and derivatized compounds) are identical for the extant and fossil samples (table S2). The extract of a seed cone of extant *Glyptostrobus pensilis* (Chinese water pine) contained 6,7-dehydroferruginol, ferruginol, sugiol, pimaric acid (b), and 18- or 19-hydroxyferruginol (c), as observed in the Miocene *Glyptostrobus oreognonis* cone, but isochamaecydin and chamaecydin could not be detected (13) (fig. S1).

Terpenoids are abundant constituents of extant conifers and are used as chemosystematic characteristics (18-21). Ferruginol, 6,7-dehydroferruginol, and sugiol are common in extant conifers, especially in the families Cupressaceae, Taxodiaceae, and Podocarpaceae (18, 20-22). The unusual triterpenoids isochamaecydin and chamaecydin have hitherto been identified in only two conifer species, Hinoki cypress (*Chamaecyparis obtusa*) and Sugi cedar (*Cryptomeria japonica*) (17, 23, 24). We were able to confirm these findings and identified isochamaecydin and chamaecydin in the extracts of seed cones of both species. *Taxodium*, *Glyptostrobus*, and *Cryptomeria* were formerly treated as members of the Taxodiaceae, and *Chamaecyparis* was assigned to the Cupressaceae, but Taxodiaceae and Cupressaceae were recently merged into one family, Cupressaceae sensu lato (s. l.) on the basis of morphological and molecular genetic data (25, 26). The terpenoid compositions detected here in fossil and extant species of former Taxodiaceae support this merger. The similarity of the terpenoids in *Taxodium* and *Glyptostrobus* is not surprising, as these genera are closely related (25). The terpenoid characteristics of fossil *Taxodium balticum* and *Glyptostrobus oreognonis* identified here are thus in accordance with their systematic assignment to the Cupressaceae s. l. based on their morphological characteristics.

The results show that polar natural product precursors can be preserved unaltered in fossil conifers and can be used as chemosystematic markers. The applied methods offer a new approach for studying the (paleo)chemosystematics and phylogeny of conifers. The low degree of degradation observed in the analyzed material may be due to the preservation of terpenoids in resinous plant material where the compounds are probably trapped in the resin and protected from degradation or bonding into kerogen. Furthermore, the clayey sediments should prevent the oxidation of the fossil plant material by oxygen-rich waters.

**References and Notes**


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**Global Biodiversity, Biochemical Kinetics, and the Energetic-Equivalence Rule**

Andrew P. Allen,* James H. Brown, James F. Gillooly

The latitudinal gradient of increasing biodiversity from poles to equator is one of the most prominent but least understood features of life on Earth. Here we show that species diversity can be predicted from the biochemical kinetics of metabolism. We first demonstrate that the average energy flow of populations is temperature invariant. We then derive a model that quantitatively predicts how species diversity increases with environmental temperature. Predictions are supported by data for terrestrial, freshwater, and marine taxa along latitudinal and elevational gradients. These results establish a thermodynamic basis for the regulation of species diversity and the organization of ecological communities.

Global gradients in biodiversity exist for all major groups of terrestrial (J), freshwater (2), and marine taxa (3), but the general principles underlying their origin and maintenance remain unclear (4, 5). Here we present a theoretical framework that explains gradients of species diversity in terms of energetics. Our model is derived by extending the well-established "energetic-equivalence rule" (6) to include temperature. In its original form, the energetic-equivalence rule states that the total energy flux of a population per unit area, $B_T$, is invariant with respect to body size. Species of different size have similar values of $B_T$ because individual metabolic rates, $B_i$, increase with body size, $M_i$, as $B_i \propto M_i^{3/4}$, whereas population densities per unit area, $N_i$, decrease with body size as $N_i \propto M_i^{-3/4}$ ($B_T = N_i B_i \propto M_i^{-3/4}M_i^{3/4} = M_0$). This inverse relation between abundance and body size is observed for plants and for endothermic and ectothermic animals; it reflects mechanistic connections between individual metabolic rates, rates of energy flow by populations, and the partitioning of available energy among species in a community (6, 7).

We can extend the energetic-equivalence rule to include temperature by incorporating the biochemical kinetics of metabolism. Recent work has shown that whole-organism metabolic rate varies with body size and temperature as $\dot{B} = b_0 M^{\alpha-1} e^{-\varepsilon T}$ (8), where $b_0$ is a normalization constant independent of size...
The Boltzmann factor, $e^{-E/kT}$, describes the temperature dependence of metabolic rate, where $E$ is the activation energy of metabolism ($-0.78$ eV or $-1.25 \times 10^{-19}$ J) ($9$), $k$ is Boltzmann’s constant (8.62 $\times$ 10$^{-5}$ eV K$^{-1}$), and $T$ is absolute temperature ($K$). The total energy flux of a population is therefore $B_t = N B_t = N b_i M_i^{3/4} e^{-E/kT}$, which yields

$$\ln(N M_i^{3/4}) = \left(E/1000k\right)(1000/T) + C_0 \quad (1)$$

where constancy of $C_0 = \ln(B_i/b_i)$ with respect to temperature follows from our extension of the energetic-equivalence rule. Temperatures of ectotherms are approximately equal to ambient environmental temperatures, $T_{env}$, whereas temperatures of endotherms are $\sim40^\circ C$. Equation 1 therefore leads to three predictions for the relation between population density and temperature: (i) for ectotherms, the natural logarithm of mass-corrected population density should be a linear function of $1000/T_{env}$; (ii) the slope of this linear relation should be $E/1000k \approx 9.0 K$ for both plants and animals because the two groups share similar activation energies for metabolism ($8$); and (iii) for endotherms, mass-corrected population density should be independent of $T_{env}$.

Abundance data compiled on a variety of plant and animal species provide strong support for all three predictions. First, the natural logarithm of mass-corrected population density for tree species throughout the world shows a positive, linear relation to inverse absolute temperature (Fig. 1A). Second, the 95% confidence interval (CI) for the slope of this relation includes the predicted value of 9.0 K ($\bar{x};$ 95% CI, 7.66 to 10.17). Data on mass-corrected population density for terrestrial vertebrate- and invertebrate-ectotherms also support the first and second predictions (slope $\bar{x};$ 95% CI, 6.61 to 16.88) (Fig. 1B). Finally, in accordance with the third prediction, mass-corrected population density shows no significant relation to environmental temperature for endothermic mammals (slope $\bar{x};$ 95% CI, $-0.82$ to 2.73) (Fig. 1C).

To control for body temperature, we multiply the population densities in Fig. 1, B and C, by the Boltzmann factor, $e^{-E/kT}$, assuming a temperature of $40^\circ C$ for mammals and temperatures equal to $T_{env}$ for ectotherms. When temperature-corrected population density is plotted against body size on a natural logarithmic scale, endotherms and ectotherms fall on approximately the same line (Fig. 2). Moreover, the slope of this relation is close to the predicted value of $-3/4$ ($\bar{x} = -0.78$; 95% CI, -0.82 to -0.74). Given that the intercept in Fig. 2 provides an estimate of $C_0 = \ln(B_i/b_i)$, that $e^{-C_0} = e^{-19.63} = B_i/b_i = 2.95 \times 10^{-9} \text{ km}^{-2} \text{ g}^{3/4}$, and that $b_i = 2.65 \times 10^{10} \text{ W} \text{ g}^{-3/4}$ (9), we can estimate $B_i$ to be $\sim80 \text{ W m}^{-2}$ regardless of taxon, body size, temperature, or geographic location.

Having established temperature invariance for $B_t$, we can now use the energetic-equivalence rule to predict changes in the diversity of ectotherms along temperature gradients. The average population density in a community composed of $J$ individuals and $S$ species is $\bar{N} = J/S$, where $A$ is the area of the plot delimiting the community and

$$J = \sum_{i=1}^{S} N_i A_i \quad (10)$$

The average metabolic rate of an ectotherm is $\bar{B} = \bar{B} e^{-E/kT_{env}}$, where $\bar{B} = b_i M_i^{3/4}$ and is calculated on the basis of the frequency distribution of body sizes for species constituting the community of interest. Holding $A$ constant across community samples, $\bar{B}_t = N \bar{B} = (J/S) \bar{B} e^{-E/kT_{env}}$. Thus, we find strong support for predictions (i) and (ii) by using two independent data sets on tree diversity along gradients of latitude in North America and elevation in Costa Rica (Fig. 3, A and B). For both data sets, the relation between the natural logarithm of species richness and inverse absolute temperature is approximately linear, and the slopes are both close to the predicted value of $-9.0 K$ (Table 1).

![Fig. 1. Effects of average ambient temperature on the natural logarithm of mass-corrected population density for trees (19, 22) (A); terrestrial ectotherms including amphibians, reptiles, and invertebrates (6) (B); and terrestrial mammals from around the world (6) (C).](fig1.png)

![Fig. 2. Effects of body size on temperature-corrected population density for endotherms and ectotherms. The data plotted here are the same as in Fig. 1, B and C. The line was fitted by ordinary least-squares regression (24) after applying a natural logarithmic transformation to both variables.](fig2.png)
Data on amphibian richness along latitudinal and elevational gradients also support these two predictions with slopes statistically indistinguishable from each other and from those observed for the trees (Figs. 3, C and D). Finally, latitudinal data on riverine fish, marine gastropods, and even the number of fish ectoparasite species per host support all three predictions of the model (Fig. 4). Overall, we see that the slopes are consistently close to the predicted value of –9.0 K (x = –9.21; range, –7.17 to –10.81), although the confidence intervals do not always include this value.

We do not mean to imply that temperature is the only variable that affects biodiversity. The significant residual variation about the relations in Figs. 3 and 4 emphasizes the importance of other variables including biogeographic history (13), habitat heterogeneity (14), area (15), and geometric constraints on species distributions (16). Indeed, we only predict the slopes of the diversity-temperature plots. The intercepts may vary by taxon, habitat, and sampling method. In particular, N, and therefore \( \frac{\Delta}{A} \), will vary as functions of plot size A, even if \( JA \) is held constant, because \( S \) increases nonlinearly with \( J \) as a consequence of sampling, turnover in species composition through space (12), and the fractal-like distribution of habitat (10, 14).

Nevertheless, our model accounts for much of the variation in biodiversity (Table 1). Of more importance, it yields testable, quantitative predictions based on first principles of biochemical kinetics and provides a theoretical framework for understanding how temperature and productivity regulate biodiversity. The species-energy hypothesis proposes that biodiversity is positively correlated with productivity because more productive environments contain more individuals and can therefore support more species populations above some minimum size required for persistence (1, 17). Data for endotherms support this hypothesis. The average population densities of mammals are temperature invariant. This implies that the observed increase in mammal diversity toward the tropics (1) results from an increase in total density, \( JA \), for mammals. By contrast, average population densities of trees and other ectotherms show an inverse Boltzmann relation to temperature \( (N \propto e^{-E/kT}) \). This result, combined with the observed Boltzmann relation of diversity to temperature for independent data collected on a variety of ecotothermal taxa \( (S \propto e^{-E/kT}) \), supports our model assumption that total ecotothermal abundance is approximately independent of temperature \( (JA = NS \propto e^{-E/kT}) \).

Temperature influences the diversity of terrestrial and aquatic ectotherms primarily through its effects on the biochemical kinetics of metabolism. Metabolic rates, in turn, dictate resource requirements at the level of the individual and rates of resource supply required of the ecosystem to maintain communities composed of multiple individuals. Evolutionary rates are ultimately constrained by generation times of individuals and mutation rates. Both of these rates are correlated with metabolic rates and show the same Boltzmann relation to temperature (9, 18). Our results therefore support the hypothesis that elevated temperatures increase the standing stock of species by accelerating the biochemical reactions that control speciation rates (5).

Fig. 3. Effects of mean annual ambient temperature on species richness for North American trees in blocks of 2.5° by 2.5° south of 50°N, and 2.5° (longitude) by 5° north of 50°N (1) (A); Costa Rican trees along a 2600-m elevational gradient on Volcan Barva (25), and (B); North American amphibians in blocks of 2.5° by 2.5° south of 50°N, and 2.5° (longitude) by 5° north of 50°N (1) (C); and Ecuadorian amphibians along a 4000-m elevational gradient in the Andes (26) (D). Temperature estimates were obtained from the sources cited. Lines were fitted by reduced-major-axis regression (21, 24).

Fig. 4. Effects of mean annual water temperature on richness for fish species in watersheds throughout the world (2) (A), numbers of marine prosobranch gastropod species per latitudinal degree band along the continental shelves of the Americas (2) (B), and ectoparasite species per host for marine teleost fish ranging from Antarctica to the tropics (27) (C). Temperature estimates were obtained from the sources cited. Lines were fitted by reduced-major-axis regression (21, 24).

Table 1. Summary of temperature-biodiversity relations in Figs. 3 and 4, including 95% confidence intervals (CI) for the slope estimates.

<table>
<thead>
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<th>Group</th>
<th>Data set</th>
<th>Slope</th>
<th>95% CI</th>
<th>Intercept</th>
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<th>( n )</th>
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References and Notes

Geographic Range Size and Determinants of Avian Species Richness

Walter Jetz1,2* and Carsten Rahbek3

Geographic patterns in species richness are mainly based on wide-ranging species because their larger number of distribution records has a disproportionate contribution to the species richness counts here. We demonstrate how this effect strongly influences our understanding of what determines species richness. Using both conventional and spatial regression models, we show that for sub-Saharan African birds, the apparent role of productivity diminishes with decreasing range size, whereas the significance of topographic heterogeneity increases. The relative importance of geometric constraints from the continental edge is moderate. Our findings highlight the failure of traditional species richness models to account for narrow-ranging species that frequently are also threatened.

Most analyses of determinants of geographic patterns in species richness have traditionally looked only at overall species richness patterns, but this does not give a representative picture for most taxa. Wide-ranging species contribute many more distribution records to a species richness pattern than do narrow-ranging species. Thus, although most species tend to have range sizes well below average (1–3), insights from conventional biogeographical analyses of overall species richness are in fact largely based on wide-ranging species. This may produce a profound bias in the presumed determinants of species richness in space that any general model should address.

Determinants of overall species richness singled out so far include measures of productivity (4, 5), habitat heterogeneity (6, 7), area (8, 9), regional and evolutionary history (10), synergism between climate and evolutionary history (11), and effects from geometric constraints imposed by distribution boundaries such as the continental edge (12–14). Here we address the potential effect of range size on the pattern of species richness and its presumed determinants (15), using a 1°-resolution database summarizing the distribution of the 1599 breeding bird species endemic to sub-Saharan Africa (Fig. 1B) (15).

We first examine potential factors one by one, using traditional general linear model (GLM) and spatial linear model (SLM) regression analyses of overall species richness (see table S1 for all single-predictor results). We focus on the latter approach, which avoids inflation of type I errors and invalid parameter estimates due to spatial autocorrelation (15–17). Our results broadly confirm the important role of net primary productivity (NPP, including a quadratic term, NPP2) and habitat heterogeneity (HabHet) on species richness asserted in previous studies (4–7). Both emerge as main predictors of overall species richness (single-predictor SLM: t = (HabHet) = 22.03; two-predictor SLM (NPP + NPP2): t (NPP) = 25.08, t (NPP2) = −15.62; all P < 0.001). These three variables together explain around 66% of the variance (SLM: r2 of fitted values against observed values, log likelihood = −12,440). Annual precipitation (Rain) also has high predictive value (single-predictor SLM: t = 26.14), but because it is strongly collinear with NPP [rS = 0.91, n = 1738; two-predictor SLM (NPP + Rain): t (Rain) = 8.69, t (NPP) = 13.66], we did not examine it further.

Other core environmental predictors include topographic heterogeneity [TopHet, measured as altitudinal range; single-predictor SLM: t = 13.77 (table S1)] and mean maximum daily temperature (MaxTemp; single-predictor SLM: t = −17.74). In contrast to the suggested direct positive link between temperature as a measure of energy and species richness (18, 19) and some of the empirical findings from South America (11), the relationship with maximum temperature is strongly negative: High-temperature quadrats support fewer species than do quadrats with more moderate temperatures. This may suggest an envelope effect of temperature on homeotherms, with both cold and hot temperatures adversely affecting species richness in addition to and in conjunction with other factors.

Distribution constraints imposed by continental boundaries, together with the tendency of ranges to be continuous at larger scales of analysis, can demonstrably influence the geography of species richness, with large levels of species richness expected in the middle of a bounded domain (12–14, 20). We found that geometric constraints modeled in two dimen-