Title: Microevolutionary Responses to Seasonality Contribute to the Latitudinal Biodiversity Gradient

Authors: Anne-Céline Granjon[1,2]†*, Michael Gerth[1,3], Jean-Philippe Lessard[4], Colin J. Garroway[5], Chloé Schmidt[6]*

Affiliations:

[1]German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig; Leipzig, Germany.

[2]Leipzig University; Leipzig, Germany.

[3]Department of Zoology, Faculty of Natural Sciences I; Martin Luther University Halle-Wittenberg, Halle (Saale), Germany.

[4]Department of Biology, Concordia University, Montreal, QC, Canada

[5]Department of Biological Sciences, University of Manitoba, Winnipeg, MB, Canada

[6]Department of Biology, Dalhousie University; Halifax, NS, Canada

*Corresponding authors. Email: anne-celine.granjon@idiv.de, chloe.schmidt@dal.ca.

†Present address: Friedrich Schiller University Jena, Faculty of Biological Sciences, Institute of Biodiversity, Ecology and Evolution, Jena, Germany.

Abstract: The latitudinal gradient in species richness is one of ecology's oldest observed patterns, yet the mechanisms maintaining it remain debated. One prominent explanation links seasonality to the evolution of broad physiological tolerances, creating evolutionary conditions that impede population divergence and speciation. We tested whether seasonality leaves detectable signatures in the genetic composition of natural populations by estimating genome-wide diversity, genetic differentiation, and effective population size across 100 mammal species at 1,426 local populations worldwide. Within species, genetic diversity was higher and genetic differentiation lower in the most seasonal parts of the range. In wide-ranging species occurring at higher latitudes, genetic diversity increased in populations toward the poleward range edge. Our results suggest that the population genetic conditions generally associated with the promotion of speciation vary systematically across latitudes in parallel with the latitudinal species diversity gradient.

Main Text: The increase in species richness from the poles toward the equator, known as the latitudinal diversity gradient, is one of the most pervasive patterns in the natural world (*1*). Despite centuries of research interest, the mechanisms responsible for this pattern remain actively debated (*2*–*5*). Though not originally developed for this question, the climate variability hypothesis (*6*, *7*) is often invoked to explain latitudinal diversity gradients because of the intuitive mechanism it proposes (*8*, *9*). It posits that poleward regions experiencing seasonal fluctuations in climatic conditions should harbor species that can tolerate a broad range of environmental conditions. This should promote connectivity and high gene flow between populations across larger geographic ranges, in turn preventing population divergence and ultimately, speciation. In contrast, lower gene flow should increase the likelihood of population divergence and speciation at lower latitudes, which could contribute to the latitudinal diversity gradient (*8*). However, the extensive theoretical and empirical attention devoted to evaluating these processes has not extended to understanding whether population-level biogeographic patterns in intraspecific genetic diversity align with these predictions. Here we revisit these classical ecological ideas through a population genetic lens to test whether the evolutionary conditions thought to promote population divergence and speciation covary with latitude and the species richness gradient.

Population genetic theory suggests that populations occupying a narrow, consistent set of conditions evolve more efficiently in response to the environment than generalists (*10*). Beneficial mutations spread more quickly, local adaptation occurs more readily, and individuals that mate and stay within their home habitat are favored, all of which accelerate divergence between populations. In comparison, organisms in seasonal environments evolve broader environmental niches, which leads to greater population cohesion, larger ranges, and fewer opportunities for divergence and speciation (*10*). The connections between seasonality and environmental niche breadth drawn by Janzen (*6*) and Stevens (*7*) can be logically extended to the latitudinal diversity gradient through their proposed effects on dispersal (*8*). Janzen (*6*) predicted that the absence of seasonality near the equator would produce organisms so narrowly adapted to local conditions that even modest altitudinal environmental gradients could become barriers to dispersal. Stevens (*7*) extended this reasoning, suggesting that greater seasonality at higher latitudes should select for broader environmental niches and therefore relieve organisms from the dispersal limitations imposed by climatic barriers, both of which would contribute to species having wider geographic ranges in these regions (*7*, *11*).

The population genetic theoretical framework and the predictions of Janzen and Stevens are thus two descriptions of the same phenomenon from different disciplinary perspectives. Both predict that seasonal environments should favor broader environmental tolerances, greater dispersal, and stronger genetic connectivity among populations. Recognizing this connection suggests that the evolutionary consequences of living in seasonal environments should be detectable in the genetic composition of natural populations across latitude, and should produce corresponding contemporary latitudinal gradients in genetic diversity. Within species, latitudinal genetic diversity gradients should be most apparent in wide-ranging species whose distributions span large latitudinal gradients in seasonality; among species, those with larger ranges positioned at higher latitudes should have higher diversity and lower population structure than species with smaller ranges near the equator. Leveraging a microsatellite database compiled from 59,587 individuals across 100 mammal species and 1,426 local populations (Fig. 1), we tested whether the predicted effects of the climate variability hypothesis were borne out in the genetic composition of populations and species. Access to genotype data enabled us to consistently estimate metrics of genome-wide diversity, contemporary effective population size, and genetic differentiation at population and species levels. We used spatially-explicit Bayesian hierarchical regression models to quantify the effects of seasonality on local population genetic composition, allowing model slopes and intercepts to vary by species. This model structure enabled us to test the consistency and generality of relationships between genetic composition and seasonality across species.

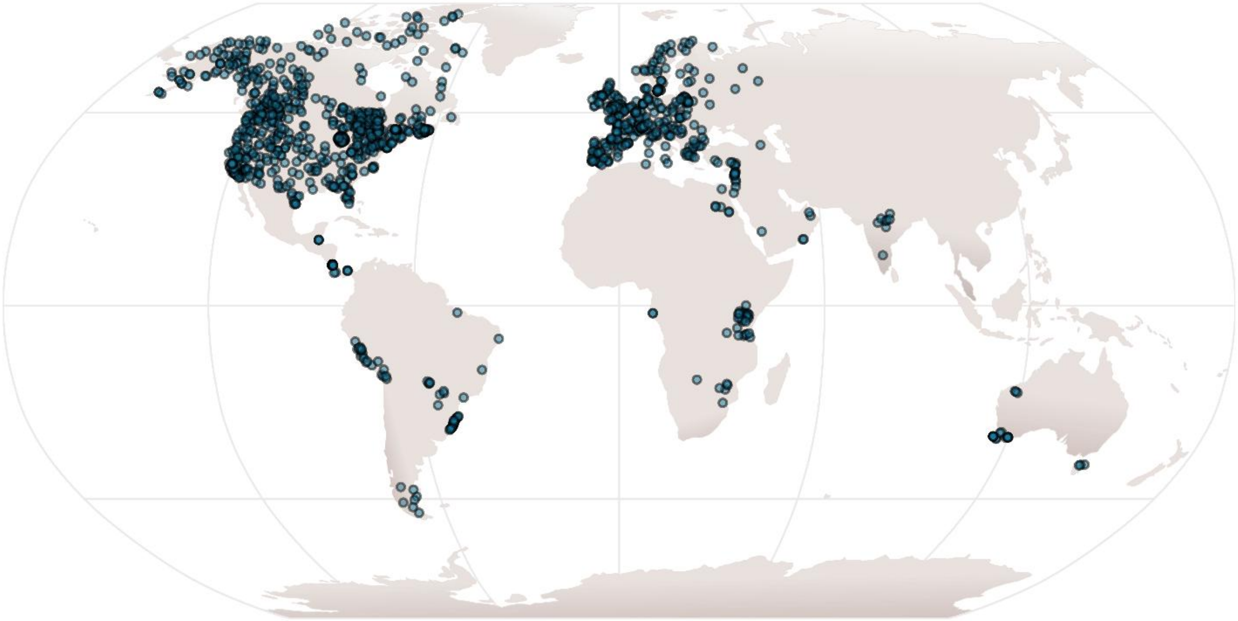

Fig. 1. Map of sample locations. The data comprised 59587 individuals sampled across 100 mammal species at 1426 locations. Each point represents a site where multiple individuals were genotyped. The median number of individuals sampled at each site was 23 (range 5 – 2444 individuals), and the median number of sample locations per species was 7 (range 1 – 82 sites).

Temperature seasonality is associated with latitudinal gradients in genetic diversity

In support of the climate variability hypothesis, we found seasonality, here measured as the annual range in temperature at a sample site, was positively associated with the genetic diversity and effective population size of local populations, and negatively associated with genetic differentiation across populations (Fig. 2). Populations in more seasonal environments were better connected with nearby populations, thus had lower levels of genetic differentiation, higher genetic diversity, and larger effective population sizes than populations in less seasonal environments. This relationship was consistent across most species (87-97%) in the dataset for all genetic metrics (Fig. 2). The consistent effects of temperature seasonality contrasted with other climatic variables including precipitation seasonality, the standard deviation of annual precipitation at a sample site. A separate set of models demonstrated that population-level relationships between genetic metrics and precipitation seasonality, mean annual temperature, and mean annual precipitation were dependent on species' latitudinal range position, with variable effects on tropical populations and consistent effects in high-latitude populations (fig. S3, table S2).

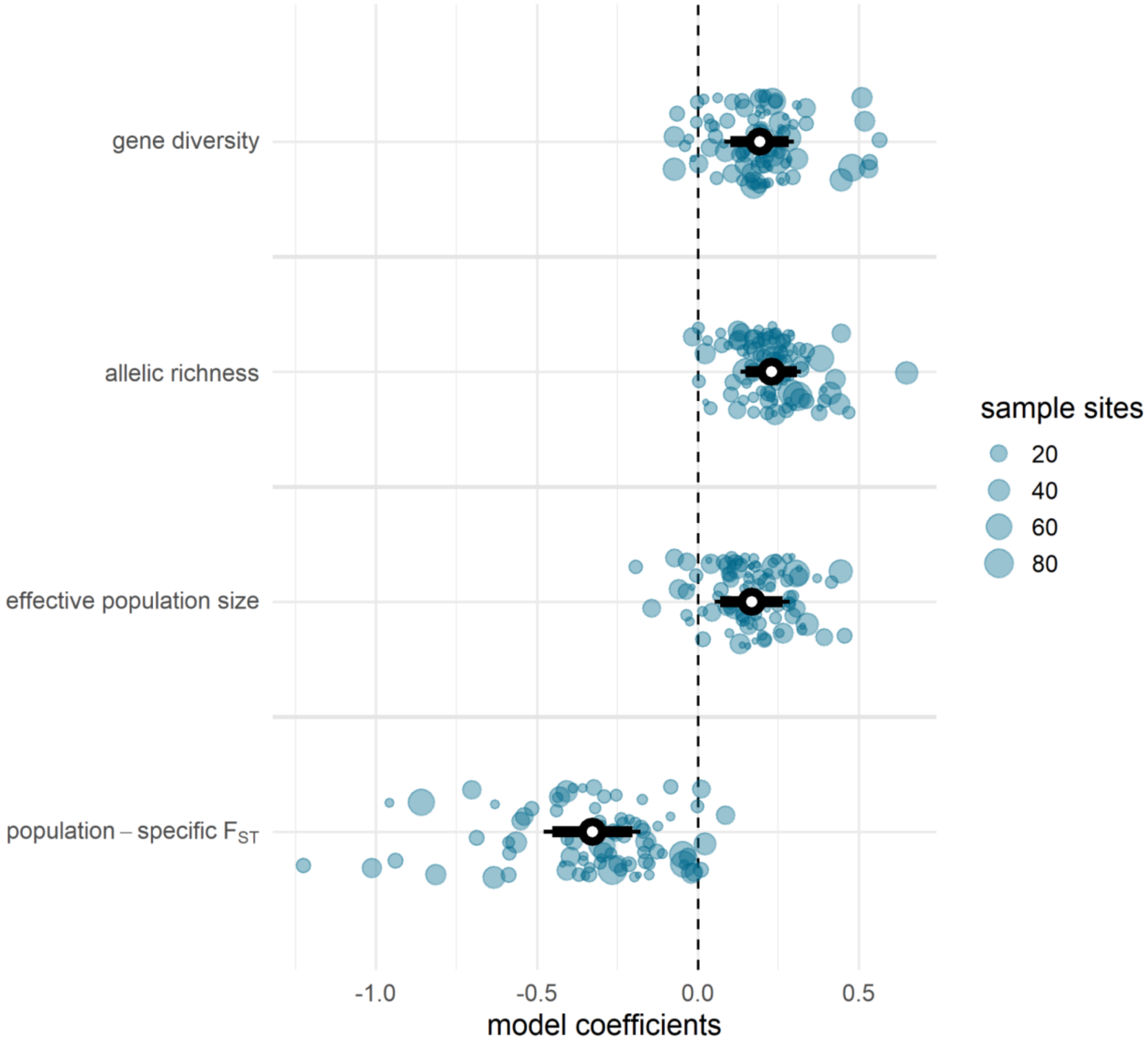

Fig. 2. Coefficient plot showing the effect of annual temperature range on genetic metrics at the site level. Open circles show the estimated overall effect of temperature range across all species, with 90 and 95% credible intervals (bold and narrow lines, respectively). Colored circles represent species-specific effects of temperature range (i.e. random slope estimates). Circle diameter is proportional to the number of locations sampled for each species. Within species, populations experiencing higher temperature seasonality show consistently higher gene diversity, allelic richness, effective population sizes and lower genetic differentiation.

Because the relationship between temperature seasonality and population genetic metrics were independent of latitudinal range position, we predicted that these patterns should be most apparent in wide-ranging species whose distributions span large latitudinal gradients in seasonality. Indeed, high-latitude species tended to have more well-connected, genetically diverse populations toward the poleward edge of their range (Fig. 3a). This relationship also held for species with larger geographic ranges (table S1, fig. S2). Our results suggest that species distributed at high absolute latitudes with larger range areas have pronounced latitudinal gradients in intraspecific genetic diversity. In contrast, no consistent latitudinal trends were detectable for species with smaller ranges or species distributed nearer the equator.

Among species, we predicted that species with larger ranges positioned at higher latitudes should have higher genome-wide diversity and lower population structure at the species level than species with smaller ranges near the equator. However, while effective population size trended in this direction, we did not detect strong latitudinal gradients across species for any genetic metric (Fig. 3b).

Links between genetic diversity and species richness

The negative association between temperature seasonality and population differentiation, and lower genetic diversity at the equatorward edge of species ranges, suggest that demographic conditions for species formation are systematically less favorable in seasonal, high-latitude environments. The contrasting relationship with temperature seasonality versus other climate factors is informative, because precipitation regimes vary in ways that do not track the simple latitudinal gradient in thermal seasonality (*12*). The consistent effect of temperature seasonality across range positions, and the absence of an equivalent effect for precipitation, therefore supports the specific mechanism invoked by the climate variability hypothesis rather than a more general climatic complexity argument.

New species form most readily when populations are genetically isolated from one another, allowing all evolutionary forces to contribute to population divergence over time (*13*–*15*). Our results align with the patterns of genetic diversity predicted in high-seasonality environments, in which seasonally varying selection pressures produce species with wider ecological niches and greater dispersal capacity (*10*). In turn, populations remain genetically connected across large areas, keeping differentiation low, maintaining genetic diversity, and slowing the accumulation of genetic differences that can eventually lead to speciation. This interpretation rests on the assumption that contemporary population genetic conditions reflect the long-term demographic environment relevant to speciation. The extent to which population differentiation predicts speciation remains debated (*15*–*18*), but our results do not require that differentiation mechanistically drives speciation in all lineages, only that the demographic conditions facilitating divergence are systematically more prevalent at low latitudes. In mammals, there is mixed evidence that speciation rates are faster and extinction rates are lower in the tropics (*19*, *20*). Intriguingly, a lighter drift load may suggest that specialist species should tend to persist over longer evolutionary time than generalists (*10*). Our results reinforce general patterns observed in mammals where geographic areas with higher species richness, and those exhibiting rapid spatial turnover in species composition, coincide with more genetically differentiated populations (*21*–*23*), highlighting an important role for spatial population demography in speciation processes relevant for broad-scale biodiversity patterns (*15*).

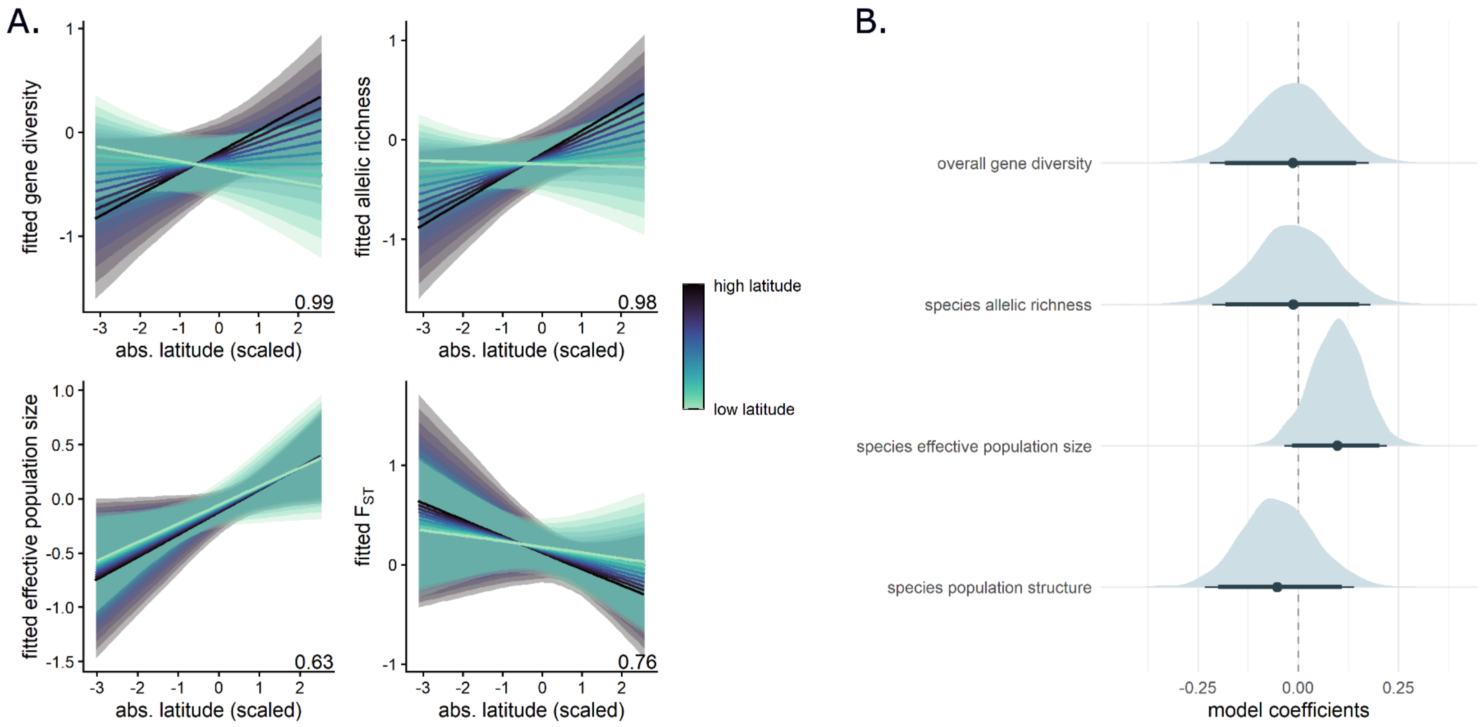

Fig. 3. Model results for intraspecific (A) and interspecific (B) genetic gradients. (A) Interactive relationships between intraspecific latitudinal gradients and absolute species level mid-range latitude. Plots show predicted genetic metrics (y axes) based on regressions including interaction terms between latitude and species level latitude. The probability of direction (the proportion of posterior draws with effects in the estimated direction) for the interaction term in each model is shown at the bottom right of all plots. Shaded regions represent 95% credible intervals. For gene diversity and allelic richness, relationships with latitude tended to become more strongly positive for high latitude species. (B) Relationships between species' absolute mid-range latitude and genetic metrics estimated at the species level. Points represent the effect of latitude flanked by 90 (bold lines) and 95% (narrow lines) credible intervals and posterior densities. Absolute latitude was not strongly related to any genetic metric at the species level, suggesting there are no gradients in genetic diversity or differentiation across species.

Reduced genetic diversity in populations nearer the poles, particularly in the northern hemisphere, is often a predicted outcome of glaciation as species expanded poleward following glacial retreat (*24*–*26*). A purely historical account would therefore predict that genetic diversity gradients should reflect expansion directionality rather than contemporary climate, be decoupled from range size, and should vary with hemisphere in ways that track glacial history rather than contemporary seasonality (*24*, *25*). Instead, we find increasingly positive intraspecific genetic diversity gradients towards the poles associated with temperature seasonality, likely reflecting the fact that species with larger ranges span greater latitudinal variation in seasonality. This pattern is more consistent with ongoing microevolutionary processes than with the residue of past demographic events.

We note that our dataset is geographically biased toward North America and Europe, regions that harbor a disproportionate number of wide-ranging species occupying highly seasonal environments (Fig. 1, fig. S1). Because the strength and direction of intraspecific latitudinal genetic gradients depend on species-level attributes such as range size and latitudinal range position (Fig. 3a), estimates of global latitudinal patterns will reflect the species composition of the dataset. Tropical and range-restricted species are comparatively underrepresented in our data (Fig 1, fig S1.), meaning our results provide strongest support for positive intraspecific diversity gradients in temperate, wide-ranging mammals. Additional sampling at low latitudes will be required to determine the extent to which the relationship between population genetics and seasonality generalizes across the full diversity of mammalian life histories and geographic distributions.

We did not detect a latitudinal gradient in genetic diversity or population structure across species (Fig. 3b). This likely reflects a limit on what contemporary intraspecific diversity can reveal about macroevolutionary history, rather than evidence against a microevolutionary role in shaping patterns of species richness. The relationship between population size and genetic diversity is far shallower than neutral theory predicts across taxa (*27*, *28*), so the range-size advantage of high-latitude species may yield only modest diversity gains that are easily obscured by variation in body size, generation time, and demographic history. In addition, anthropogenic habitat loss and fragmentation reduce effective population sizes and interrupt gene flow, with mammals showing particularly consistent declines in genetic diversity in disturbed landscapes (*29*–*31*). Because this erosion is concentrated in heavily modified landscapes that are not distributed uniformly across latitude, it can introduce spatial noise into contemporary diversity patterns, further obscuring any underlying macroevolutionary signal.

Reconciling latitudinal genetic patterns across markers and metrics

The latitudinal gradients in genetic diversity we find contrast with known gradients in species richness, endemic species richness, functional diversity, phylogenetic diversity, and with previous descriptions of latitudinal gradients of genetic diversity. The literature on latitudinal gradients in genetic diversity is small but growing, and there is no empirical consensus on whether gradients in genetic diversity exist (*32*–*34*). Part of the reason for this is unclear terminology surrounding the types of latitudinal genetic diversity gradients being quantified. For instance, latitudinal gradients of genetic diversity may include latitudinal gradients in intraspecific (*35*, *36*) or interspecific mitochondrial genetic diversity (*26*), mitochondrial genetic differentiation (*37*), multispecies averages of mitochondrial genetic diversity (*38*–*41*), interspecific chloroplast genetic diversity (*26*), intraspecific nuclear genetic diversity (*22*, *23*, *36*, *42*, *43*), nuclear genetic differentiation (*44*), and gene-specific diversity (mitochondrial cytochrome oxidase I and cytochrome b: *38*–*41*, MHC: *45*). Predictions differ for the genetic diversity of local populations or genetic differentiation, and, as we demonstrate, depend on whether such patterns are quantified at the population or species level. Our results are generally consistent with previous work on intraspecific mitochondrial genetic differentiation, where populations in low-latitude bins within species ranges were found to be more genetically differentiated than those in high latitude bins (*37*), however our findings contrast with latitudinal gradients in interspecific mitochondrial diversity (*38*). Importantly, however, different genetic markers reflect distinct evolutionary processes that can be considered holistically, but not interchangeably, in the broader context of understanding how latitudinal biodiversity gradients are maintained (*4*).

Conclusions

The latitudinal diversity gradient is one of the oldest and most conspicuous patterns in ecology, yet the mechanisms responsible for its persistence remain debated. Our results suggest that the population genetic conditions associated with population divergence vary predictably with seasonality and across latitude in ways consistent with the climate variability hypothesis. More broadly, our results suggest that the population genetic conditions associated with population divergence and species formation are unevenly distributed across latitude and continue to leave detectable signatures in the genetics of contemporary populations. This adds a new contemporary evolutionary perspective to ideas long invoked to explain the latitudinal diversity gradient.

Materials and Methods

Genetic data

We used a previously compiled database of publicly available microsatellite genotypes for terrestrial mammals to test for latitudinal relationships (*46*). In brief, these data were compiled by programmatically querying DataONE (https://www.dataone.org/) and the Dryad Digital Repository (https://datadryad.org/) with a list of species names and the search term “microsat*” (e.g., *Tamias striatus* microsat*). Because we were interested in generally describing contemporary latitudinal patterns of genetic diversity, we applied the following filters to the database: removing sites located outside species’ native ranges as identified by the authors of original works; removing hybrid species as identified by the original authors; removing historical samples where identified (pre-1900); and removing a cosmopolitan, human-associated species (*Mus musculus*). Finally, we also excluded island sites due to specific processes that may cause systematic downward biases in island genetic diversity relative to the mainland independent of latitude (i.e., bottlenecks and reduced gene flow). The final database encompassed 100 mammal species, 1426 sample locations (sites) and 59587 individuals (Fig. 1). The median number of individuals sampled at each site was 23 (range 5 – 2444 individuals), and the median number of sample locations per species was 7 (range 1 – 82 sites). We use *dataset* to refer to a single genotype file for one species of a given study (a unique combination of species and study).

To describe latitudinal patterns of genetic diversity and differentiation, we estimated four genetic metrics at site and species levels using the *adegenet* and *hierfstat* packages in R (*47*, *48*). First, we used two alternative metrics of genetic diversity: gene diversity and allelic richness. Gene diversity is the probability of sampling two different alleles in a non-random mating population (*49*). We estimated gene diversity at each site, and at the species level we estimated the overall gene diversity across all sites within each dataset. Allelic richness is a count of alleles in a sample of individuals standardized using sample-based rarefaction to account for variation in sample size across sites (*50*). The genetic database only retains sites with a minimum of 5 sampled individuals, thus we rarefied allelic richness to a minimum of 10 alleles across the entire database to ensure comparability. To estimate allelic richness at the species level, we grouped all individuals within a dataset into a single population and re-estimated allelic richness, retaining a 10-allele minimum for rarefaction because this was the smallest sample size across all datasets.

Next, we estimated contemporary effective population size, a measure of the strength of genetic drift, using the linkage disequilibrium method implemented in NeEstimator v2 (*51*). Contemporary effective population size measures signatures of genetic drift in the parental generation of sampled individuals at each locality. The linkage disequilibrium method performs well for small effective sizes, however returns estimates of infinity if too few individuals were sampled and sampling error overwhelms the signal of genetic drift, or if effective population sizes are very large (*52*). We set estimates of infinity to NA and removed them from the final analysis. At the species level, we analyzed the average effective population size of local populations within a hierarchical model using random intercepts for species. We used the average effective population size of species rather than pooling all individuals within datasets because this would estimate a metapopulation effective population size which is only appropriate under high migration rates (*53*).

Finally, we estimated genetic differentiation per site and overall population structure at the species level. At the site level we used population-specific F_{ST} (*54*), which estimates how genetically differentiated sites are from a single common ancestor of all sites in the sample. Genetic differentiation is only estimable when at least two sites were sampled in original datasets, thus datasets with single populations were omitted from all F_{ST} analyses. We estimated a species-level measure of population structure using G'_{ST} (*55*). G'_{ST} is a variant of G_{ST} (*49*), which estimates F_{ST} for multiallelic markers. Maximum G_{ST} values are determined by the genetic diversity of subpopulations, and are thus not comparable across datasets or species. G'_{ST} addresses this issue by rescaling G_{ST} to remove its dependency on the average genetic diversity of subpopulations.

Species attributes

We obtained spatial distribution data for terrestrial mammals from the International Union for the Conservation of Nature (*56*). We filtered species range data to retain only regions where species were recorded as extant, native, and resident. We identified the mid-range latitude for each species by taking the latitude of the range centroid using the *sf* package (*57, 58*). We used the function st_area() to calculate the size of each distribution range.

We obtained species body mass (g) data from PanTHERIA (*59*) using the *traitdata* package version 0.0.1 (*60*). We manually added body masses for species with missing data (6 species) using reference information from the Global Biodiversity Information Facility (www.gbif.org/species).

Climate data

We downloaded raster maps of bioclimatic variables from the WorldClim database (*61*) at a spatial resolution of 5 arc-minutes. We focused on four major climate variables: annual mean temperature (BIO1), temperature annual range (BIO7), annual precipitation (BIO12), and precipitation seasonality (BIO15). We extracted the mean climate value within a 10 km buffer around each sampling location using the *terra* package (*62*). Locations with missing climate data were excluded from the climate model analyses (4 observations).

Analysis

We used hierarchical Bayesian generalized linear models to test our predictions related to seasonality and inter- and intraspecific latitudinal gradients in genetic metrics. We fit all models with *brms* (*63*) using normally distributed priors (mean 0, SD 1) for fixed effects, and default priors for all other parameters. To retain the same directionality for latitudinal relationships across hemispheres, we used absolute latitude in all models. We log-transformed effective population size, body mass and range size, and scaled and centered all predictor and response variables before analysis. All analyses were conducted in R Version 4.3.2 (*64*).

Intraspecific models. We modeled the effect of temperature seasonality on each genetic metric in a series of hierarchical linear regressions incorporating random slopes and intercepts for species. To account for spatial autocorrelation in model residuals, we used spatial simultaneous autoregressive models implemented in *brms*. Our genetic response variables included site-level measures of gene diversity, allelic richness, effective population size, and population-specific F_{ST}, resulting in a total of 4 models. In this model structure, random intercepts account for variation in the means of each genetic metric across species, and random slopes allow the relationship between genetic metrics and temperature seasonality to vary per species.

To test for latitudinal genetic gradients within species, we used the same model structure as above with site-level latitude as a predictor. By using random slopes, relationships with latitude are estimated for each species. This means we did not make assumptions about the strength or direction of latitudinal genetic patterns of individual species; we instead asked the extent to which latitudinal genetic relationships are consistently negative or positive across all species in the sample. An overall effect size of zero for latitude may therefore indicate that genetic metrics for all species do not vary with latitude (all species-specific slopes near zero), or alternatively that the effect sizes for individual species relationships with latitude vary from negative to positive, effectively balancing out to a zero overall effect size.

One species, *Apodemus flavicollis*, had a markedly large effect size for gene diversity due to a study-level difference in this metric that was confounded with latitude. In our database, 31 species were represented in multiple studies. This means that using species as a random effect does not fully account for study-specific variation across datasets. However, a majority (69%) of species are from single studies, and some studies include multiple species, making it infeasible to simultaneously account for species- and study-level variation with random effects in our models.

We addressed this issue in two ways. First, because *A. flavicollis* was the only strong outlier, we ran a parallel set of models coding these two studies as separate species (i.e., Apodemus_flavicollis1 and Apodemus_flavicollis2). Second, we ran intraspecific models using a dataset-specific grouping factor (genotype file name) for random slopes and intercepts instead of species. Dataset as a random effect uniquely identifies each species-study combination. . However, due to biases toward the study of temperate species in the database, they were overrepresented in models with dataset as a random effect, pulling overall effect estimates closer to those of temperate species. Because of this, we chose to present models with species as a random effect with *A. flavicollis* coded as two species in the main text.

Interspecific models. We then tested for evidence of interspecific latitudinal gradients, which may emerge if species' genetic diversity, effective population size, or overall population structure were related to the latitudinal positions of their range or gradients in range size. We fit a series of models regressing species' mid-range latitude on genetic metrics. We fit simple linear regressions with species-level estimates of gene diversity, allelic richness, or population structure as the response variable. We did not have enough replication of species across studies to account for study-level variation with random effects, thus we took the median allelic richness and mean gene diversity or population structure in cases where one species had estimates from multiple studies. For effective population size, we fit a hierarchical model including random intercepts for species with population-level effective population size as the response and species mid-range latitude as predictor. In this model, species random intercepts estimate the average effective population size of species.

Interaction models. We next tested the extent to which relationships between genetic metrics and seasonality were consistent across latitude. To do this, we modeled each genetic metric as a function of site-level temperature seasonality, species mid-range latitude, and their interaction. We retained the same species-level random effects and spatial autoregressive terms as in the intraspecific models described above. Here, the interaction term describes how estimated effects of temperature seasonality vary depending on species range position.

We were primarily interested in the effects of temperature seasonality on populations, however other climate factors may also affect population genetic diversity and differentiation. We therefore ran parallel analyses using three other climate variables estimated at each sample location: mean annual temperature, mean annual precipitation, and precipitation seasonality. With this set of models, we were able to determine whether temperature seasonality had a unique effect on population genetic metrics, or whether its effects were correlated with climatic gradients in general.

Finally, we predicted that stronger seasonality gradients toward the poles should cause genetic diversity gradients within species ranges to become increasingly steep with increasing range size and latitudinal range position. We tested whether range size and latitudinal range position (midrange latitude) moderated the strength and direction of latitudinal patterns across species for each genetic metric. We additionally tested whether body size affected intraspecific genetic diversity gradients because it is correlated with range size and also tends to increase with latitude in mammals (Bergmann's Rule). We included each species-level predictor (mid-range latitude, range size, body mass) and their interactions with site-level latitude as additional predictors in our intraspecific models. Interaction terms allowed the effect of site-level latitude to vary conditional on each species-level variable. We modeled each species-level variable separately for a series of three models per genetic metric. We log-transformed, scaled, and centered body mass and range size for comparability across models. We scaled and centered the absolute values of midrange latitude.

To better describe the conditional effects of latitude dependent on interaction terms with species-level variables, we assessed the probability that latitudinal relationships were negative or positive conditional on low and high values for body size, range size, and mid-range latitude. We did this using the hypothesis() function in *brms* to test whether the effect of latitude was greater or less than 0 while conditioned on body size, range size, or mid-range latitude being large (+1 SD) or small (-1 SD).

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Author contributions:

Conceptualization: ACG, CS, MG, CJG, JPL

Data curation: ACG, CS

Methodology: ACG, CS, CJG

Investigation: ACG, CS, MG, JPL

Visualization: ACG, CS

Funding acquisition: ACG, CS, MG

Project administration: ACG, CS

Writing – original draft: ACG, CS, CJG, JPL

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Supplementary Materials

Figs. S1 to S3

Tables S1 to S2

Supplementary Materials for

Microevolutionary Responses to Seasonality Contribute to the Latitudinal Biodiversity Gradient

Anne-Céline Granjon*, Michael Gerth, Jean-Philippe Lessard, Colin J. Garroway, Chloé Schmidt*
Corresponding authors: anne-celine.granjon@idiv.de, chloe.schmidt@dal.ca

The PDF file includes:

Figs. S1 to S3
Tables S1 to S2

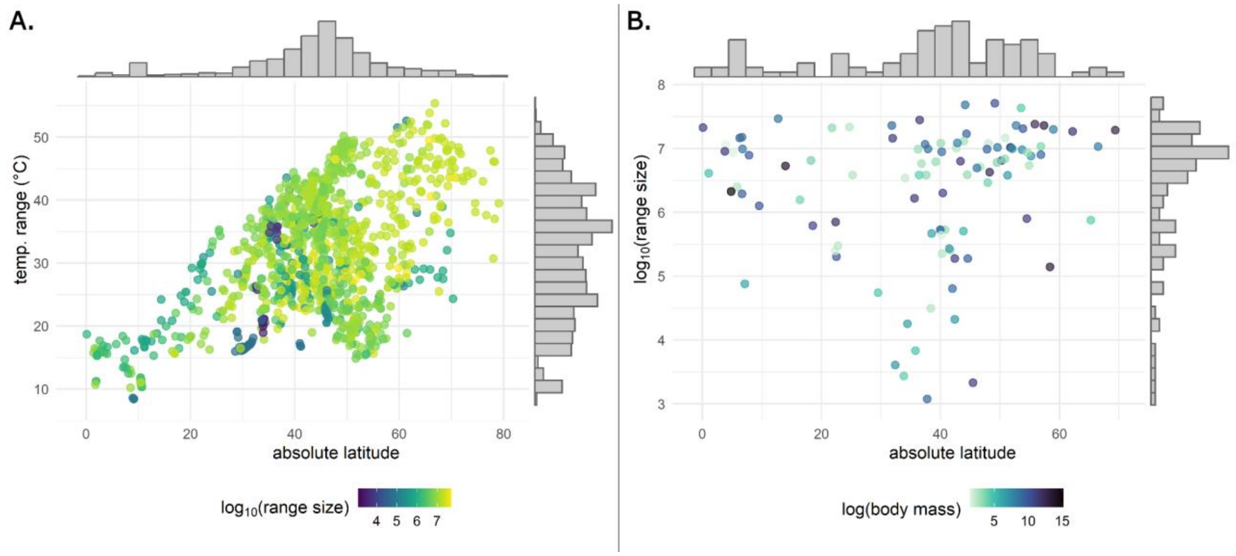

Fig. S1. Raw data summary. (A.) Distribution of annual temperature range of populations in our database across absolute latitudes and species range size. Each point represents one population, color gradient represents the species' range size (log10 scale). (B.) Distribution of species in our database across latitudinal range position (midrange latitude), range size, and body mass. Each point represents one species, color gradient represents body mass (log scale) with 100 species sampled in total.

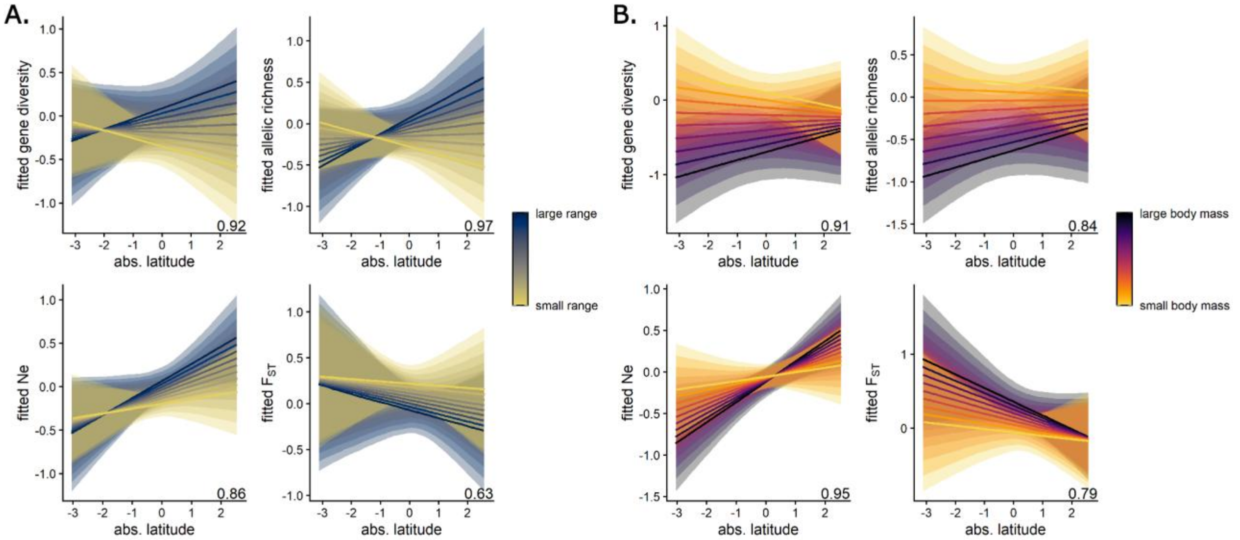

Fig. S2. Interactive relationships between local population latitude and species-level attributes: log range area (A) and log adult body mass (B). Plots show predicted genetic metrics (y axes) based on regressions including interaction terms between scaled absolute latitude and species-level attributes for different levels of each attribute. The probability of direction (the proportion of posterior draws with effects in the estimated direction) for the interaction term in each model is shown at the bottom right of all plots. Shaded regions represent 95% credible intervals. Populations of species with large body sizes and species with large geographic range areas tended to have higher genetic diversity at the poleward edge of their range (Table S1).

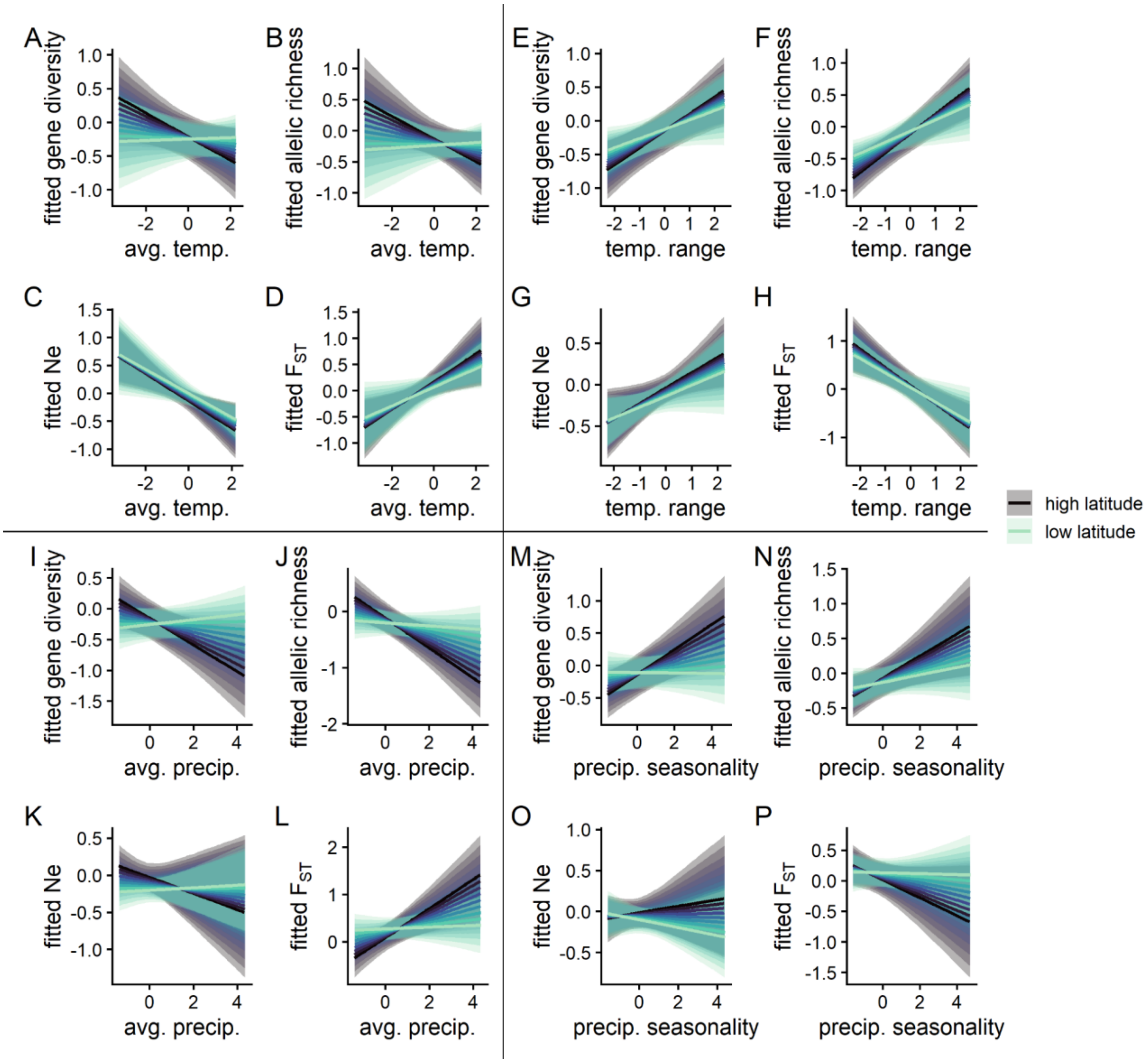

Fig. S3. Interactive relationships between local climate variables and species mid-range latitude, including: average temperature (A-D), temperature range (E-H), average precipitation (I-L), and precipitation seasonality (M-P). Plots show predicted values of genetic metrics (y axes) based on regressions including interactions between species mid-range latitude and (scaled) population-level climate variables. Shaded regions represent 95% credible intervals. The strength of the interaction was variable across all climate variables and genetic metrics, but there was no evidence for a variable effect of temperature seasonality depending on latitude (Table S2). Instead, temperature seasonality had a consistent relationship with genetic metrics across all latitudes (Table S2).

Table S1.

Results summary for models including latitude of local populations, species attributes (mid-range latitude, range size, or body mass), and their interaction as predictors for each genetic response variable (gene diversity, allelic richness, effective population size, and population-specific F_{ST}). Effect sizes (with 95% credible intervals), and sample size (number of species, number of local populations) are reported for each model.

	Gene Diversity	**Allelic Richness**	**Effective Population Size**	**Population-specific F_{ST}**
Predictors	*Estimate* *CI (95%)*	*Estimate* *CI (95%)*	*Estimate* *CI (95%)*	*Estimate* *CI (95%)*
Latitude	0.07 -0.08 – 0.22	0.11 -0.04 – 0.26	0.19 0.34 – 0.35	-0.11 -0.32 – 0.10
Mid-range Latitude	0.08 -0.17 – 0.31	0.05 -0.18 – 0.28	-0.04 -0.20 – 0.13	-0.03 -0.24 – 0.19
Latitude x Mid-range Latitude	0.14 0.02 – 0.25	0.12 0.01 – 0.24	0.02 -0.09 – 0.12	-0.05 -0.20 – 0.09
Latitude	0.01 -0.13 – 0.15	0.03 -0.10 – 0.17	0.15 0.03 – 0.27	-0.11 -0.29 – 0.07
Body Mass	-0.40 -0.63 – -0.18	-0.39 -0.59 – -0.20	-0.03 -0.16 – 0.09	0.21 0.03 – 0.40
Latitude x Body Mass	0.10 -0.04 – 0.23	0.07 -0.06 – 0.20	0.09 -0.01 – 0.21	-0.07 -0.25 – 0.10
Latitude	0.02 -0.13 – 0.16	0.05 -0.10 – 0.19	0.13 0.00 – 0.26	-0.06 -0.24 – 0.13
Range area	0.22 0.06 – 0.37	0.17 0.03 – 0.32	0.13 0.03 – 0.23	-0.14 -0.28 – -0.00
Latitude x Range area	0.11 -0.04 – 0.26	0.14 -0.00 – 0.29	0.07 -0.06 – 0.21	-0.03 -0.21 – 0.15
n_{species}	101	101	100	84
n_{sites}	1426	1426	1128	1387

Table S2.

Results summary for models including local climate, species mid-range latitude, and their interaction as predictors for each genetic response variable (gene diversity, allelic richness, effective population size, and population-specific F_{ST}). Effect sizes (with 95% credible intervals), probabilities of direction, and sample size (number of species, number of local populations) are reported for each model. The probability of direction is the probability that a given effect is positive or negative, measured here as the proportion of posterior draws with the same sign as the median.

	Gene Diversity	**Allelic Richness**	**Effective Population Size**	**Population-specific F_{ST}**
Predictors	*Estimate* *CI (95%)*	*Estimate* *CI (95%)*	*Estimate* *CI (95%)*	*Estimate* *CI (95%)*
Latitude	0.02 -0.20 – 0.24	0.06 -0.15 – 0.27	-0.06 -0.22 – 0.09	0.04 -0.14 – 0.22
Mean Temperature	-0.08 -0.19 – 0.04	-0.08 -0.22 – 0.06	-0.23 -0.37 – -0.09	0.22 0.07 – 0.37
Latitude x Mean Temperature	-0.09 -0.20 – 0.01	-0.10 -0.22 – 0.01	-0.02 -0.12 – 0.09	0.04 -0.07 – 0.16
Latitude	-0.02 -0.24 – 0.20	-0.02 -0.22 – 0.18	0.05 -0.09 – 0.18	0.03 -0.19 – 0.24
Temperature seasonality	0.19 0.08 – 0.30	0.24 0.14 – 0.33	0.16 0.03 – 0.29	-0.34 -0.49 – -0.18
Latitude x Temp. seasonality	0.06 -0.04 – 0.16	0.07 -0.03 – 0.16	0.03 -0.08 – 0.14	-0.04 -0.18 – 0.10
Latitude	0.05 -0.16 – 0.25	0.05 -0.12 – 0.22	0.09 -0.02 – 0.21	-0.10 -0.28 – 0.09
Mean precipitation	-0.09 -0.18 – 0.02	-0.14 -0.25 – -0.04	-0.05 -0.17 – 0.09	0.16 0.03 – 0.29
Latitude x Mean precipitation	-0.13 -0.20 – -0.05	-0.12 -0.19 – -0.04	-0.06 -0.16 – 0.06	0.14 0.04 – 0.24
Latitude	-0.02 -0.22 – 0.18	0.03 -0.14 – 0.19	0.04 -0.08 – 0.17	-0.06 -0.23 – 0.12
Precipitation seasonality	0.09 0.01 – 0.17	0.11 0.02 – 0.20	-0.00 -0.10 – 0.11	-0.08 -0.19 – 0.04
Latitude x Precip. seasonality	0.10 0.03 – 0.17	0.05 -0.02 – 0.13	0.04 -0.05 – 0.13	-0.07 -0.16 – 0.02
n_{species}	101	101	100	84
n_{sites}	1426	1426	1128	1387