

## Supplementary Methods

### *Diversification, speciation and latitude in New World birds*

Figure 4A revisited the analysis of Ricklefs<sup>100,101</sup>, which examined differences in species richness of North American and South American clades of passerine birds. We collected new data (rather than simply reproducing his original figure) because both the systematics of birds and estimates of divergence times have changed considerably in the past decade.

To identify clades, we used the exemplar tree of all birds by Jetz et al.<sup>102</sup>, which was also used to produce Figure 4B, and so is comparable. Using the OneZoom platform<sup>103</sup>, we systematically walked through the tree of passerines and identified nodes that led to clades of birds currently distributed exclusively (or nearly exclusively; see below) in either North America or South America. For each node we recorded the number of species and the crown age estimated from the dating analysis of Jetz et al.<sup>102</sup>. Following Ricklefs<sup>100,101</sup>, we did not distinguish between tropical and temperate species in the analysis. However, the vast majority of South American species in our dataset are tropical, and the vast majority of North American species are in the temperate regions. We only included singletons if they represented monotypic families. We did not consider any clades in which North and South American species were interspersed. We ended up with 39 North American clades and 40 South American clades containing a total of 1939 species. In a few cases, some primarily North American or primarily South American clades contained a small number of species currently distributed in either Central America or the Old World. The clades were retained but these species were removed from the data set. Clade definitions, species counts, and age estimates are included in Supplementary Table 1.

### *Patterns in alpha genetic diversity in mammals and amphibians*

Patterns of alpha genetic diversity in terrestrial mammals and amphibians were obtained from data in Miraldo et al.<sup>104</sup>, who estimate nucleotide diversity per base,  $\hat{\pi}$ , within cells of size  $386 \times 386 \text{ km}^2$  of an equal area grid placed on a global map. For every species present in each grid cell on islands and continents, the authors calculated  $\hat{\pi}$  using mtDNA sequences from Genbank and BOLD that had been annotated with geographical coordinates. Quality control steps are explained in Miraldo et al.<sup>104</sup>. We assumed that genetic diversity for a given species in a given cell represented an approximate estimate of alpha (within-population) diversity.

Identities and geographic coordinates of grid cells (central point, Behrmann map projection) were kindly provided by A. Miraldo and M. K. Borregaard. Behrmann projection coordinates were converted to latitude and longitude (coordinate system WGS84) using the *rgdal*<sup>105</sup> package in R 3.3.2<sup>106</sup>. Following ref<sup>107</sup> only species whose latitudinal ranges spanned at least 8 degrees were included in our subsequent analyses. To emphasize species on continents and nearby islands, we also removed oceanic islands, Madagascar and New Zealand from our analysis.

To compare alpha diversity among species living at different latitudes, we calculated  $\bar{\pi}$  for each species, the mean of alpha diversities, by taking the weighted average value of  $\hat{\pi}$  across all grid cells in which the species was present. This average was weighted by the number of sequences used to calculate each value of  $\hat{\pi}$ . Mid-latitude of the geographic range of each species was calculated as the midpoint between the latitudes of the most northern and the most southern grid cell for which an mtDNA sequence was available. For mammal and amphibian species separately, we regressed  $\bar{\pi}$  against the absolute value of mid-latitude. Residuals were highly skewed with some outliers present. We used two strategies to address this. First, we used beta regression in R, using the *gam* function in the *mgcv* package<sup>108</sup>, setting the smoothing parameter to yield an effective number of parameters of 2. We also used robust linear regression using *rlm* in the *MASS* package<sup>109</sup> in R. Fitting the data with beta regression often produced a warning that the saturated likelihoods might be inaccurate, so we relied on the robust regression coefficients, which led to similar fitted values.

A consistent relationship between mean alpha genetic diversity and species' midpoint latitude was not detected. For mammals, the regression slope was slightly negative: -0.00029 ( $\pm$  0.00017 SE)  $\bar{\pi}$  units per base per 10 degrees latitude. For amphibians, the regression slope was slightly positive: 0.00024 ( $\pm$  0.00045)  $\bar{\pi}$  units per 10 degrees latitude. Approximate 95% confidence intervals, calculated as  $\pm$  2 standard errors (SE), for both taxa overlapped zero.

To investigate patterns of alpha diversity with latitude within species, we carried out robust linear mixed model regression using the *robustlmm* package<sup>110</sup> in R, treating grid values of  $\hat{\pi}$  as the response data, the absolute value of grid latitude as the predictor variable, and species as a random effect. Weighted regression was used, to account for variation among grid cells in the number of sequences available per species.

For both mammals and amphibians the regression slopes from the robust method were negative: -0.00047 ( $\pm$  0.00015 SE)  $\hat{\pi}$  units per base per 10 degrees latitude in mammals and -0.002030 ( $\pm$  0.00063 SE)  $\hat{\pi}$  units per base per 10 degrees latitude in amphibians. We obtained slightly steeper estimates of slope with larger standard errors when we repeated the analyses using the *nlme* package<sup>111</sup> in R, with species and the interaction between species and latitude as random effects. The interaction allowed for the possibility that slopes of regressions of alpha diversity on the absolute value of latitude differed among species.

- 100 Ricklefs, R. E. Global variation in the diversification rate of passerine birds. *Ecology* **87**, 2468-2478 (2006)
- 101 Ricklefs, R. E. Estimating diversification rates from phylogenetic information. *Trends Ecol. Evol.* **22**, 601-610 (2007)
- 102 Jetz, W., Thomas, G. H., Joy, J. B., Hartmann, K. & Mooers, A. O. The global diversity of birds in space and time. *Nature* **491**, 444-448 (2012)
- 103 Rosindell, J. & Harmon, L. J. OneZoom: a fractal explorer for the tree of life. *PLoS Biol* **10**, e1001406 (2012)
- 104 Miraldo, A. *et al.* An Anthropocene map of genetic diversity. *Science* **353**, 1532-1535 (2016)
- 105 Roger, B., Tim, K. & Barry, R. *rgdal*: Bindings for the geospatial data abstraction library. 1.2-5 (2016).

- 106 R Development Core Team. R: A language and environment for statistical computing (R  
Foundation for Statistical Computing, Vienna, Austria, 2008).
- 107 Martin, P. R. & McKay, J. K. Latitudinal variation in genetic divergence of populations and the  
potential for future speciation. *Evolution* **58**, 938-945 (2004)
- 108 Wood, S. N. Fast stable restricted maximum likelihood and marginal likelihood estimation of  
semiparametric generalized linear models. *J. Roy. Stat. Soc. Ser. B. (Stat. Method.)* **73**, 3-36  
(2011)
- 109 Venables, W. N. & Ripley, B. D. *Modern applied statistics with S*. 4th edn, (Springer, 2002).
- 110 Koller, M. *robustlmm*: An R package for robust estimation of linear mixed-effects models. *J.*  
*Stat. Softw.* **75** (2016)
- 111 Pinheiro, J. C. & Bates, D. M. *Mixed-effects models in S and S-PLUS*. (Springer, 2000).

Supplementary Table 1. Data used in Figure 4A.

Clade	No. species	Age (my)	Continent	Notes
<i>Poecile</i>	7	8.03	North	
<i>Empidonax</i>	15	6.15	North	3 Central American spp excluded
<i>Lessonia + Muscisaxicola + allies</i>	49	9.76	South	
Chat-tyrants + allies	29	12.6	South	
<i>Casiornis + Rhytiptema</i>	5	1.97	South	
<i>Sirystes</i>	2	1.72	South	
Attilas	7	5.97	South	
<i>Myiozetetes</i>	4	5.35	South	
<i>Ramphotrigon + Deltarhynchus</i>	4	9.79	South	
Tyrannulets + Elaenias + allies	96	14.9	South	
<i>Myiophobus, Myiotriccus + allies</i>	8	12.1	South	
Spadebills + <i>Neopipo</i>	8	18.8	South	
Pygmy-Tyrants, Flatbills + allies	103	22	South	
<i>Piprites</i>	3	17.4	South	
<i>Oxyruncus cristatus</i>	1	25	South	
Contingidae	30	20.4	South	
Tyrant-flycatchers	9	19	South	
Pipridae + Contingidae	117	23.5	South	
Antbirds + Antipittas + Overbirds + allies	652	31.2	South	
Greenlets	15	15.5	South	
<i>Auriparus flaviceps</i>	1	30.4	North	
<i>Beaolophus</i>	5	10	North	
<i>Psaltriparus minimus</i>	1	4.99	North	
<i>Regulus</i>	2	34.6	North	Some Old World species excluded
Silky flycatchers	3	21.9	North	
<i>Bombycilla</i>	2	10.9	North	
Nuthatches	3	15.2	North	Some Old World species excluded
<i>Certhia americana</i>	1	1.7	North	
<i>Microbates</i>	2	3.43	South	
<i>Hylorchilus + Catherpes + Salpinctes</i>	4	14.3	North	
<i>Microcerculus</i>	4	9.06	South	
<i>Odontorchilus</i>	2	5.18	South	
<i>Cyphorhinus</i>	3	5.82	South	
<i>Cinnycerthia</i>	4	8.34	South	
<i>Thryothorus + Thryomanes</i>	2	10	North	
Woodwrens + allies	15	11	South	

<i>Dumetella carolinensis</i>	1	6.63	North	
<i>Toxostoma</i>	10	9.64	North	
<i>Mimus</i>	5	3.42	South	
<i>Cinclus mexicanus</i>	1	13.4	North	
<i>Cinclus</i> (SA clade)	2	6.77	South	
<i>Sialia</i>	3	5.1	North	
<i>Cichlopsis</i> + <i>Entomodestes</i>	3	7.87	South	
<i>Catharus</i>	3	1.41	North	
<i>Turdus thrushus</i> + allies	28	7.76	South	
<i>Turdus robins</i>	2	0.609	North	
<i>Peucedramus taeniatus</i>	1	31.4	North	
<i>Coccothraustes</i>	2	10.2	North	One Old World species excluded
<i>Carpodacus</i> finches	3	11.4	North	
<i>Leucosticte</i>	3	0.246	North	
<i>Carduelis flammea</i> + <i>Loxia</i>	4	5.35	North	
<i>Carduelis</i> goldfinches	3	3.47	North	
Siskins	11	1.67	South	
Emberizidae	6	16.9	North	
<i>Verminova</i> + <i>Parula</i>	10	8.4	North	
<i>Seiurus</i> + <i>Mniotilta varia</i>	3	7.56	North	
<i>Prothonotaria</i> + <i>Limnothlypis</i>	2	7.52	North	
<i>Oporornis</i>	4	5.16	North	
<i>Dendroica</i> spp + allies	25	5.6	North	Some Caribbean species excluded
<i>Basileuterus</i> + allies	17	7.41	South	
<i>Wilsonia</i> + <i>Myioborus</i>	5	5.26	North	
<i>Myioborus</i>	10	3.32	South	
Orioles	10	4.8	North	
<i>Psarocolius</i> + allies	22	6.56	South	
<i>Quiscalus</i>	3	2.46	North	Some Caribbean species excluded
<i>Macroagelaius</i> + allies	19	5.59	South	
Brush-finches	16	6.69	South	
<i>Chlorospringus</i> Tanagers	9	6.89	South	
<i>Amphispiza</i> + allies	9	8.85	North	
<i>Atlapetes</i>	14	6.11	South	
<i>Atlapetes</i>	3	2.84	South	
<i>Zonotrichia</i> + <i>Junco</i> + <i>Spizella</i>	10	6.78	North	
Buntings	7	8.26	North	
<i>Habia</i> + <i>Chlorothraupis</i>	9	11	South	
<i>Piranga</i> tanagers	8	10.7	North	
Tanagers + grosbeaks + saltators + allies	391	18.7	South	
<i>Amaurospiza</i> + <i>Cyanocompsa</i>	6	9.01	South	

<i>Pipilo</i>	4	2.81	North	
<i>Passerculus</i> + allied sparrows	14	6.84	North	