59 by the number of ecosystems within a 1° grid cell (Rahbek & Graves 2001). We measured habitat  
60 richness as the number of habitats covering a minimum of 1% of a cell's area, using the USGS  
61 vegetation cover data, which comprises 24 different habitat types (U.S. Geological Survey, 2012). We  
62 do expect habitat diversity to affect SR rather than PD.

63

64 *S1b) Using a subset of the 10,000 available trees to estimate PD per cell*

65 Due to computational limitations we used of a subset of the 10,000 available trees. To determine  
 66 how many trees were necessary to produce a stable estimate of PD for a cell we undertook a pilot  
 67 analysis on 20 randomly chosen cells from across the world. The species richness for these cells  
 68 varied between 16 and 387 species per cell. We calculated PD values for each cell, using a random  
 69 subset of 1000 trees (Rubolini *et al.*, 2015) out of the 10,000 phylogenetic trees from Jetz *et al.*  
 70 (2012). We then calculated the change in the coefficient of variance of PD values per cell as more  
 71 trees were added. We determined that using 200 of 1000 trees resulted in a coefficient of variance  
 72 below 0.005 for 90% of the cells, i.e. the precision in PD increased to only a small extent if more than  
 73 200 trees were considered. Therefore, we subsequently calculated mean PD for all cells using 200  
 74 randomly chosen trees from the 10,000 available trees (*Figure S1*).

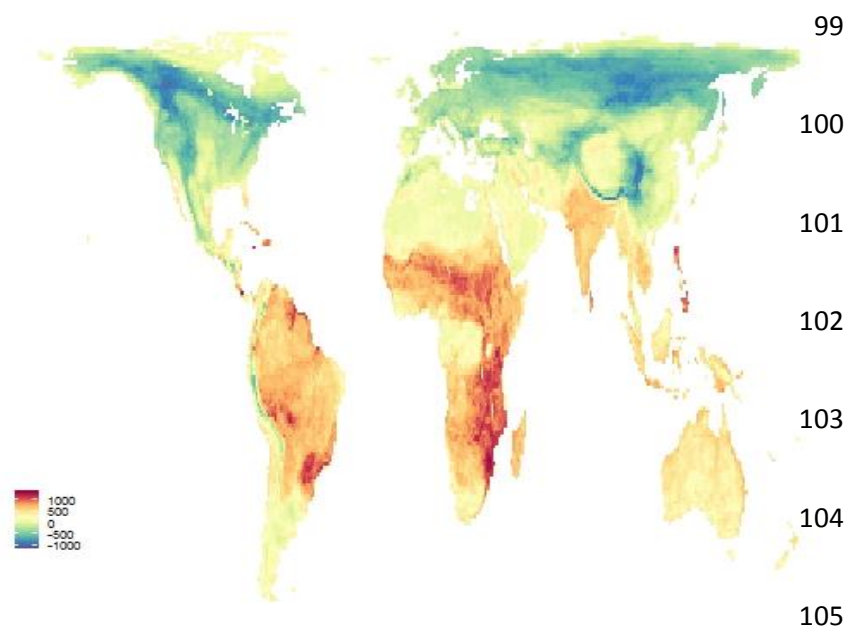


75  
 76 **Figure S1:** The coefficient of variation (for 20 randomly chosen grid cells) for PD plotted against the  
 77 number of trees used to calculate PD. The black line indicates the coefficient of variation threshold  
 78 of 0.005. Coloured lines and points represent data for individual cells. Cells had a SR between 16 and  
 79 219 species.

80

81 *S1 c) Alternative modelling method to investigate the relationship between SR and PD*

82 To analyse the relationship between species richness (SR) and phylogenetic diversity (PD) we used a  
83 locally weighted regression (LOESS). The method was chosen to make the results of this study  
84 comparable to previously published similar work (Fritz & Rahbek, 2012). It is assumed to be “akin to  
85 using the global relationship between species richness and phylogenetic diversity as a simple null  
86 model, in order to account for sampling effects arising from different levels of species richness  
87 among grid cells” (Fritz & Rahbek, 2012). Using this method it is difficult to disentangle potential real  
88 effects from sampling effects and there for the assumption that the modelled association reflects a  
89 null relationship could be untrue. The given rPD value for a grid cell is always relative to the  
90 surrounding values within the window of the LOESS regression. To double check the pattern of the  
91 residuals of the LOESS regression, we have split the data into five blocks based on their SR. We have  
92 fitted a generalized (Michaelis- Menten) saturating curve to a random data sample (n=1000) of each  
93 of the blocks and then predicted to the whole dataset. We repeated this process 50 times, taking  
94 new random samples each time. We then took the average residual value from the fitted curve for  
95 each grid cell. This gives us an average residual value for each grid cell that is not relative to only  
96 those grid cells with similar SR values but the whole dataset. We then compared the residuals of the  
97 LOESS regression (Figure S3) and the average residuals from the predictions of the generalized  
98 saturating curve (Figure S2).



106 **Figure S2:** The residuals of the generalized (Michaelis- Menten) saturating curve. Red indicating  
107 areas of unusually high PD given the SR and blue indicating unusually low PD given the SR.

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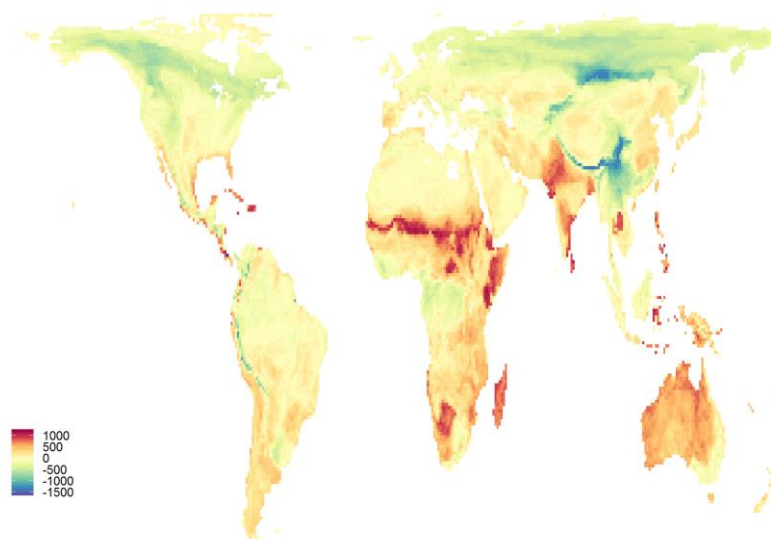
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116 **Figure S3:** The residuals of the LOESS regression. Red indicating areas of unusually high PD given the  
117 SR and blue indicating unusually low PD given the SR.

118

119 *S1d) Selecting the climate variable for the global and the realm model*

120 Several climate variables were highly correlated (Pearsons' correlation,  $r > 0.70$ ), so they were not  
121 used in combination to explain PD. Instead, we first sequentially produced models of PD including all  
122 potential response variables, but only one of the climate variables each time. For each combination  
123 of model explanators (i.e. each with a different climate variable) we used a model selection  
124 approach (Burnham & Anderson, 2002; Burnham *et al.*, 2011), calculating the mean AIC across a  
125 1000 random subsamples (using the AICcmodavg package in R; (Mazerolle, 2014). The random  
126 samples were drawn using the blocking method described in supplementary material S1e. The  
127 climate variable contained in the model set that had the lowest mean AIC were used for all  
128 subsequent modelling.



129 *S1e) Blocking method used to draw sub samples for the models*

130 To minimise potential effects of spatial autocorrelation in analyses of PD, we used a blocking method  
131 that divided the globe into 36 sub-blocks containing an equal number of cells. The 36 sub-blocks  
132 were divided into two groups in a checkerboard pattern (*Figure S4*). For modelling, we repeatedly  
133 drew random subsets of ten percent of the grid cells from each block, using blocks from only one of  
134 the two checkerboard groups each time (datasets were drawn equally from the two checkerboard  
135 groups). This resulted in approximately 1700 randomly selected cells being drawn broadly from  
136 across the globe, for each iteration of the global model.

137



138 **Figure S4:** The 36 blocks across three latitudinal bands used for data subsampling – see methods.

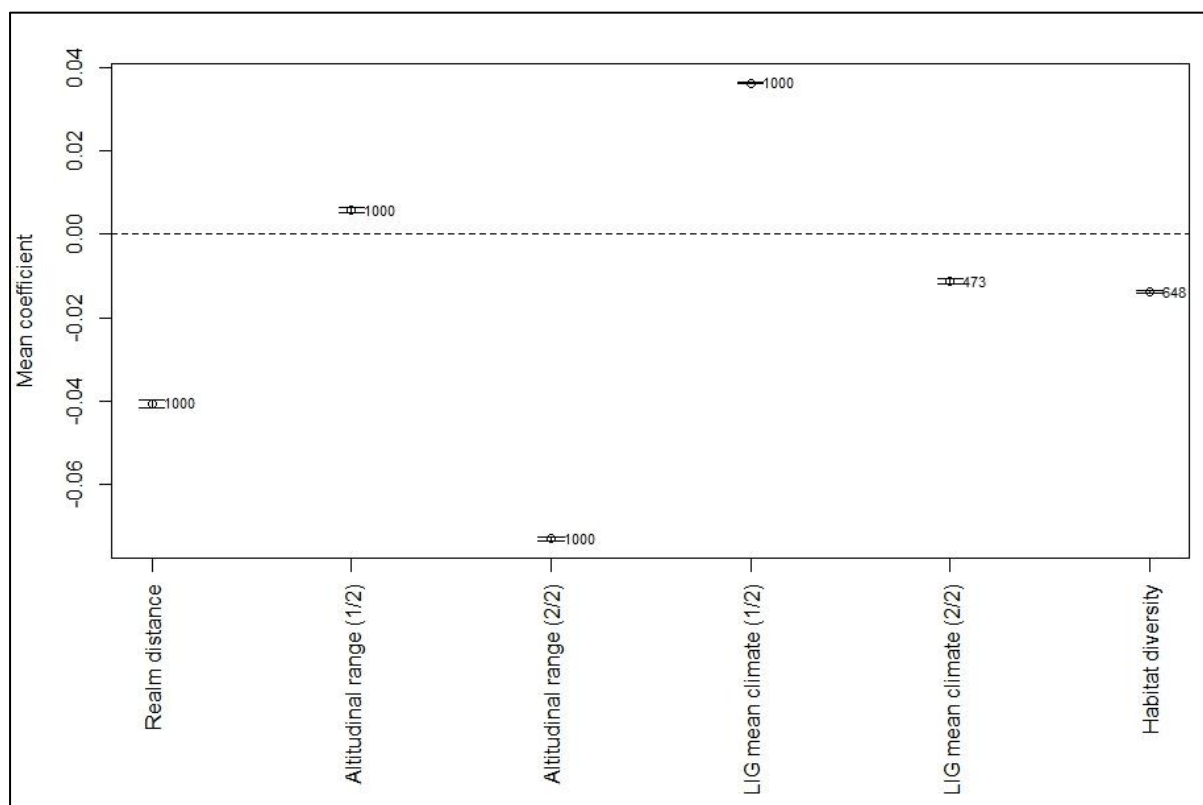
139 The blocks were divided in two groups using a checkerboard pattern.

140 *S1f) Selecting variables for the final model*

141 After selecting the best climate variable the full model was run over 1000 randomly selected subsets

142 and only those variables which were consistently in the best model were kept for the final model

143 (Figure S5)



144

145 **Figure S5:** The mean coefficients (+/- 95% confidence intervals) of the full global model including:

146 habitat diversity, neighbouring realm distance, altitudinal range, and mean climate stability (over

147 125 ka). Numbers alongside points indicate how often each variable was in the best model across

148 1000 randomly selected subsets of data. SR has been excluded from the graph to show the

149 coefficients of the other variables more distinct.

150

151 *S1g) Critical discussion of the used phylogeny*

152 The phylogeny by Jetz *et al.* (2012) has been focus of academic discussion due to the methods used  
153 to compose it. Using a previously defined backbone (which included 158 major bird clades in the  
154 case of the backbone based on Hacket *et al.* (2008) that we used) to define the tree's outline might  
155 result in restricted variation in higher order relatedness between avian species. It is possible that  
156 avian evolution might be better described by another tree (Ricklefs & Pagel, 2012), and amendments  
157 to phylogenetic trees are frequently proposed. Furthermore, the uncertainty around estimating  
158 branch length, inferred from time-dated trees (Venditti *et al.*, 2010), can introduce additional bias  
159 (Ricklefs & Pagel, 2012). Spatial differences in the degree to which bird populations are distinguished  
160 at the species level contribute another potential source of uncertainty. Areas such as North America  
161 and Europe, with finely distinguished populations, may contain artefactually inflated species  
162 diversification compared to areas with less resolved populations (Ricklefs & Pagel, 2012). All three of  
163 these sources of uncertainty could affect the total branch length calculated for a community and,  
164 therefore, affect the observed pattern of avian PD.

165

166 *S1h) Ongoing amendments to the avian taxonomy*

167 Research in the field of avian taxonomy is ongoing, and the rapid advances are demonstrated  
168 through recent amendments. For instance, the recently published genomes of 48 species  
169 representing all Neoaves by Jarvis et al. (2014), resulted in a rearrangement of some of the early  
170 branches in the tree of life. Since then, Prum et al. (2015) have published a comprehensive  
171 phylogeny, based on more species (198) but sampling only genetic regions rather than whole  
172 genomes. The latter contradicts some of Jarvis et al.'s (2014) findings, as with, for example, the  
173 splitting of Neoaves into five rather than two groups. Advances are also continuously made on  
174 subsets of the avian phylogenetic tree (e.g. Rocha et al. (2015)). Such work will inevitably lead to a  
175 more accurate tree of all living birds, which will refine the global geographic patterns of avian PD and  
176 rPD we observe. The backbone that we used in this study (Hackett et al. 2008) is broadly similar to  
177 the most recent phylogeny of Prum et al. (2015) for terrestrial birds (our focal species). Moreover,  
178 among the many possible trees that the phylogeny of Jetz (2012) produces, variance in PD resulting  
179 from applying different potential trees was small (Figure S6 Appendix S1i).

180

181 *S1i) Variance among the 200 phylogenetic trees sampled per grid cell*

182 We explored the variance around the derived PD values from the 200 randomly chosen phylogenetic  
183 trees per cell. Only 5% of the grid cells have a coefficient of variance of 0.06 or higher, these are  
184 mainly located in areas with very low species richness.



185

186 **Figure S6:** The coefficient of variation for the mean PD derived from the 200 trees within each grid  
187 cell. Dark blue indicating cells with a low coefficient of variation, light blue areas indicating a higher  
188 coefficient of variation.

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