Is species richness mediated by functional and genetic divergence? A global analysis in birds (Supplementary Material)

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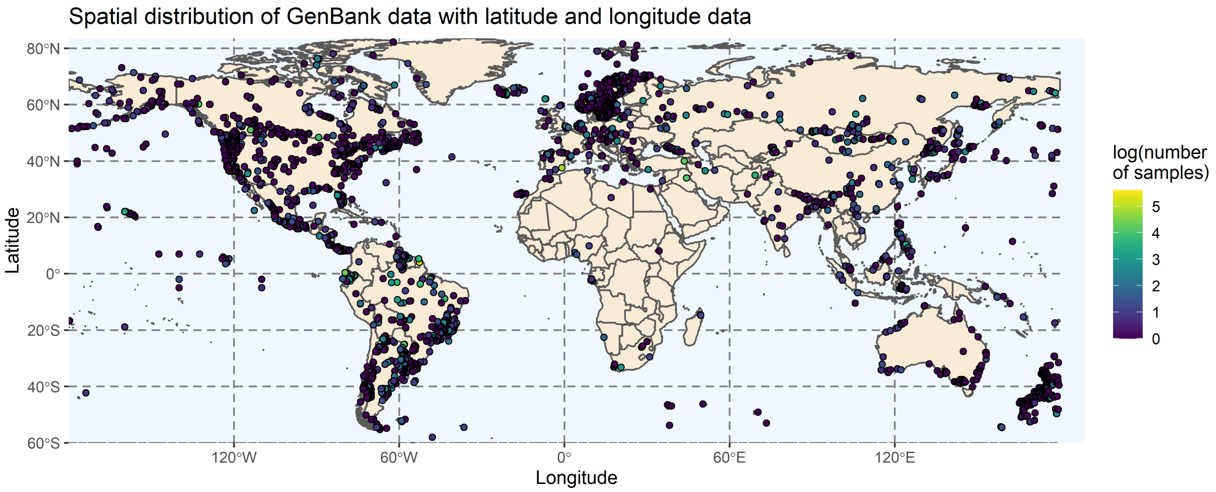

Figure S1: Spatial distribution of CO1 samples downloaded from GenBank containing GPS coordinates.

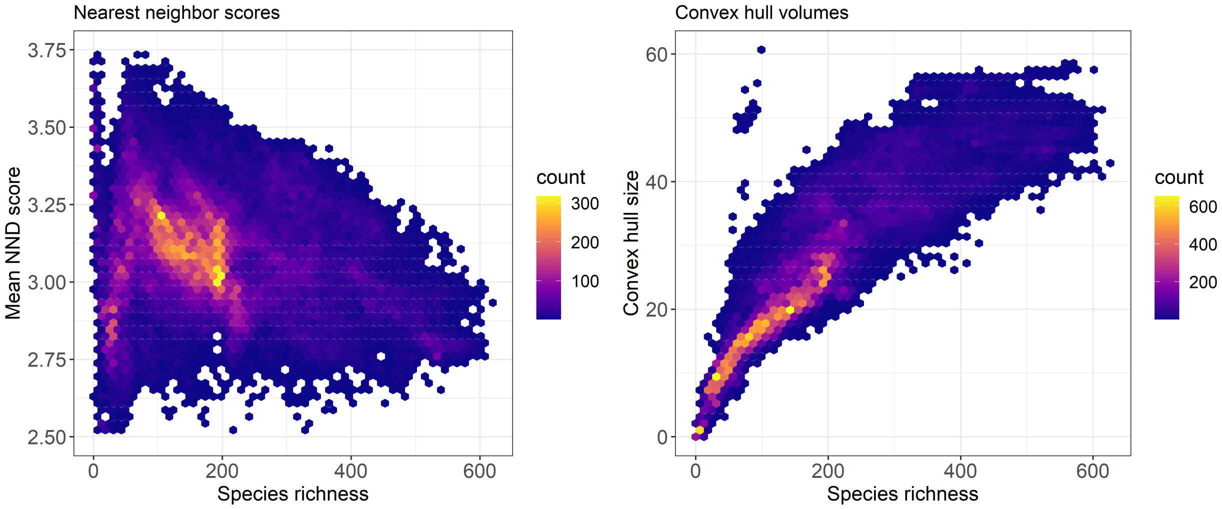

Figure S2: Relationship between species richness and nearest neighbor distances (*left*) and convex hull volumes (*right*) highlighting the variation in grid cells with the corresponding values.

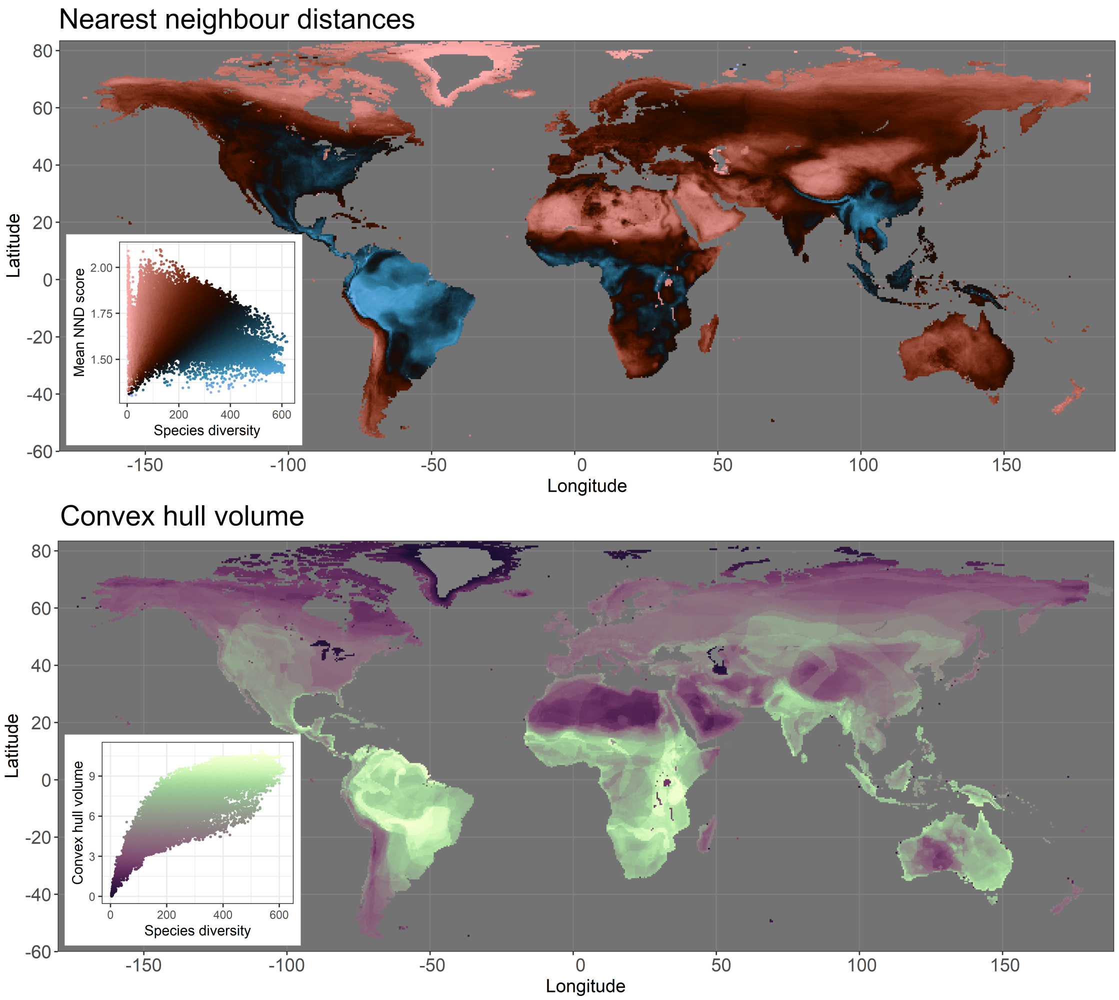

Figure S3: Global variation in nearest-neighbor distances and convex hull volumes when analyzing only beak traits. Inset panels in both images show the relationship between the corresponding variable and species richness across the globe.

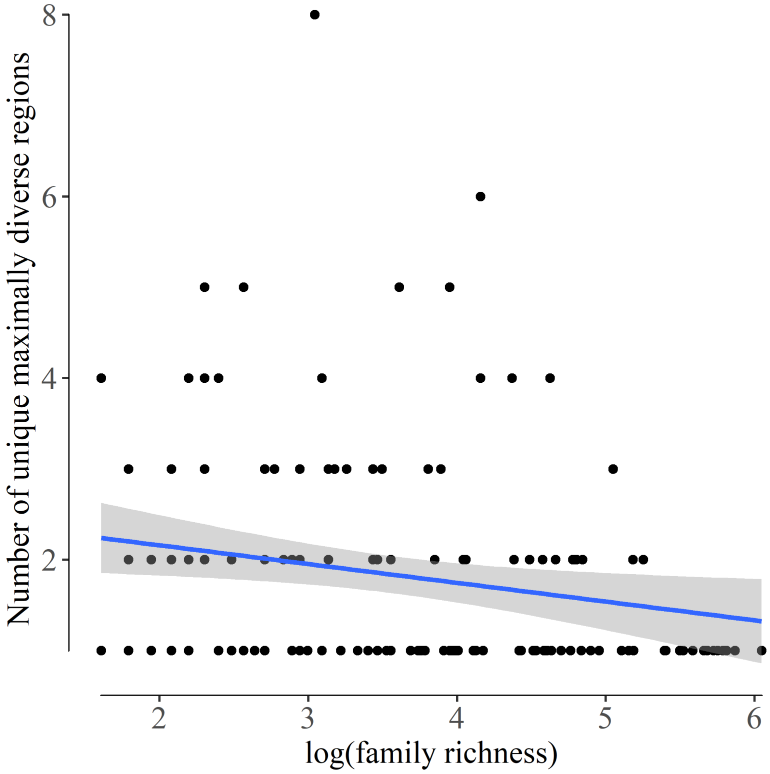

Figure S4: Relationship between within-family species richness and the number of maximally diverse regions of its constituent species.

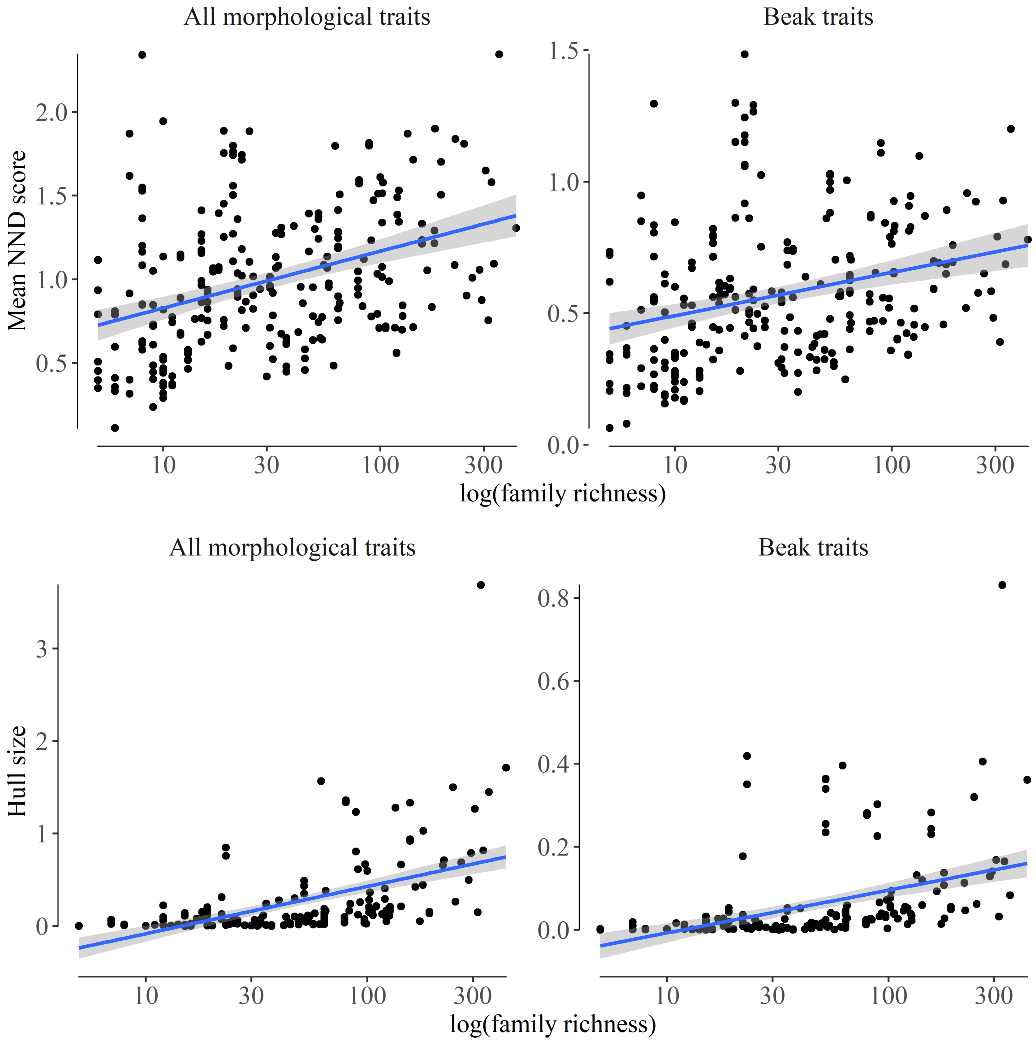

Figure S5: Relationship between within-family species richness and mean nearest-neighbor-distance scores (*top*) and hull size (*bottom*).

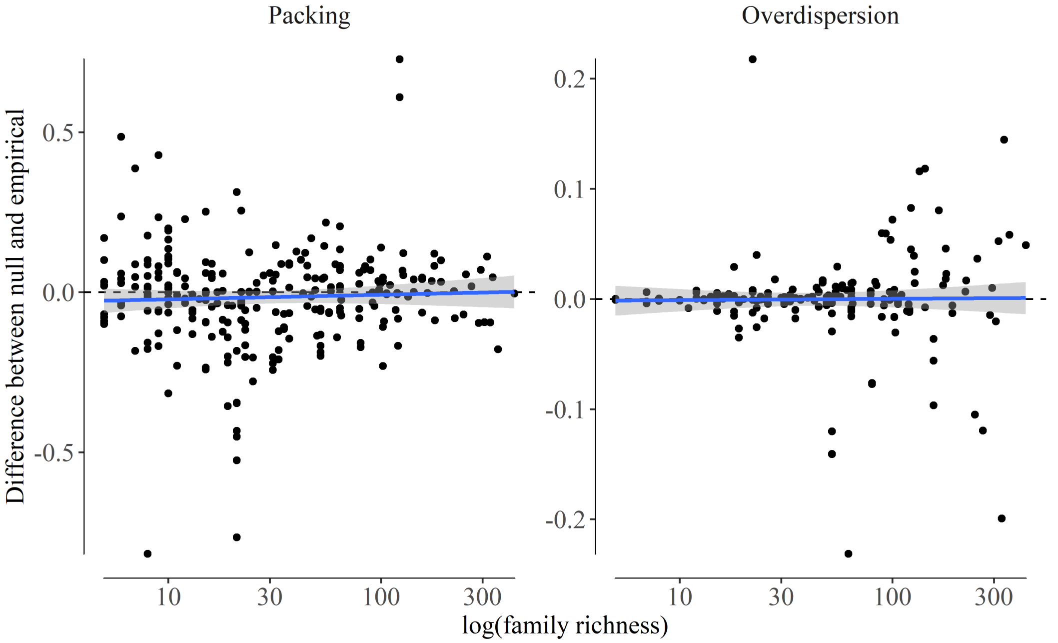

Figure S6: Relationship between within-family species richness and packing (*left*) and overdispersion (*right*) when only analyzing beak traits.

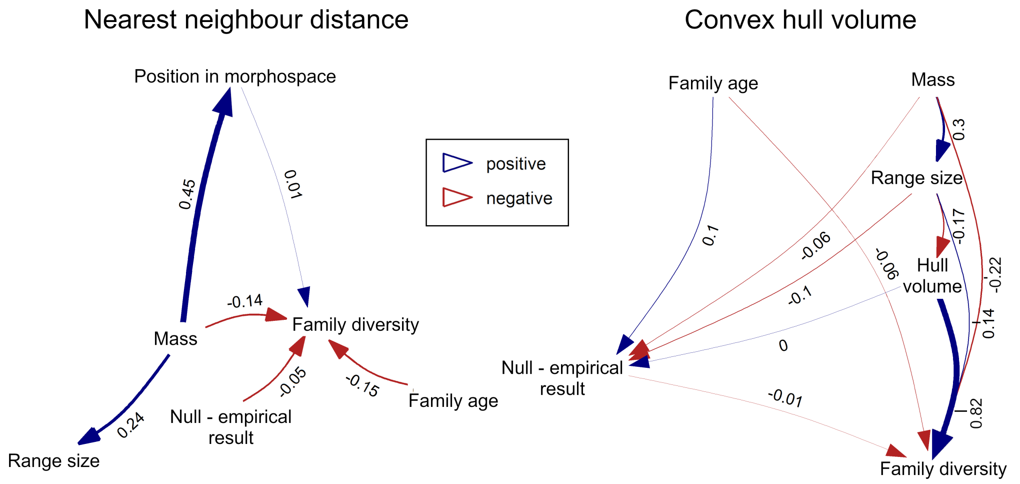

Figure S7: Model-averaged path analysis results for nearest-neighbor distances and convex hull volumes respectively. “Null – empirical result” is the difference between the observed value for the area of maximum species richness minus the mean value from a random distribution of species.

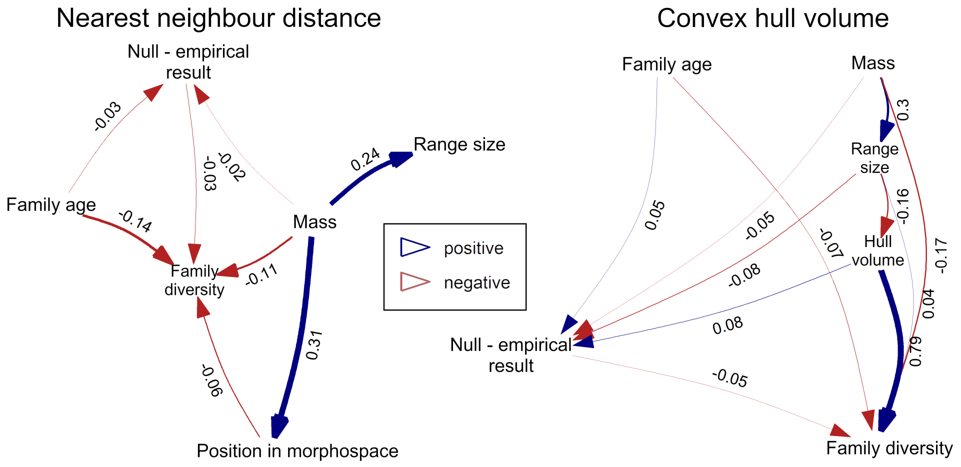

Figure S8: Model-averaged path analysis results for nearest-neighbor distances and convex hull volumes respectively. Null – empirical result reflects the difference between the observed value for the area of maximum species richness minus the mean value from a random distribution of species.

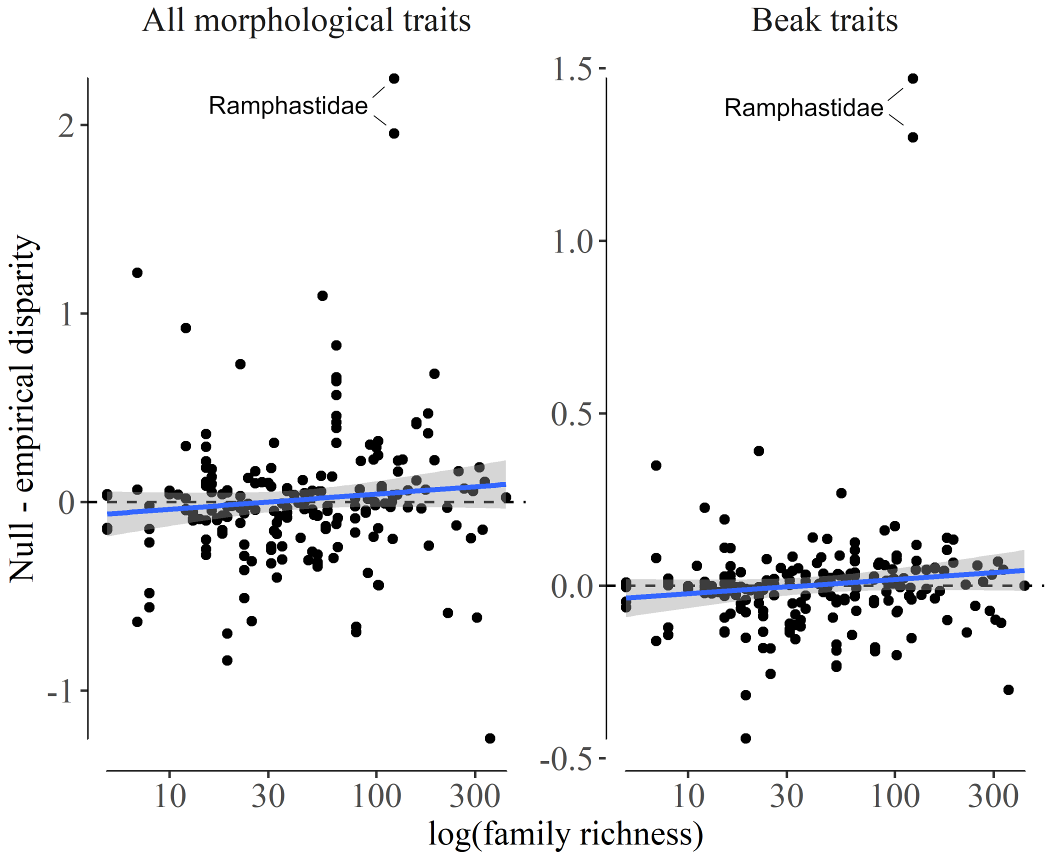

Figure S9: Relationship between within-family species richness and packing (*left*) and overdispersion (*right*) when calculated using multivariate disparity.

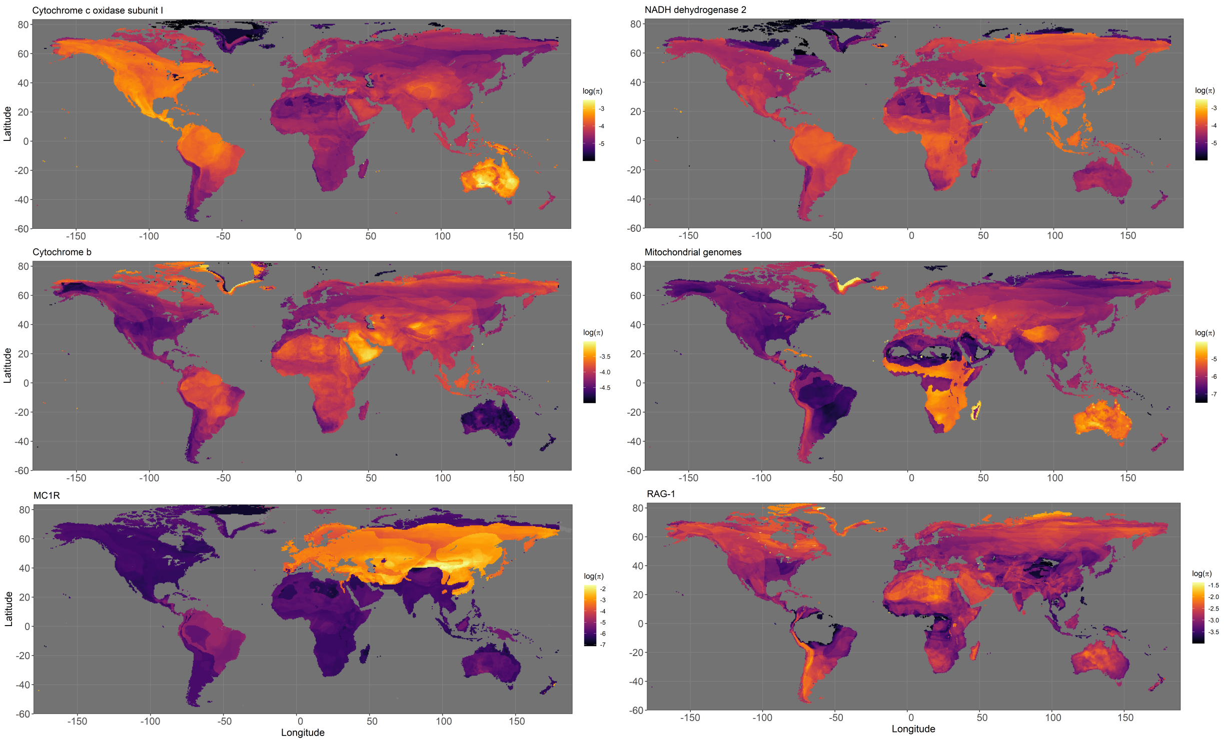

Figure S10: Global variation in nucleotide diversity (π) between the six genes analyzed in this study.

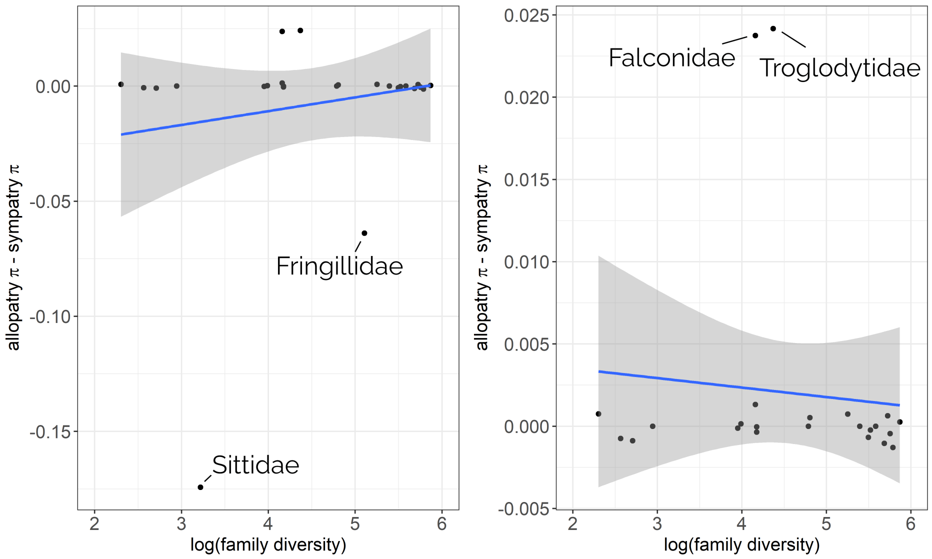

Figure S11: Relationship between family species richness and the difference in nucleotide diversity (π) between allopatric and sympatric species excluding one outlier (Certhiidae). The right-hand panel shows the relationship with the exclusion of the families Sittidae and Fringillidae.

Analysis	**Morphological data**	**Estimate**	**p**	λ
Nearest neighbor distance	All morphological traits	-0.004	0.75	1e-07
	Beak traits	-0.002	0.85	1e-07
Convex hull volume	All morphological traits	-0.002	0.92	1e-07
	Beak traits	0.001	0.74	1e-07

Table S1: Estimates of the effect of family diversity on nearest neighbor distances and convex hull volumes while accounting for shared evolutionary history. λ is the estimated phylogenetic signal from each model respectively.

Comparison	Gene	t	p	Effect size	Magnitude	n1	n2	Where π is largest
Allopatry (defined using sister species)	CO1	0.16	0.87	0.01	Negligible	800	1405	Allopatry
	CYTB	-3.00	0.00	-0.13	Negligible	866	1178	Sympatry
	ND2	-4.91	0.00	-0.20	Small	1059	1381	Sympatry
	mtDNA	0.31	0.76	0.05	Negligible	84	102	Allopatry
	RAG1	-1.31	0.19	-0.19	Negligible	104	95	Sympatry
	MC1R	0.58	0.57	0.13	Negligible	37	47	Allopatry
Allopatry (defined using all confamilial species)	CO1	0.97	0.34	0.20	Negligible	27	2081	Allopatry
	CYTB	-4.47	0.00	-0.58	Moderate	52	1992	Sympatry
	ND2	-0.85	0.37	-0.12	Negligible	49	2310	Sympatry
	mtDNA	-2.84	0.04	-1.23	Large	5	175	Sympatry
	RAG1	1.20	0.35	0.78	Moderate	3	193	Allopatry
	MC1R	-4.54	0.00	-0.74	Moderate	2	76	Sympatry
Tropical and temperate species	CO1	7.07	0.00	-0.49	Small	286	602	Tropical
	CYTB	6.43	0.00	-0.46	Small	238	831	Tropical
	ND2	5.52	0.00	-0.41	Small	213	1157	Tropical
	mtDNA	0.06	0.95	-0.01	Negligible	33	45	Temperate
	RAG1	-1.63	0.12	0.47	Small	22	45	Temperate
	MC1R	-1.14	0.26	0.42	Small	16	14	Temperate

Table S2: Comparison of log-transformed nucleotide diversity (π) between different geographic states. t is the result of a two-sided t-test, and p the associated significant of the test. Effect size is Cohen's D estimate of effect size, with magnitude the interpretation of the effect size. n1 and n2 refer to the sample sizes for allopatry/sympatry and temperate/tropical respectively. The final column describes which geographic state has the largest mean value of π.

Gene	**Correlation**	**Sample size**
CO1	-0.02	2434
CYTB	0.09	2401
ND2	0.05	2617
mtDNA	0.16	199
RAG1	0.05	208
MC1R	0.11	85

Table S3: Correlation between branch length and nucleotide diversity (π) across the six genes analyzed in this study. Sample size is the number of species used to test the correlation. Species with π scores of 0 were excluded as the data were required to be log-transformed prior to analysis.