Electronic Supplementary Material

Historical contingency, niche conservatism and the tendency for some taxa to be more diverse towards the poles

Ignacio Morales-Castilla[1,2] *, Jonathan T. Davies[3] and Miguel Á. Rodríguez[1]

[1]Departament of Life Sciences, University of Alcalá, 28871, Alcalá de Henares, Spain
[2]Department of Organismic and Evolutionary Biology, Harvard University, 26 Oxford St, Cambridge, MA, 02138, USA
[3]Botany, forest & conservation sciences, University of British Columbia, 2212 Main Mall, Vancouver, BC, V6T 1Z4, Canada

*Correspondence to:
I. Morales-Castilla
E-mail: moralescastilla@fas.harvard.edu

Appendix S1 Species list and classification.

Appendix S2 Detailed results from MEMs.

Appendix S3 Model verification.

Appendix S4 Moran's *I* spatial autocorrelation analyses.

Appendix S5 Phylogenetic analyses of variation in richness-temperature slopes.

Appendix S6 Cross-predictions among phylogenetic models of climatic tolerances.

Appendix S7 Diversification analyses for the subsets of colonizers and sedentary mammal species.

Appendix S1.

Data will be provided as a .csv formatted dataset, upon publication of this ms. and can be requested to the corresponding author.

Appendix S2. Detailed results of four modelling techniques applied to build MEMs.

Table S2. Species richness models utilizing five environmental predictors: net primary productivity (NPP), mean annual temperature (TEMP), temperature seasonality (SEAS), mesoclimatic effects measured as the interaction between temperature and elevation (TEMP*RIE), range in elevation (RIE). Spearman rank correlation (*ρ*) was calculated between observed species richness and predicted species richness of each model. All Spearman correlations were significant (*p*<0.001). For each model and predictor variable, values of regression coefficients (GLM), smoothing coefficients (GAM), variable importance (GBM), mean decreases in accuracy (Random Forests) are provided, indicating that TEMP and NPP are the stronger predictors in all cases.

Model	Taxa	Region	n	NPP	TEMP	SEAS	TEMP*RIE	RIE	Spearman *ρ*
GLM	P-N colonizer	Nearctic	2244	0.000	-0.006	0.000	0.000	0.000	0.823
		Palaearctic	4162	0.000	-0.018	0.000	0.000	0.000	0.673
	N-P colonizer	Nearctic	2244	0.000	0.004	0.000	0.000	0.000	0.789
		Palaearctic	4162	0.000	0.016	0.000	0.000	0.000	0.736
GAM	P-N colonizer	Nearctic	2244	5.925	8.285	4.855	1.995	2.584	0.877
		Palaearctic	4162	8.141	8.543	5.819	1.600	5.607	0.776
	N-P colonizer	Nearctic	2244	5.121	7.974	7.138	2.623	3.696	0.833
		Palaearctic	4162	8.504	6.088	6.015	4.210	3.678	0.790
GBM	P-N colonizer	Nearctic	2244	13.150	42.430	11.834	8.031	24.556	0.908
		Palaearctic	4162	26.069	41.761	8.740	8.908	14.521	0.817
	N-P colonizer	Nearctic	2244	36.771	27.493	10.781	10.933	14.021	0.876
		Palaearctic	4162	46.115	18.785	19.273	8.240	7.588	0.828
Random Forest	P-N colonizer	Nearctic	2244	3.942	12.402	5.836	4.549	7.198	0.933
		Palaearctic	4162	5.603	9.839	7.049	3.728	2.921	0.903
	N-P colonizer	Nearctic	2244	4.356	5.125	1.816	1.590	1.223	0.888
		Palaearctic	4162	6.549	5.484	6.178	1.669	1.365	0.906

Appendix S3 Model verification

Table S3. Model verification results utilizing a tenfold procedure. Each dataset was randomly divided into a modelling subset (70% of the data) and a calibration subset (30% of the data) 1,000 times, in order to evaluate model accuracy. MEMs predictions from the modelling subset were utilized to predict species richness of the calibration subset. Spearman rank correlations were recorded for each of the 1,000 replications and are shown together with 95% Confidence Intervals. Note that model accuracy is consistently superior for P-N colonizers than for N-P colonizers.

Model	Taxa	Region	n	Spearman's ρ	-95%CI	+95%CI
GLS	P-N colonizer	Nearctic	2244	0.822	0.789	0.837
		Palaearctic	4162	0.673	0.626	0.694
	N-P colonizer	Nearctic	2244	0.427	0.364	0.475
		Palaearctic	4162	0.431	0.392	0.459
GAM	P-N colonizer	Nearctic	2244	0.892	0.873	0.906
		Palaearctic	4162	0.797	0.775	0.814
	N-P colonizer	Nearctic	2244	0.466	0.407	0.504
		Palaearctic	4162	0.487	0.442	0.521
GBM	P-N colonizer	Nearctic	2244	0.856	0.831	0.872
		Palaearctic	4162	0.759	0.730	0.778
	N-P colonizer	Nearctic	2244	0.462	0.370	0.510
		Palaearctic	4162	0.480	0.430	0.510
Random Forest	P-N colonizer	Nearctic	2244	0.988	0.983	0.990
		Palaearctic	4162	0.982	0.977	0.984
	N-P colonizer	Nearctic	2244	0.481	0.396	0.520
		Palaearctic	4162	0.539	0.491	0.566

Appendix S4 Moran's *I* spatial autocorrelation analyses.

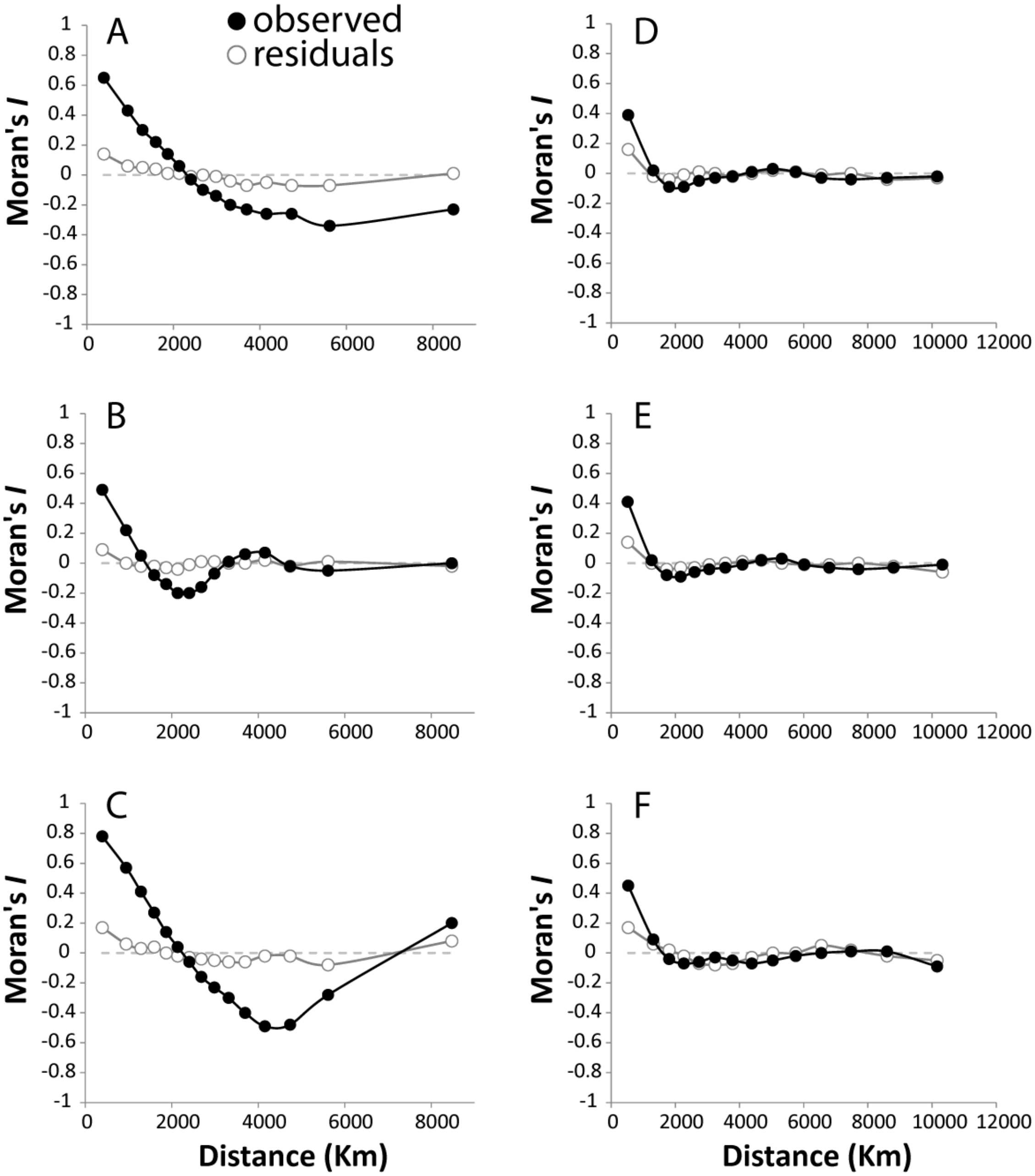

Figure S4. Moran's *I* values are depicted for observed and residual species richness from averaged MEMs. Panels represent MEMs within the Nearctic for P-N colonizers (A), N-P colonizers (B) and N sedentaries (C), and, within the Palaearctic for P-N colonizers (D), N-P colonizers (E) and P sedentaries (F). The lack of residual autocorrelation in all cases (Moran's *I* < 0.2) indicates that most spatial structure in species richness is absorbed by the five environmental predictors utilized to build MEMs.

Appendix S5 Phylogenetic analyses of variation in richness-temperature slopes.

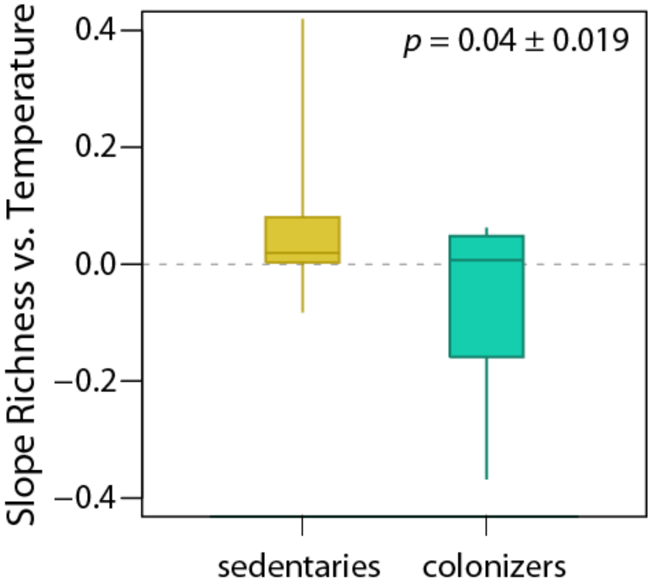

Figure S5. Boxplots comparing the climate-richness relationships between sedentary and colonizer mammal families. Climate-richness relationships are measured by the slopes of fitted GLS models between species richness and temperature, and are computed at the family level. Sedentary families are those without genera participating in the biotic exchanges through the Bering Strait and colonizer families those with at least one genera participating. The distribution are significantly different according to a phylogenetic ANOVA, and a post-hoc comparison of means.

Table S5. Results from phylogenetic generalized least squares models (PGLS) fitting statistical relationships between variation in the fitted slopes between species richness and temperature, computed at the family level, and three predictors: classification as sedentary-colonizer of each family coded as 0-1 respectively ("colonizing"), average log-body mass of each family, and total range size of each family.

Model	Predictor	Estimate	Std. Error	*p*-value	R^2_{adj}	$\lambda_{residual}$
Colonizing	intercept	0.033	0.026	0.208	0.108	0.000
	colonizing	-0.085	0.041	0.048		
Colonizing + Body mass	intercept	-0.042	0.055	0.455	0.152	0.000
	colonizing	-0.103	0.042	0.020		
	log-body mass	0.012	0.008	0.140		
Colonizing + Body mass + Range size	intercept	0.046	0.107	0.674	0.335	0.000
	colonizing	-0.105	0.054	0.072		
	log-body mass	0.022	0.009	0.020		
	log-range size	-0.023	0.015	0.149		

Appendix S6 Phylogenetic cross-predictions of climatic tolerances.

In order to establish the extent to which the predictive ability among MEMs of exchanged species was due to phylogenetic conservatism of climatic tolerances, we inspected the ability of phylogenetic relationships represented by eigenvectors to cross-predict the climatic tolerances of each group of exchanged and non-exchanged species. The procedure is as follows. First we characterized each species climatic tolerance regarding mean annual temperature (TEMP) and net primary productivity (NPP), since both variables were those most strongly correlated with species richness (see Appendix S2). For each species we calculated mode values of TEMP and NPP for the lowest quartile of each variable within each species' geographic range. These values are representative of the lowest temperatures and productivities that each species experiences and thus, were used as surrogates for the climatic tolerances of species, which are the response variables of this analysis. Second, we extracted a mammal phylogeny for each subset of exchanged and non-exchanged species by pruning Fritz et al.'s (2009) phylogeny. Each phylogeny was transformed into a set of phylogenetic eigenvectors (see details in Diniz-Filho et al. 1998) and for each subset, a number of eigenvectors were selected to minimize residual phylogenetic autocorrelation (see Griffith & Peres-Neto 2006) after regressing them against the response variables (TEMP and NPP). Finally, we repeated the same MEMs procedure (see Material and Methods in main text) to make cross-predictions among exchanged species in different biogeographic regions and among non-exchanged and exchanged species, but in this case utilizing the phylogenetic eigenvectors as predictors and the climatic tolerances for TEMP and NPP as response variables.

Table S6. Phylogenetic cross-predictions utilizing phylogenetic eigenvectors selected according the method proposed by Griffith and Peres-Neto (2006) as predictor variables and mode values of NPP and TEMP across the lowest quartile within each species geographic range, as response variables. Although the predictions among subsets of exchanged species are higher than between non-exchanged and exchanged species, the ability of phylogenetic eigenvectors to predict climatic tolerances is limited in all cases.

Taxa	Model	Response variable	Spearman's ρ	p-value
P-N colonizers	origin to destination	NPP	0.388	0.005
		TEMP	0.295	0.036
N-P colonizers	origin to destination	NPP	0.160	0.240
		TEMP	0.085	0.533
P-N colonizers	sedentary species	NPP	-0.001	0.994
		TEMP	-0.149	0.020
N-P colonizers	Sedentary species	NPP	0.003	0.959
		TEMP	0.048	0.455

References

1. Diniz-Filho, JAF, de Sant'Ana, CER, Bini, LM. 1998 An eigenvector method for estimating phylogenetic inertia. *Evolution*, **52**(5), 1247-1262.

2. Fritz, SA, Bininda-Emonds, OR, Purvis, A. 2009 Geographical variation in predictors of mammalian extinction risk: big is bad, but only in the tropics. *Ecol lett*, **12**(6), 538-549.

3. Griffith, DA, Peres-Neto, PR. 2006 Spatial modeling in ecology: the flexibility of eigenfunction spatial analyses. *Ecology*, **87**(10), 2603-2613.

Appendix S7 Diversification analyses

Table S6. Net diversification rates calculated for exchanged species to the Nearctic, exchanged species to the Palaearctic and for non-exchanged species. Although diversification rates of exchanged species are slightly higher than rates for non-exchanged species, all values are proximal.

Taxa	Net diversification rate
Exchanged species to Nearctic	0.044042
Exchanged species to Palaearctic	0.044216
Non-exchanged species	0.039793

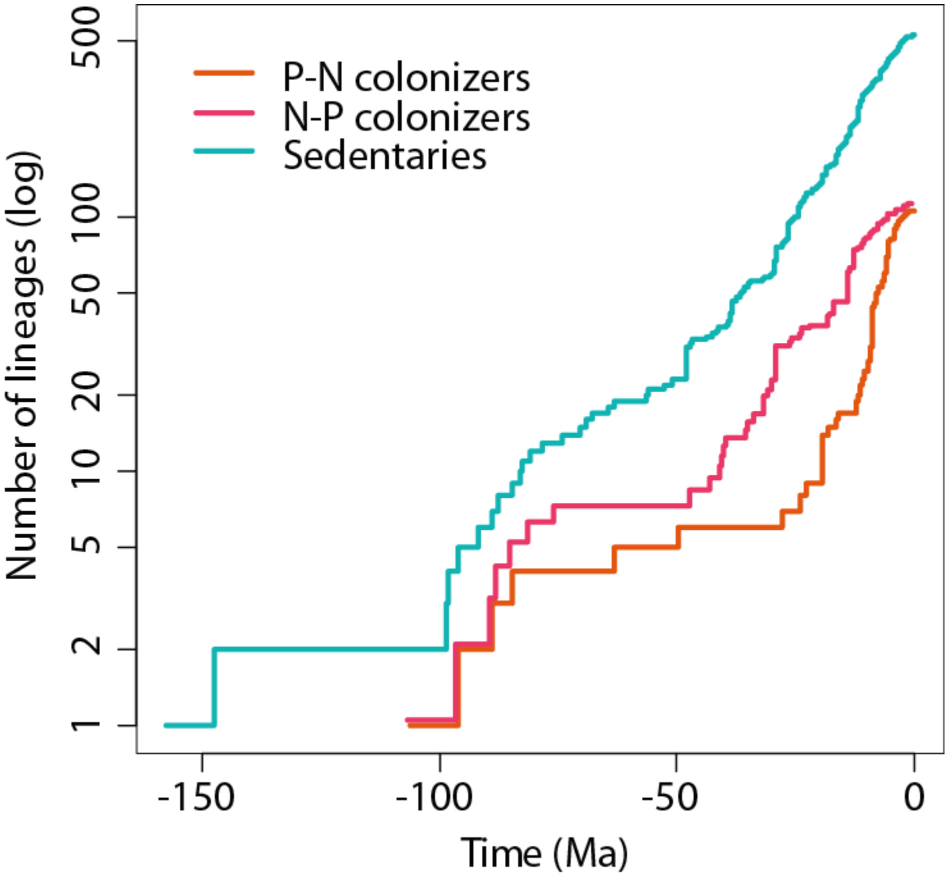

Figure S7. Lineage Through Time (LTT) plot, representing the diversification process of each group of exchanged species and non-exchanged species. Note that non-exchanged species start to diversify before but the slopes are similar for the three lines. Most accumulation of exchanged species is relatively recent and thus might have occurred posterior to their ancestors crossing the Bering Strait.