

The global distribution of diet breadth in insect herbivores

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Understanding variation in resource specialization is important for progress on issues that include coevolution, community assembly, ecosystem processes, and the latitudinal gradient of species richness. Herbivorous insects are useful models for studying resource specialization, and the interaction between plants and herbivorous insects is one of the most common and consequential ecological associations on the planet. However, uncertainty persists regarding fundamental features of herbivore diet breadth, including its relationship to latitude and plant species richness. Here, we use a global dataset to investigate host range for over 7,500 insect herbivore species covering a wide taxonomic breadth and interacting with more than 2,000 species of plants in 165 families. We ask whether relatively specialized and generalized herbivores represent a dichotomy rather than a continuum from few to many host families and species attacked and whether diet breadth changes with increasing plant species richness toward the tropics. Across geographic regions and taxonomic subsets of the data, we find that the distribution of diet breadth is fit well by a discrete, truncated Pareto power law characterized by the predominance of specialized herbivores and a long, thin tail of more generalized species. Both the taxonomic and phylogenetic distributions of diet breadth shift globally with latitude, consistent with a higher frequency of specialized insects in tropical regions. We also find that more diverse lineages of plants support assemblages of relatively more specialized herbivores and that the global distribution of plant diversity contributes to but does not fully explain the latitudinal gradient in insect herbivore specialization.

host range | latitudinal gradient | niche width | Pareto distribution | specialization

Variation in dietary specialization among individuals, populations, and species drives numerous ecological and evolutionary processes. Differences in diet breadth and composition mediate the coexistence of competitors (1), the persistence of species in the face of environmental disturbance (2), the diversity of interactions, and the stability of entire networks of interacting species (3, 4). At the ecosystem level, the top-down effect of predators on primary productivity can be controlled by the level of herbivore specialization (5). At the scale of evolutionary

diversification, differences among lineages in rates of speciation and extinction can be understood in terms of variation in dietary specialization (6). Progress in addressing all of these issues has been limited by disparity in the methods used to quantify specialization (7) and the rarity of comparative datasets encompassing large numbers of species and regions (8).

Herbivorous insects have long served as models for the study of specialization (9), because they use a variety of plant resources

Significance

Dietary specialization determines an organism's resource base as well as impacts on host or prey species. There are important basic and applied reasons to ask why some animals have narrow diets and others are more generalized, and if different regions of the Earth support more specialized interactions. We investigated site-specific host records for more than 7,500 species of insect herbivores. Although host specialists predominate, the proportion of specialists is affected by the diversity of hosts and shifts globally, supporting predictions of more exclusive tropical interactions. These results not only affect our understanding of the ecology of food webs, but also have implications for how they respond to environmental change, as well as for ecosystem management and restoration.

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in many different ways, and their host plants are discrete resources; thus, diet breadth of a given herbivore species can be quantified as the number of plant taxa that it eats. In addition to serving as models for the study of diet breadth, herbivorous insects are important in their own right as one of the most abundant and diverse forms of life on Earth, and the consumption of plant material by insect herbivores is a dominant mover of energy and matter through terrestrial ecosystems (10). Although herbivorous insects are known collectively for narrow diet breadth, species vary significantly in the number of host plant taxa that they attack, and this variation has scarcely been described in a quantitative manner (11). It is unclear, for example, whether species with relatively specialized and generalized diets anchor the ends of a continuum or if diet breadth is discontinuous, with specialists and generalists forming distinct modes. Researchers have most commonly treated diet breadth as bimodal, distinguishing only generalists and specialists (7). In some cases, this distinction is a simplification for theoretical discussion (12), and in other cases it is simply a convenience (13, 14).

A quantitative description of the relative frequencies of specialists and generalists is important for understanding the evolution and ecology of plant–insect interactions. Because specialists can evolve from generalists and vice versa (6), species presumably pass through stages of intermediate diet breadth; thus, a bimodal distribution of the number of hosts attacked would suggest that intermediate levels of diet breadth are maladaptive. Similarly, if the distribution of diet breadth is continuous, the relative frequencies of herbivores in different diet breadth categories could be examined in the context of environmental determinants of niche width. It has also been suggested that treating herbivores as either specialists or generalists creates errors in estimates of the diversity of ecological communities, including the number of species of arthropods on Earth (15). Here, we quantify herbivore host ranges from field collections of larval and adult insects. We focus many of our analyses on larval Lepidoptera (caterpillars), for which we have the most geographically extensive data, but also include herbivorous insects from other feeding guilds as well as limited samples of parasitoids (flies and wasps) that feed on caterpillars. Parasitoids potentially offer an informative contrast with insect herbivores, because they are also highly specialized but feed at a higher trophic level (16).

Our global dataset of plant–insect interactions encompasses thousands of species of herbivores from 17 localities spanning 63° latitude from Canada to Brazil in the Western Hemisphere and from the United Kingdom and Japan to Papua New Guinea in the Eastern Hemisphere (Fig. 1*A* and *SI Appendix*, section *S1*). In addition to our primary objective of characterizing the distribution of specialists and generalists among insect herbivores, the latitudinal breadth of our samples allows us to address hypotheses concerning global patterns of ecological interactions. In particular, several explanations for the higher diversity of species at lower latitudes assume that interactions in tropical regions are more specialized (17).

For example, a greater presence of specialists at lower latitudes could promote diversification of plant traits (18), and herbivory by specialists can contribute to coexistence among competing plants (19). However, evidence both for and against global gradients in interaction specificity has been reported (20–22), and we do not know if latitudinal trends in specificity might result from heterogeneity of resources or other factors.

Results

The distribution of taxonomic diet breadth is characterized by a highly skewed, concave distribution that is well-fit by a discrete, truncated Pareto power law. Examples of diet breadth distributions for both Lepidoptera and other herbivores are shown in Fig. 1*B* and *C*. Also shown in Fig. 1 are visualizations of fit to other distributions that are commonly used for ecological count

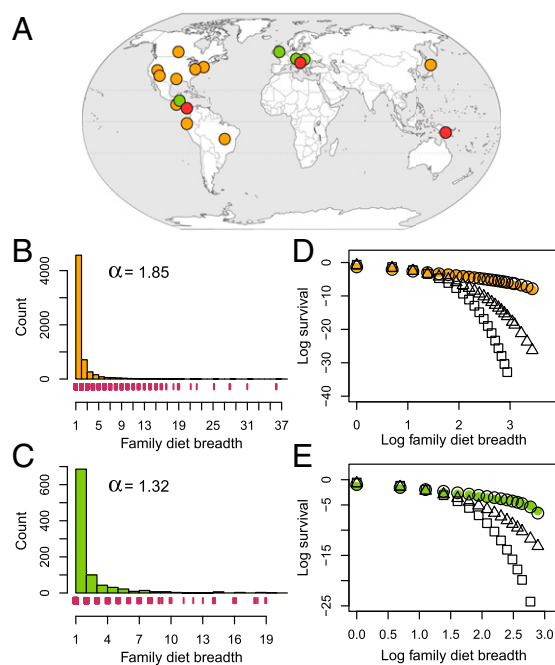


Fig. 1. (A) Study locales and the distribution of diet breadth for (B) Lepidoptera and (C) all other herbivores. Points on the globe are shown in orange for Lepidoptera study sites, green for other herbivore study sites, and red for study sites for both. Histograms in *B* and *C* illustrate counts of the numbers of herbivores associated with different numbers of host plant families; also shown is the shape parameter (α) from the discrete, truncated Pareto distribution. Tick marks under histograms indicate individual observations for visualization in the thin tail of the distributions. (D and E) Survival plots illustrate the fit of the Pareto (white circles), geometric (triangles), and Poisson (squares) distributions to the data (colored symbols). Log survival on the y axis is $\ln(P(X > x))$, which is the natural logarithm of the probability of herbivores having a greater diet breadth (X) than the corresponding value (x) on the x axis. Note that most analyses focus on diet breadth at the scale of individual sites; for simplicity, diet breadth is shown here across sites.

data (Fig. 1*D* and *E*). Compared with the truncated Pareto distribution, the geometric and Poisson distributions fit the diet breadth data poorly. We use the discrete, truncated Pareto, because the long tail of the empirical distributions of diet breadth (Fig. 1*B*) suggests a power law, and the discrete, truncated formulation is appropriate to the particular data being modeled (the number of hosts attacked by herbivores is a discrete count, and truncation results from the number of plant taxa attacked by any one herbivore always being less than the total number of plant taxa sampled). Furthermore, the shape parameter (α) of the discrete, truncated Pareto is more informative than measures of central tendency, such as the mean, for highly nonsymmetrical distributions. Higher values of α indicate a greater proportion of more specialized herbivores.

The distributions in Fig. 1*B* and *C* illustrate family-level diet breadth (the number of host plant families attacked), which is highly correlated with species-level diet breadth (the number of host plant species attacked): Pearson's correlation coefficient between family- and species-level diet breadth across all herbivores = 0.89 ($P < 0.001$) (*SI Appendix*, section *S2*). Species-level diet breadth is also closely fit by the discrete, truncated Pareto (*SI Appendix*, Fig. *S2*); high values of α , indicating a concentration of specialists and a long tail of generalists, characterize most of the taxonomic and functional subsets of the global data (*SI Appendix*, Table *S3*). Based on these data, an average of 69% of caterpillar species are associated with a single host family at each site; above 25° latitude, this value is 60%, and at sites less than

25° latitude, it is 83%. Among the sampled guilds of herbivorous insects, 76% of species associate with a single host family, although values for individual guilds vary widely (species-level diet breadth for the different feeding guilds as well as Lepidoptera shows similar patterns) (*SI Appendix, Table S3*).

Geographically, the discrete, truncated Pareto shows a consistently good fit across latitudes (*SI Appendix, Fig. S4*), whereas the shape parameter (α) increases toward the equator ($P = 0.0046$; $F_{2,10} = 8.87$; $R^2 = 0.64$) (Fig. 2A). The increase in α toward the equator for larval Lepidoptera corresponds to a greater relative frequency of specialized herbivores. In contrast, maximum diet breadth does not change with latitude, although a greater number of potential hosts is available in the tropics (white symbols in Fig. 2B). Although the upper limit of the distribution is unchanged with latitude, there is a shift throughout the distribution toward more specialized diets, such that most insect herbivores become more specialized toward the equator, which is illustrated in Fig. 2B (*SI Appendix, Figs. S5 and S6*).

Taxonomic diet breadth is a convenient but incomplete index of host range or dietary niche width, because herbivores attack particular plants for a variety of reasons (e.g., phytochemistry or geography) that may or may not be captured by simply counting the number of species eaten. As a complementary approach to investigating the latitudinal gradient in specialization, we calculated phylogenetic diet breadth (23) for Lepidoptera species associated with angiosperms, for which a robust phylogeny is

available at the family level (24). Phylogenetic family-level diet breadth, as measured by phylogenetic distance (PD) among hosts, changes globally: mean PD declines toward lower latitudes ($P < 0.001$; $F_{2,10} = 11.58$; $R^2 = 0.70$) (Fig. 2C), despite the greater phylogenetic diversity of tropical compared with temperate plants (25). This result is driven by the increase in the number of specialists (species with low PD) at lower latitudes. Thus, when specialists (i.e., herbivores associated with a single host family) are removed from the analysis, PD does not change with latitude (white symbols in Fig. 2C).

Previously, insect herbivores were reported to be more specialized at lower latitudes in the Western Hemisphere (21), whereas no latitudinal trend in specialization was found in the Eastern Hemisphere, where the sampled vegetation had been standardized for latitudinal differences in phylogenetic diversity (20). Results from this analysis for both taxonomic and phylogenetic diet breadth suggest that data from both hemispheres conform to a single global latitudinal gradient (Fig. 2A and C). These analyses differ from previous studies in a number of ways: we have focused on a single life history stage (larvae), we have included phylogenetic information for insect hosts from all sites, and we have increased the number of sites from both hemispheres. The inference of a global gradient in herbivore specialization is supported by temperate and tropical comparisons among different feeding guilds, which is illustrated by variation in α for family- and species-level diet breadth in Fig. 3. Average α across samples of species-level diet breadth rarefied to the lowest number of hosts in each comparison is significantly higher in tropical than temperate samples (Wilcoxon signed rank test, $P = 0.016$), and the same is true for family-level diet breadth if the one apparent exception, phloem suckers, is removed ($P = 0.031$; without phloem suckers removed, $P = 0.16$). Guilds with the most intimate host plant associations (gallers and leaf miners) show the highest levels of specialization (26), and it is noteworthy that such interguild differences are evident, despite latitudinal variation (Fig. 3). Among the most generalized guilds are mobile adult chewers, such as leaf beetles (family Chrysomelidae), that are able to move among individual plants to a greater extent than sessile or wingless life stages and may achieve a broader diet than larvae through selection of plant tissues that limit exposure to phytochemicals (27).

Variation in specialization among lineages and regions is addressed by theories of adaptive radiation and coevolution (28), which predict a negative relationship between the diversity of available resources and the diet breadth of consumers. Unexploited resources, for example, allowed the Hawaiian honeycreepers to evolve into a large number of specialized species (29). Thus, for herbivorous insects, it has been hypothesized that lower latitudes might harbor more specialized herbivores because of the diversity of hosts; similarly, the most species-rich lineages of plants might allow for the evolution of a greater number of specialists (30–32). However, these patterns have been difficult to evaluate empirically given the scope of many previous studies. Based on more than 6,000 species of Lepidoptera, we investigated connections between herbivore diet breadth and plant diversity and found that host plant families with high global species richness are associated with assemblages of herbivores with relatively narrow species-level diet breadth ($P < 0.001$; $R^2 = 0.56$) (Fig. 2D). This relationship holds when linear models contain covariates associated with plant families, including sample size (the number of experimental rearings from a family), phylogenetic age, and latitudinal extent of geographic range (*SI Appendix, Table S4* shows analyses of latitudinal subsets of herbivores). The relationship between host richness and dietary specialization could inform our understanding of the latitudinal gradient in herbivore specialization if lower latitudes contain more diverse lineages of hosts. This possibility was addressed with path analysis, including a direct effect of latitude

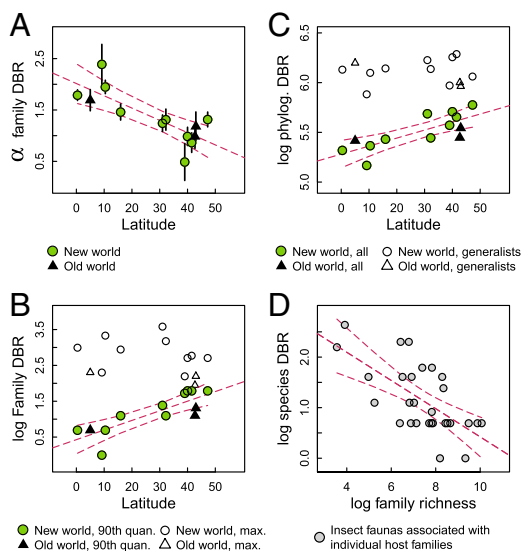


Fig. 2. Patterns in the distribution of diet breadth (DBR) for Lepidoptera. (A) Latitudinal trend in the shape parameter (α) for family-level DBR with bootstrapped SEs for individual sites; larger values of α indicate distributions with a higher density of herbivores having more narrow DBRs. (B) Maximum observed DBR (white symbols) and DBR in the 90th quantile of the DBR distributions (colored symbols) vs. latitude. Lower values of the 90th quantile correspond to a distribution in which more herbivores are compressed toward lower, more specialized DBRs. (C) Latitudinal patterns in phylogenetic DBR among sites for all species are shown with colored symbols, and more generalized species that attack more than one host family are shown with white symbols (log units on the y axis are in millions of years). (D) Relationship between median species-level DBR (as the number of host species attacked; y axis) for herbivores associated with particular families and the species richness of the plant families (x axis); more species-rich plant families host more specialized herbivores (*SI Appendix, section S4* shows analyses on latitudinal subsets of herbivores). For all panels, 95% confidence limits are shown around linear relationships, and the natural logarithm is used in all cases. In A–C, circles (white and green) are New World sites, and triangles (white and black) are Old World sites; differences between white and colored symbols in B and C are specific to B and C.

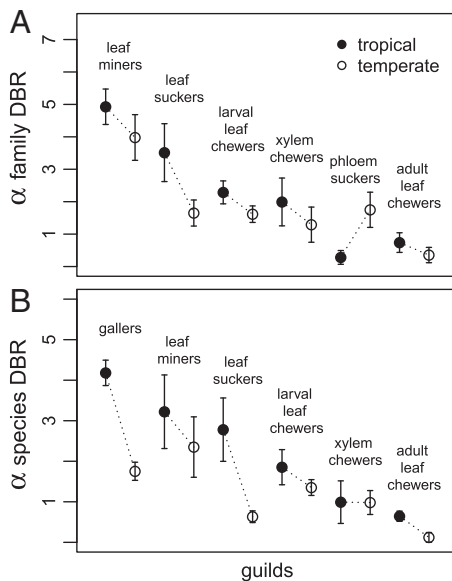


Fig. 3. Diet breadth (DBR) comparisons for herbivore guilds from tropical and temperate communities for (A) family-level DBR and (B) species-level DBR. Higher values of the shape parameter (α) indicate more specialized diets. Means and SDs are based on rarefaction to the lowest number of host taxa sampled in each pairwise comparison connected by dotted lines. More than one community is represented by some but not all of the points (*SI Appendix, section S1*). Note that not all guilds could be analyzed for both species- and family-level DBR (*Materials and Methods* and *SI Appendix* contain more details).

on specialization as well as an indirect effect of latitude mediated through plant richness (the number of plant families and species encompassed by insect sampling at each site). We found that the effect of latitudinal variation in plant richness on specialization is approximately one-fourth the direct effect of latitude on the global trend in specialization (*SI Appendix, Fig. S7*), indicating that plant diversity may contribute to variation in specialization but does not fully explain the global pattern of interactions (33).

Discussion

In summary, the distribution of diet breadth for insect herbivores conforms to a power law, with a majority of species associated locally with a single plant taxonomic family or species and a long tail of more generalized herbivores. The distribution of specialization shifts globally with latitude (Fig. 2A), which confirms the long-standing expectation that interactions are more specific at lower latitudes (17) and contributes to our understanding of the latitudinal diversity gradient. Plant diversity affects insect diet breadth (Fig. 2D and *SI Appendix, Fig. S7*), which may, in turn, feed back onto plant diversity through either coevolutionary (30) or ecological (12, 34) interactions, although the investigation of such feedback processes is beyond the scope of this study (35).

When interpreting the frequencies of insects in different diet breadth categories (Fig. 1), it is important to note that we have focused on local estimates of diet breadth derived from collections and rearings at focal sites. The alternative approach (using host records that encompass entire geographic ranges of herbivores) has less relevance for understanding ecological determinants of diet breadth (36) and faces the additional challenge that widespread generalists may often be composed of cryptic, localized specialists (37). Clearly, the distribution of herbivore diet breadth is continuous (specialists and generalists are not separated by a gap in frequency distributions) (Fig. 1), although it may be useful to consider herbivores as belonging to either the great majority of specialists or the long, thin tail of generalists. A

similar frequency distribution is apparent in the diet breadth of insect parasitoids (*SI Appendix, Fig. S3*), suggesting that the highly concave, skewed distribution could be inherent to the parasitic habit, of which insect herbivores are only one example, albeit the most well-studied (38). In general, the predominance of specialists is relevant to issues in natural resource management and challenges the idea that, in human-impacted systems, the interactions among novel suites of co-occurring species will be comparable in structure with less-degraded systems (39, 40).

Recent approaches to studying biotic networks include comparisons of distributions of natural interactions with theoretical and mathematical predictions. In randomly assembled networks of interactions, the frequency of highly connected nodes drops rapidly beyond the mode, such as in a Poisson distribution (41, 42), and some natural networks (for example, plant–pollinator interactions) deviate from that pattern by having a small portion of relatively overconnected nodes, which we have observed with generalist herbivores (41, 43, 44). For these more heterogeneous networks, it has been suggested that facilitating processes underlie the long, thin tail of the frequency distribution (45). In the case of herbivore diet breadth, the process of host range expansion could be such a process: initial expansion of diet breadth might be rare, but after more than one host plant family has been colonized, adaptations for generalized feeding could facilitate the colonization of new hosts (46). This possibility is consistent with the observation that highly polyphagous species of butterflies are more likely to use novel hosts (47, 48), and the ubiquity of the highly peaked, skewed distribution of diet breadth suggests that any processes facilitating dietary generalization operate not only in different regions of the globe, but also within different lineages and guilds of herbivores. An additional mechanism for the observed frequencies of diet breadth could be disruptive selection, favoring either extreme specialization or increasing generalization. However, the biological factors that favor dietary generalism as an ever-present but relatively infrequent life history strategy in herbivorous insects must await additional study.

Materials and Methods

Data Collection. Rearing of field-collected caterpillars (Lepidoptera) to establish consumer–host relationships was undertaken at 13 sites in North, Central, and South America, Papua New Guinea, Japan, and central Europe (Fig. 1A and *SI Appendix, Table S1*). Collections and rearings focused on externally feeding caterpillars, mostly macrolepidopterans, with broader sampling at some sites. Site-specific details are provided in *SI Appendix* for each dataset and site or a collection of sites when more than one site has been managed in a similar way. We tabulated data for other herbivores to study variation in diet breadth within and among ecological guilds, with the goal of encompassing both sucking and chewing feeding modes, species using various plant resources (including leaves, phloem sap, and wood), and species having diverse life histories, from species intimately connected with plants, such as miners and galls, to those that are mobile, either as larvae or adults (Fig. 3). Data were compiled from seven sites (three sites in common with the Lepidoptera data and four additional sites) (Fig. 1A and *SI Appendix, Table S2*). As with Lepidoptera, all data for these herbivores are based on field collections for both larval and adult stages (depending on the herbivore taxa).

Heterogeneity among sites in methodology and sampling effort is almost always present in global datasets, which emphasizes the importance of statistical controls (covariates) to account for variation in sampling effort. Although this approach has a well-established history in ecology, covariates introduce complexity to models and reduce degrees of freedom for main effects; however, substantial power is gained by the inclusion of additional sites, despite differences in design. Variation in sampling effort could be particularly important when considering variation in diet breadth: an understudied herbivore community might seem more specialized, because not all plant–insect interactions will have been sampled, or less specialized if rare species are mostly specialists (and missed by sampling). Furthermore, the discovery of interactions will necessarily take more time in areas with more diverse floras and faunas. However, our most diverse sites are tropical and extremely well-sampled, with 71 site-years of sampling below 30° latitude just for Lepidoptera (*SI Appendix, Table S1*). We use the number of

years of study along with other appropriate covariates (including the number of rearing records and the geographical area of study sites) to address sampling issues throughout our analyses, which are described below and in *SI Appendix*. Ultimately, biological signal is evident at multiple scales (in latitudinal patterns and the consistent fit of the Pareto distribution among sites), despite differences in methodologies and sampling effort. It can also be noted that the number of rearing records per Lepidoptera species does not vary with latitude ($F_{1,11} = 0.84$; $R^2 = 0.0071$; $P = 0.38$). Although we have been successful in detecting relationships among our focal variables, future research in the area of global interactions could reasonably strive for a greater number of sites with standardized methodologies that would potentially increase explained variance in analyses, such as the path models in *SI Appendix*, Fig. S7.

To determine host associations for each herbivore species, data from each site were subjected to site-specific preanalysis filters appropriate to the methods of collection and taxonomic knowledge at each site (*SI Appendix*, section S1). Data for Lepidoptera from some of the sites were analyzed previously in the works by Dyer et al. (21) and Novotny et al. (20). Here, we updated those previous datasets with additional years (more than double the previously examined number of years for some sites) and added new locations for Lepidoptera (Ohio, Great Basin, and Japan). We also added 18 datasets for other herbivores that had not previously been brought together into one analysis (*SI Appendix*, section S1). Identification procedures varied among sites, but voucher specimens have been deposited at appropriate museums, and both insect and plant species were identified by knowledgeable taxonomists in so far as possible; several sites additionally used DNA barcoding to validate species identifications.

Pareto Distribution. Because the distribution of diet breadth is highly skewed (Fig. 1), the core of our statistical approach is the use of a theoretical distribution appropriate to the structure of the data. We have used a version of the Pareto distribution, from which a shape parameter (α) can be extracted that serves as a useful summary statistic; higher values of α correspond to diet breadth distributions that are more highly peaked, with a greater density of specialists. The Pareto distribution (49) is widely used in a number of fields of science, and the truncated Pareto has been proposed as an important extension (50). Here, we use a form of the Pareto that is truncated and discrete, and thus, it is appropriate for ecological count data (51); in our case, we are interested in counts of host plant families and host plant species associated with specific herbivore species. We say that a random variable X has a truncated discrete Pareto distribution with parameters α , β , and γ if

$$P(X=x) = \frac{\frac{1}{x^\alpha} - \frac{1}{(x+1)^\alpha}}{\frac{1}{\gamma^\alpha} - \frac{1}{(\beta+1)^\alpha}}$$

for any natural number of host plant taxa (x), such that $\gamma \leq x \leq \beta$. Here, α is any real number, and γ and β are positive integers. Parameters γ and β are the lower and upper truncation parameters, respectively, for which maximum likelihood estimates were used: the sample minimum for γ and the sample maximum for β . We estimated α by minimizing the sum of squares of the differences between the model survival function and the empirical survival function. The distribution was fit to data using custom R scripts (*SI Appendix*, section S5).

As a measure of goodness of fit or closeness of the modeled discrete truncated Pareto distribution to the empirical distribution of the data, we used the maximum absolute difference between the modeled and the empirical cumulative distribution functions. This approach provides the largest difference between probabilities computed using the model and the relative frequency from the data, and it gives an intuitive notion of closeness (52). Fits of the discrete, truncated Pareto to our data were visualized using plots of survival functions, as in the work by Aban et al. (50), which are useful for comparing values in the tail of the distribution with predictions generated by theoretical distributions (53–55). We compared the discrete, truncated Pareto with the geometric and Poisson distributions; in Fig. 1, it can be seen that the Pareto (white circles) predict the observations (colored symbols) throughout the tail of the distribution.

Relationships between parameters from the Pareto distribution fitted to diet breadth (e.g., the shape parameter, α) and latitude were investigated for Lepidoptera with linear models that included sample size (the number of experimental rearings per site), area (of sampled locations), the number of herbivore species, and the number of years (over which sampling was conducted) as covariates. For other herbivores, we did not have the same well-sampled latitudinal gradient but were able to make pairwise comparisons between temperate and tropical sites (*SI Appendix*, Table S2). Because

these analyses did not involve multiple regression models, we did not include covariates associated with sampling effort or other factors as in the Lepidoptera analyses. Instead, we used a rarefaction approach based on the number of plant taxa (families and species) sampled, which is a key axis along which datasets differ: when one dataset includes 15 hosts and another includes only 10 hosts, the latter will potentially be biased toward a more narrow observed diet breadth among herbivores. For each set of comparisons (for example, matrices of plant–insect associations for leaf miners from tropical and temperate communities), we subsampled each matrix down to the lowest number of plant taxa sampled for any of the matrices involved in the comparison, and we did this 1,000 times using the sample function in R and inspected means and variances across resampled replicates.

Phylogenetic Analyses. To investigate phylogenetic diet breadth of Lepidoptera species, we used PD among host plant families calculated with the R package *picante* and using the angiosperm phylogeny from the work by Davies et al. (24), which was the most complete angiosperm phylogeny available at the time of analysis (nonangiosperm host records were excluded from these analyses). As with parameters from the fitted Pareto distributions (see above), the relationship between PD and latitude was investigated using linear models and covariates to account for sampling effort.

Plant Diversity. Diversity of resources (host plants) can affect the evolution of consumer traits by providing opportunities for local adaptation and specialization, a possibility that we have investigated in two complementary ways: using plant lineages (for which resource diversity is global species richness of plant families) followed by using geographic sites as replicates (for which resource diversity is richness of sampled plant taxa). For the first approach, multiple regression used median species-level diet breadth of insect herbivores as the response variable and the following independent variables: species richness (number of species within plant families), relative age (extracted from the angiosperm phylogeny) (24), latitudinal range, and sample size (the number of times in which an insect was reared from any species in a host plant family). Median diet breadth was used here instead of α from the Pareto, because comparisons were being made among subsets of data (insects associated with plant families) that varied greatly in sample size, and the Pareto could not always be fit to the smallest sample sizes. However, the use of the median is conservative, because shifts in the tail of the distribution may not be reflected in the median value when comparing two distributions that have similar numbers of extreme specialists. Species richness (the total number of species within plant families) for these analyses was taken from the angiosperm diversity website maintained by the Missouri Botanical Garden (www.mobot.org/MOBOT/research/APweb/), which was also used as a reference to standardize family names from the different databases used in this project. Latitudinal range (the maximum extent of north–south latitude occupied by any species in the plant family) was taken from family-level distribution maps in Heywood (56). Only plant families for which all measures were available (richness, relative age, and latitudinal range) were included in analyses. Furthermore, a sample size cutoff was used to avoid plant families that were less well-characterized from the perspective of insect rearings: we considered families from which insects had been reared at least 100 times. To investigate the robustness of results, the multiple regression using these variables was repeated with subsets of the data, specifically only using insects for which rearing records were restricted to sites either greater than 25° or less than or equal to 25° latitude.

Our second approach to understanding the influence of plant diversity on dietary specialization involved path analyses and variation among sites in dietary specialization and plant richness. Path analysis is useful in this context, because it allows for the simultaneous analysis of direct and indirect effects. Specifically, path analyses included the α shape parameter from the Pareto distributions and plant richness per site as endogenous variables (plant richness for each site is the number of plant families and species associated with the sampled herbivores). The exogenous variable was simply latitude, which pointed directly to α and indirectly to α through plant richness (allowing for the possibility that latitude affects α through resource diversity but also has effects that are not explained by global variation in plant richness). The model was evaluated using plant richness as both the number of plant species and the number of plant families sampled at sites.

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The global distribution of diet breadth in insect herbivores

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Supporting Information, Appendices S1 – S6

Appendix S1, Collection and curation of data

We used the most complete assemblage of site-specific plant-herbivore interaction data in existence, but a dataset of this size is characterized by inconsistencies and sampling artifacts that cannot be entirely mitigated. The data used in this study are comparable in that they are all based on collections and rearings of individual herbivores to document local plant-insect interactions. Some collections utilized identical methods across numerous sites, and these miscible subsets yield the same patterns that we report for the global data. For the full complement of sites, differences among datasets necessarily exist, and unique methods of collection and processing are described below for each dataset or collection of datasets (with additional details in Tables S1 and S2). In particular, datasets differ in the extent to which pre-analysis filters were applied. For example, at the first five sites described below (Lepidoptera from Arizona, Costa Rica, Ecuador, Great Basin and Louisiana), an insect has to have been found in association with a specific plant at least five times to be considered for analysis. For the majority of our other datasets (e.g. Lepidoptera from the Czech Republic and Papua New Guinea, and most of the guild-specific datasets), singletons were excluded (i.e. a plant-insect association that was observed only once is not analyzed). In a smaller number of additional cases, a quantitative filter was not applied (e.g. Japan, Belize), typically because the data were considered sufficiently reliable by the primary investigators, and some of these include already-published, stand-alone datasets (e.g., Canada).

Methods unique to each dataset, Lepidoptera

Arizona, Costa Rica, Ecuador, Great Basin, and Louisiana. Collecting at all five sites covered a broad range of latitude and longitude within the respective states and countries, including all of Arizona (USA; most collecting was at approximately 31°53'N, 109°12'W), all of Louisiana (USA; collecting was centered at 29°56'N, 90°7'W), all of Costa Rica (most collecting was at La Selva Biological Station, 10°26'N, 84°0'W), all of Ecuador (collecting centered at approximately 0°35'S, 77°53'W), and a large number of sites across the Sierra Nevada mountains and Great Basin desert (collecting centered at approximately 39°39'N, 119°46'W). Lepidopteran larvae at all sites were collected both opportunistically along trails, watercourses, and on undirected walks through the forests, and quantitatively using 10 m diameter plots as search areas. Plots were divided into four equal wedges, and one person spent 30 min looking for caterpillars on all the plants within each wedge. At all sites caterpillars were collected from all plant taxa and growth forms (herbs, vines, shrubs, trees) on which they were encountered.

48 All collected caterpillars were reared individually in clear plastic bags or glass jars in
 49 rearing facilities at ambient temperature and humidity. Fresh food in the form of new foliage
 50 from the same plant species from which the caterpillar was collected was placed in containers
 51 as needed. All pupae were checked daily to collect any adult Lepidoptera or parasitoids that
 52 emerged.

53 Voucher specimens of the focal plants and all first-time food plants were collected and
 54 pressed to insure accurate taxonomic identification and deposited at appropriate institutions.
 55 Initial identifications of insects were made by parataxonomists and then confirmed by taxonomic
 56 specialists. Voucher specimens of the insect species can be found at Tulane University, InBio
 57 (Costa Rica), the Museo Nacional de Ciencias Naturales (Ecuador), and other collaborating
 58 institutions (see www.caterpillars.org for a list of participating institutions). Tachinid parasitoids
 59 reared from caterpillars at the Ecuador site were mounted, identified to genus (using Wood and
 60 Zumbado (1) and other resources) and sorted into morphospecies by JOS. When possible,
 61 specimens were identified to species with the aid of D.M. Wood and/or reference to specimens in
 62 the U.S. National Museum of Natural History and the Canadian National Collection of Insects
 63 (Ottawa, Canada). Some morphospecies were confirmed using mtDNA COI sequences. A pre-
 64 analysis filter of at least 5 observations (for any plant-insect interaction) was implemented for all
 65 of these datasets.

66

Table S1. Thirteen focal sites, with covariates used in analyses examining latitudinal gradients in specialization, including: latitude (decimal degrees), area and years sampled, the number of Lepidoptera species, and the number of rearing records studied; also the number of plant families and species studied at each site in the last column.

Site	Degrees lat.	Lep. species	Records	Area (ha)	Years	Plant fam. / sp.
Canada	47.25	671	131,431	80,000,000	20	27 / 257
Czech Republic	43.00	74	1,475	300	3	10 / 15
Japan	42.68	174	1,181	1000	2	18 / 51
Connecticut	41.50	116	744	1,437,100	26	45 / 175
Ohio	40.00	273	3,294	500,000	4	35 / 98
Great Basin	39.00	25	7,615	3,000,000	5	14 / 29
Arizona	32.21	186	14,229	3,000,000	18	47 / 176
Louisiana	31.00	328	14,505	500,000	12	67 / 196
Brazil	15.92	568	5,614	10,000	12	42 / 109
Costa Rica	10.42	1,321	35,103	2,400	22	81 / 454
Panama	9.17	401	4,536	1,600	10	50 / 210
Papua New Guinea	5.00	229	18,632	1,500	14	30 / 88
Ecuador	0.41	2,122	90,622	28,000,000	13	79 / 318

67

68

69

70 **Brazil.** We collected lepidopteran larvae in cerrado sensu stricto areas near Brasilia, DF, Brazil
71 (15°45'S, 47°50'W) from 1991 to 2005. The region experiences a marked dry season from May
72 through September (mean month precipitation of 24 mm). Caterpillars were collected
73 opportunistically but on most of the plant species we collected once a week throughout a year.
74 The plants examined included shrubs, trees and some herbs, varying in height from 0.50 to 2.50
75 m. All were censused during morning hours. The caterpillars were individually reared in plastic
76 jars on leaves of the plant on which they were found, at ambient temperature and humidity.
77 Leaves were replaced every two days, and any parasitoid emergence was recorded. Voucher
78 specimens are housed at the Entomological Collection of Zoology Department, University of
79 Brasilia, and were identified by Vitor Osmar Becker, Associate Researcher, Department of
80 Zoology, University of Brasilia. A pre-analysis filter of 5 observations was implemented for the
81 Brazil Lepidoptera data.

82
83 **Canada.** Collection records of individual caterpillars or groups of caterpillars that yielded adult
84 Lepidoptera (moths) were entered from hand-written rearing records provided by the Canadian
85 Forest Insect Survey (CFIS, now the Forest Insect Disease Survey), Sault Ste. Marie, Ontario,
86 Canada. Larvae were collected from 1936-1955 by hand picking and beating foliage throughout
87 the provinces of southern Canada (centered at approximately 53°N, 101°W). Collectors included
88 forest biology rangers and associates of the CFIS (2). Collected larvae were reared at regional
89 centers on foliage from the host plant on which they were collected. Identifications of larvae and
90 reared adults were made by the Insect Systematics Unit of the Survey. A combination of
91 published data from these surveys (3-6) and the original hand-written rearing records were used
92 to construct the caterpillar-host plant database. Plant and insect nomenclature were updated as
93 needed to reflect the current state of taxonomic understanding.

94
95 **Connecticut.** Caterpillars (Lepidoptera) were collected both opportunistically (1988-2013)
96 across many communities throughout the state of Connecticut and in adjoining areas of
97 Massachusetts and Rhode Island (centered at approximately 41°33'N, 72°39'W), as well as
98 quantitatively using haphazardly chosen branches from focal tree taxa at three sites in Middlesex
99 County, Connecticut (2004-2012). For quantitative sampling, collection effort on each of eight
100 tree taxa (*Quercus rubra* group, *Quercus alba*, *Fagus grandifolia*, *Carya* spp. (Eucarya group),
101 *Prunus serotina*, *Acer rubrum*, *Betula lenta*, and *Hamamelis virginiana*) was equalized per
102 collection day. Saplings and low branches of larger trees were sampled (ground level-3 m in
103 height). Much of the opportunistic and all of the quantitative collecting occurred during the peak
104 caterpillar season in Connecticut (May- July), although limited collecting efforts extended
105 throughout the growing season (May-October).

106 Caterpillars were reared individually in vials, plastic cups, bags, or boxes in the
107 laboratory under ambient conditions. Caterpillars were fed foliage from the plant taxon upon
108 which they were collected. Reared adults were spread to facilitate taxonomic identification.
109 Identifications were based on reared adult specimens, or, for relatively distinct and well-
110 described species, on larval features using Wagner (7) and Wagner et al. (8-10), or both.
111 Voucher specimens are housed at the University of Connecticut (Storrs) and Wesleyan
112 University.

113 To correct for possible bias due to the combination of opportunistic and restricted
114 quantitative sampling approaches, we limited the host records used here to a randomly chosen set
115 of 116 species of Zygaenoidea, Papilionoidea, and macrolepidoterans meeting certain criteria.

116 The random set of species was drawn from a Connecticut state checklist of Lepidoptera (2410
117 species) compiled by DLW. We used a random number generator to choose candidate species
118 from the numbered checklist. Criteria for inclusion were: 1) externally feeding larvae (including
119 leaf-tiers), 2) host range including at least some woody plants, and 3) the availability of and our
120 confidence in rearing records of larvae on natural, reliably identified host plants. If a randomly
121 chosen species met these criteria, it was included. If not, it was discarded and a new randomly
122 chosen species was considered. This iterative process continued until the data set included 116
123 species, which we estimated (based on previous experience with similar data) was a sufficiently
124 large sample size for analysis.

125
126 **Czech Republic.** We collected all externally feeding, leaf-tying and rolling caterpillars
127 (Lepidoptera) from accessible foliage of 15 focal, locally-common woody plant species (14
128 species listed in Novotny et al. (11) and *Acer pseudoplatanus*) in the Poodri Protected Area
129 (18°03-13'E, 49°42-48'N, 200 m asl., Czech Republic). The study area of 300 ha included three
130 fragments of the primary floodplain forest along a 20 km long section of the Odra River. The
131 forest vegetation was dominated by *Quercus*, *Ulmus*, *Tilia*, *Prunus* and *Fraxinus*. The study
132 plant species represented $85 \pm 2.4\%$ of the total forest basal area according to 62 plots of 25 x 25
133 m each, where all plants ≥ 5 cm in diameter at breast height (DBH) were recorded. The annual
134 average temperature was 7-8.5°C, the annual average rainfall 600-800 mm. Insect sampling
135 effort amounted to 150 m² of foliage inspected per tree species. Each caterpillar was provided
136 with fresh leaves of the plant species from which it was collected and only those that fed were
137 retained in the analyses. Larvae were identified to morphospecies and/or reared to adults. All
138 insects assigned to morphospecies were later verified and identified by taxonomic specialists.
139 Vouchers are deposited at the University of Ostrava, Ostrava. The pre-analysis filter of excluding
140 singleton observations was implemented for the Czech Republic Lepidoptera.

141
142 **Ohio.** We sampled caterpillars (Lepidoptera) from temperate deciduous forest fragments in
143 Southwestern Ohio (ca. 39°N, 84°W) from 2006-2009. All woody plant feeding caterpillars, as
144 well as some herbaceous feeding species, were collected along 100m transects from 19 forest
145 fragments ranging in size from 6 to 800 ha. Each fragment was sampled with between 2 and 20
146 transects. All caterpillars within one meter on each side of the transect line, from ground level to
147 a height of ca. 2.5 m, were recorded and collected. Caterpillars were placed in plastic bags with
148 foliage from their host plants and later transferred to plastic tubs placed in an environmental
149 chamber with temperatures and light regimes mimicking the seasonal temperatures and light
150 regimes of the region. Every other day they were fed new leaves of plant species on which they
151 were found until they died, pupated, or a parasitoid emerged. When they were near pupation,
152 plant material was replaced with moistened peat moss in which they could pupate.

153 All caterpillars collected were identified to the lowest taxonomic level possible based on
154 morphological appearance, distribution, host plant use, and seasonality using Wagner (7). Once
155 adults emerged, specimens were mounted and identified with the use of Covell (12), Wagner (7),
156 Microleps.org, The North American Moth Photographer's Group
157 (<http://mothphotographersgroup.msstate.edu>), and other traditional and digital resources. Some
158 specimens were taken to the Ohio State University insect collection for comparison and
159 identification. Specimens that could not be identified retained morphospecies designations.
160 Vouchers of all taxa were deposited in the Wright State University insect collection. Insects that
161 were only observed once from a single plant were excluded from analyses.

162

163 **Panama.** We collected caterpillars (Lepidoptera) on Barro Colorado Island (BCI), Panama (9°N,
164 80°W) from 1996-2005 with some additional collections in 2013. The island is maintained and
165 protected by the Smithsonian Tropical Research Institute and is part of a larger forested corridor
166 that extends from the Atlantic to Pacific coasts. BCI experiences a marked dry season that is
167 usually four months long, and the vegetation is classified as tropical, moist forest (13-15).

168 Caterpillars were collected opportunistically from the island's diverse understory of
169 shade-tolerant plants representing a variety of life histories. The plant species included shrubs,
170 juvenile lianas and immature trees with growth strategies that differed widely, even within plant
171 genera. We reared all caterpillars individually in closed plastic containers or plastic bags at
172 ambient temperature in a screened and shaded porch. We fed them leaves of the same species
173 and age as those on which they were initially found. Leaves were replaced with fresh ones at
174 least every other day. We photographed and reared specimens and entered them into our
175 database (<http://www.biology.utah.edu/~coley/database.htm>). Using larvae and adult specimens,
176 we identified the lepidopterans to the lowest taxon possible. Voucher specimens are stored on
177 BCI, and some duplicate specimens are with experts for identification. Host plants were
178 identified to species using Croat (14) and by comparison with herbarium specimens.

179

180 **Papua New Guinea.** All externally feeding caterpillars (Lepidoptera), including leaf-tiers and
181 rollers, were sampled from 88 woody species of plants, representing all major lineages of
182 flowering plants, at three study sites (Baitabag, Ohu, and Mis Villages; 145°41-8' E, 5°08-14' S,
183 0-200 m asl., Papua New Guinea) within a 10 x 20 km area, encompassing a mosaic of
184 secondary and primary lowland hill forest. The annual average temperature was 26.5°C, and the
185 annual average rainfall 3,600 mm. The sampling took place within approximately 1,500 ha of
186 primary and secondary forests. Each tree species was sampled for at least one year between
187 1994-2008. The sampling effort amounted to 1,500 m² of foliage per tree species, obtained from
188 multiple conspecific individual trees. All caterpillars were provided with fresh leaves of the plant
189 species from which it was collected and only those that fed were retained in the analyses. Larvae
190 were identified to morphospecies; adults were identified by genitalia, DNA barcoding and
191 consultation with taxonomic specialists. Vouchers are deposited at the National Agricultural
192 Research Institute of Papua New Guinea and Smithsonian Institution, Washington. See Novotny
193 et al. (16, 17, 11) for more information. Any singleton observations were excluded from the
194 Papua New Guinea Lepidoptera data.

195 Parasitoids were reared from the above caterpillar sampling encompassing 38 tree
196 species. Reared parasitoids were linked with their host through caterpillar morphospecies.
197 Parasitoids were mounted, morphotyped by JH and identified by taxonomists listed in Hreck et
198 al. (18). A selection of the parasitoid specimens was DNA barcoded and any identifications in
199 conflict with DNA barcodes were re-examined. Parasitoids belonged to Hymenoptera:
200 Braconidae, Ichneumonidae, Chalcidoidea and Bethyilidae, and Diptera: Tachinidae; see Hreck et
201 al. (18) for more information. Singleton observations were excluded prior to analysis.

202

203 **Japan.** We collected caterpillar (Lepidoptera) at the Tomakomai Research Station in Hokkaido,
204 Japan (42° 42'N, 141° 36'E) from 2008 to 2009. This cool-temperate mixed forest receives 1,161
205 mm of annual precipitation, and the average annual temperature is 5.6°C. Maple (*Acer mono*),
206 linden (*Tilia japonica*), and oak (*Quercus crispula*) dominate the forest. The canopy ranges from
207 15 m to 25 m in height. Deciduous trees break bud in early to mid-May and shed their leaves in

208 late October. Caterpillars were collected using truck-mounted elevated work platforms (cherry-
209 pickers) on 51 plant species representing 18 families including four conifer species. Samples
210 were taken twice (spring and summer) for each year, in total four times during the survey. For
211 each sampling occasion, three branches from three tree individuals, i.e. 9 branches in total, were
212 sampled (5.1 ± 3.1 , mean \pm sd cm in diameter) and all the caterpillars were picked up by hand.
213 The caterpillars were individually reared in plastic cups on leaves of the plant on which they
214 were found at ambient temperature and humidity. Voucher specimens are housed at the Chiba
215 University.

216

217 **Methods unique to each dataset, all herbivores**

218

219 **Guilds studied in Papua New Guinea.** Seven guilds (listed below, classified as in Novotny et
220 al. (19), with some modifications) were studied near the villages of Baitabag, Mis and Ohu near
221 the town of Madang (Papua New Guinea), within a 20×10 km area comprising a successional
222 mosaic of disturbed and mature lowland rainforest ($5^{\circ}08' - 14'S$, $145^{\circ}7' - 41'E$, 50–200 m above sea
223 level, Madang Province). The vegetation has been classified as mixed evergreen rain forest on
224 Latosol (16, 17, 19) with a humid climate (mean annual rainfall 3600 mm), a mild dry season
225 from July to September, and mean annual temperature of $26^{\circ}C$. All trophic interactions were
226 confirmed by feeding experiments for adults or rearing for larvae. Plant-herbivore trophic
227 interactions supported by singletons were excluded from the analysis. Plant vouchers are
228 deposited at the PNG National Herbarium (Forestry Research Institute, Lae), insect vouchers at
229 the Smithsonian Institution (USA) and the Institute of Entomology of the Academy of Sciences
230 (Ceske Budejovice, Czech Republic).

231

232 **Adult leaf chewers, Papua New Guinea.** All externally feeding adults (Orthoptera,
233 Phasmatodea and Coleoptera) were sampled in Madang from 59 native rainforest woody species
234 representing 19 families. Insects were hand-collected from 1500 m^2 of foliage per plant species
235 over the period of approximately 12 months, sampling young and mature foliage from multiple
236 individual trees. The sampling took place from 1995 to 2002 (16, 23, 24). All individuals were
237 tested in a no-choice feeding experiment on the leaves of the plant species they were collected
238 from; only feeding individuals were included in the analysis. As described above, singleton
239 observations were excluded.

240

241 **Larval leaf chewers, Papua New Guinea.** All externally feeding, leaf rolling and leaf tying
242 holometabolous larvae (Lepidoptera and Coleoptera) were sampled in Madang from 88 woody
243 species representing 31 plant families. Insects were hand-collected from 1500 m^2 of foliage per
244 plant species over the period of approximately 12 months, and reared to adults as far as possible.
245 The sampling continued from 1995 to 2008 (15, 17, 23, 24). As described above, singleton
246 observations were excluded.

247

248 **Leaf miners, Papua New Guinea.** All leaf-mining larvae (Lepidoptera, Coleoptera, Diptera)
249 were sampled in Madang from 76 woody species representing 31 plant families. Insects were
250 hand-collected from 1500 m^2 of foliage per plant species over the period of approximately 12
251 months, and reared to adults as far as possible. The sampling continued from 2006 to 2008 (19,
252 23). Only reared adults were analyzed. As described above, singleton observations were
253 excluded.

Table S2. Datasets of herbivore feeding guilds, with details relevant to pairwise comparisons between tropical and temperate communities, including the numbers of plant families and species associated with insects used in analyses, as well as the numbers of herbivore species. For other details, see supplementary text, and note that plant species data were not available for two datasets (leaf and phloem suckers from Germany). The sites listed below are only partially overlapping with the sites used for analyses involving only Lepidoptera; see Table S1 and Fig. 1A.

Site	Feeding guild	Major herbivore taxa	Herbivore species	Plant fam. / sp.
Tropical datasets				
Papua New Guinea	Adult leaf chewers	Orthoptera, Phasmatodea, Coleoptera	245	19 / 59
Papua New Guinea	Larval leaf chewers	Lepidoptera, Coleoptera	326	30 / 86
Papua New Guinea	Leaf miners	Lepidoptera, Coleoptera, Diptera	124	28 / 63
Belize	Leaf miners	Lepidoptera, Coleoptera, Diptera	81	20 / 60
Papua New Guinea	Leaf suckers	Auchenorrhyncha: Typhlocybinae	36	13 / 33
Papua New Guinea	Phloem suckers	Auchenorrhyncha	29	8 / 14
Papua New Guinea	Gallers	Diptera, Coleoptera, Lepidoptera, Hymenoptera	76	13 / 27
Papua New Guinea	Xylem chewers	Cerambycidae	40	14 / 23
Panama	Xylem chewers	Cerambycidae	22	6 / 9
Temperate datasets				
Czech Republic	Adult leaf chewers	Coleoptera	20	9 / 14
Czech Republic	Larval leaf chewers	Lepidoptera, Hymenoptera, Coleoptera	94	10 / 15
Great Britain	Leaf miners	Lepidoptera, Coleoptera, Diptera	31	11 / 20
Poland	Leaf miners	Lepidoptera, Coleoptera, Diptera	34	10 / 17
Great Britain	Leaf suckers	Auchenorrhyncha: Typhlocybinae	55	10 / 32
Germany	Leaf suckers	Auchenorrhyncha	81	12 / -
Germany	Phloem suckers	Auchenorrhyncha	84	17 / -
Czech Republic	Gallers	Diptera, Hymenoptera, Sternorrhyncha	43	7 / 9
Czech Republic	Xylem chewers	Cerambycidae	46	11 / 22

Leaf suckers, Papua New Guinea. Mesophyll-sucking larvae (Auchenorrhyncha, Cicadellidae: Typhlocybinae) were sampled in Madang from 56 woody species representing 22 plant families. Insects were hand-collected from 1500 m² of foliage per plant species over the period of six months and reared to adults (26). Only reared adult males were used in the analysis; in Typhlocybinae, the taxonomy is based mostly on the morphology of male genitalia whereas

262 females are often impossible to identify morphologically. As described above, singleton
263 observations were excluded.

264

265 **Phloem suckers, Papua New Guinea.** Phloem-sucking larvae of leafhoppers and planthoppers
266 (Auchenorrhyncha) were sampled in Madang from 14 woody species representing eight plant
267 families. Insects were hand-collected from 1500 m² of foliage per plant species from 2007 to
268 2009 and reared to adults on live saplings caged in forest understorey (27). Only reared adults
269 were used in the analysis. As described above, singleton observations were excluded.

270

271 **Gallers, Papua New Guinea.** Insect-induced galls were collected from 32 species of woody
272 plants, representing all major lineages of flowering plants in Madang, from August 2010 to
273 March 2011. Galls were hand-collected from the accessible foliage of multiple conspecific
274 individuals of each species, representing a total sampling effort of approximately 69 hours of
275 searching for galls on each tree species. Harvested galls were initially morphotyped according to
276 gall morphology within host plant and reared in clear plastic bags for a period of one month in
277 order to obtain adults. In addition, immature insect stages were obtained from gall dissections.
278 Reared insects were identified to morphospecies, and to species where possible by taxonomic
279 specialists, and both adults and/or immature insects of as many morphospecies as possible were
280 DNA barcoded. Gallling insects were used in analyses of species-level diet breadth, but not
281 family-level diet breadth because all insect species were specialists with a diet breadth of one
282 host plant family, from which a distribution of diet breadth could not be estimated. As described
283 above, singleton observations were excluded.

284

285 **Xylem chewers, Papua New Guinea.** Wood-boring beetles (Cerambycidae) were reared from
286 standardized timber baits of freshly cut wood from 26 tree species representing 15 families in
287 Madang from 2000 to 2003. Eight trunk sections, each weighing 20 kg, per tree species were
288 sawn from freshly felled trees and exposed to ovipositing females in the forest canopy and
289 understorey. After three weeks each section was individually enclosed in a rearing cage and
290 emerging insects collected for six months (19). As described above, singleton observations were
291 excluded.

292

293 **Leaf miners, Belize.** All leaf-miners (Coleoptera, Diptera, Lepidoptera) were sampled from low
294 vegetation along trails in deciduous seasonal and deciduous semi-evergreen seasonal forest near
295 the Las Cuevas Research Station (Chiquibul Forest Reserve) in south-west Belize. All vegetation
296 up to a height of 2 m was sampled within 34 plots 100 x 2.5 m and miners reared to adults as far
297 as possible. Mining species were morphotyped using the morphology of mines and adults. The
298 sampling continued for one year, from 1997 to 1998. Overall, 70 plant species from 25 families
299 were sampled in proportion to their abundance in the study plots (25).

300

301 **Xylem chewers, Panama.** Cerambycid beetles were reared from standardized timber baits
302 exposed in canopy and understorey of lowland wet forests in San Lorenzo Protected Area
303 (9°16'56"N, 79°58'26"W; 150-180 m asl, Colón Province; mean annual temperature 26.0°C,
304 mean annual rainfall 3,139 mm), then caged for rearing. 12 tree species from nine families were
305 sampled using 8 baits with combined weight ca 100 kg of wood per tree species. Singleton
306 observations of plant-insect interactions were removed.

307

308 **Adult leaf chewers, Czech Republic.** All adult herbivores (Coleoptera) were sampled from
309 accessible foliage of 15 focal, locally common woody plant species in the Poodri Protected Area
310 (49°42-48'N, 18°03-13'E; 200 m above seas level, mean annual temperature 7-8.5°C, mean
311 annual rainfall 600-800 mm). The study area of 300 ha included three fragments of the primary
312 floodplain forest dominated by *Quercus*, *Ulmus*, *Tilia*, *Prunus* and *Fraxinus*. The study plant
313 species represented ~85% of the total forest basal area of trees in the forest. Insect sampling
314 continued throughout the growing seasons during 1999-2001. Sampling effort amounted to 150
315 m² of foliage inspected per tree species. Each herbivore was tested in a no-choice experiment on
316 the leaves of the plant it was collected from. Only feeding individuals were retained in the
317 analysis. Plant-herbivore trophic interactions supported by singletons were excluded from the
318 analysis (11).

319
320 **Larval leaf chewers, Czech Republic.** All externally feeding, leaf-tying and rolling larvae
321 (Lepidoptera, Hymenoptera, Coleoptera) were sampled from the same trees as mobile chewers
322 (see above). Larvae were identified to morphospecies and/or reared to adults. All insects
323 assigned to morphospecies were later verified and identified by taxonomic specialists. Plant-
324 herbivore trophic interactions supported by singletons were excluded from the analysis (11).

325
326 **Leaf miners, Great Britain.** Leaf-miners were sampled from 20 herbaceous species and 11
327 families in a damp semi-natural grassland 1.8 ha in size (Rush Meadow) at Silwood Park,
328 Berkshire, UK (51°24'48"N, 0°39'02"W) from May to October 1999. Leaves containing living
329 miners were placed in sealed plastic tubs to rear hosts. Diapausing hosts were over-wintered at
330 ambient temperatures in a well-ventilated outdoor shed. The trophic interactions recorded are
331 based on unstandardized collections made in a stratified manner throughout the site, and reflect
332 only sampled hosts that were reared to generate identifiable adult leaf-miners.

333
334 **Leaf miners, Poland.** The data on leaf-mining insects of the Białowieża National Park, Poland
335 (52°45'N, 23°53'E; 145-175 m above sea level, mean annual temperature 6.8°C, mean annual
336 rainfall 641 mm) were published by Michalska (28). They include all leaf-miners and their host
337 plants recorded in the national park, i.e. 152 km² of predominantly old growth-forest (forest
338 associations *Circaeo-Alnetum*, *Carici elongatae-Alnetum*, *Peucedano-Pinetum*, *Querceto*
339 *Carpinetum stachyetosum* and *Pineto-Quercetum serratuletosum*) during the years 1967-1972.
340 The present analysis includes only leaf miners on woody plant species.

341
342 **Leaf suckers, Great Britain.** Feeding records for mesophyll-sucking leafhoppers
343 (Auchenorrhyncha, Typhlocybinae) were collected from woody host species at 22 study sites in
344 Great Britain and confirmed by rearing of larvae (29). Trophic interactions supported by at least
345 5 rearing records were included in the analysis.

346
347 **Leaf and phloem suckers, Germany.** Mesophyll cell and phloem sucking Auchenorrhyncha
348 were sampled within the 1,117 km² area of the administrative district of Göttingen, Germany
349 (51°17-38'N, 9°32'-10°22'E, 120-530 m above sea level, mean annual temperature 8.7°C, mean
350 annual rainfall 645 mm) for 25 years (1990 – 2014). Insects were collected from woody plant
351 species mainly between May and October through sweep-netting and direct search on the host,
352 without any standardized design but aiming at extensively covering all potential host species.
353 The study area is a semi-open landscape with fields and managed forests, as well as numerous

354 hedgerows, alleys and single trees. Singletons were removed prior to analyses; data are detailed
355 in Nickel (30, 31).

356
357 **Gallers, Czech Republic.** All galls were as far as possible completely sampled from plants
358 with DBH>5cm at two 0.1 ha plots in broadleaf floodplain forest in Southern Moravia, Czech
359 Republic (48°48'N, 17°5'E, 152 asl, and N48°41', E16°56', 164 m above sea level, mean annual
360 temperature 9°C, mean annual rainfall 525 mm). The terrain was flat and the dominant trees
361 included species of *Quercus*, *Fraxinus*, *Carpinus*, *Acer* and *Populus*. Galls were collected from
362 83 plant individuals representing nine tree species. The total sampling effort amounted to 12,500
363 m² of foliage. The sampling was carried out during the 2013 vegetation season. Canopies were
364 accessed by tree-felling at one of the 0.1 ha plots and from an elevated work platform (cherry-
365 picker) at the second one. In the felled plot, sampling was carried out during the peak of miner
366 abundance (mid May – mid June), and in the cherry-picker plot samples were taken throughout
367 the whole season from May to August. Galls were morphotyped and reared to adults for further
368 identification by specialists. Note that galling insects were used in analyses involving species-
369 level diet breadth (e.g. Fig 3), but were not used in analyses involving family-level diet breadth
370 because the temperate gallers (as well as the tropical gallers, from Papua New Guinea, see
371 above) all had a family-level diet breadth of 1 (host family), from which it was not meaningful to
372 estimate a diet breadth distribution. Singleton observations of interactions were excluded.

373
374 **Xylem chewers, Czech Republic.** Cerambycid beetles were studied in the lowland and foothill
375 forests along the Dyje river in the Podyji National Park and the Lower Moravia UNESCO
376 Biosphere Reserve (N48°46-51', E15°50'-16°50'; 160-350 m above sea level; mean annual
377 temperature 9 °C, mean annual rainfall 524 mm). The dominant trees include *Quercus* spp.,
378 *Fraxinus* spp., *Carpinus betulus*, and *Acer* spp. Historically, the forests had been managed as
379 coppice, coppice with standards or pasture woodland. The cerambycids were reared from
380 standardized timber baits of 22 woody plant species representing 11 families, including two
381 conifers. Each plant species was sampled using 12 baits with average weight of 15 kg each,
382 exposed in canopy and understorey and subsequently caged for insect rearing. Singleton
383 observations of interactions were excluded.

384
385

385 **Appendix S2, Taxonomic and phylogenetic diet breadth**

386

387 Most of the analyses that we report utilized both family and species-level diet breadth, and
388 results obtained with the two indices were always similar, which is perhaps not surprising as
389 family and species-level diet breadth are highly correlated, as can be seen in Fig. S1. Examples
390 of the distribution of both species and family-level diet breadth are shown in Fig. S2 for
391 Lepidoptera; and an example of family-level diet breadth is shown in Fig. S3 for parasitoids.

392 The shape parameter (α) from the truncated, discrete Pareto distribution fit to family-level
393 diet breadth changes with latitude, as can be seen in Fig. 2A (main text). The relationship
394 between α and latitude is significant when modeled with the number of rearing records as a
395 covariate proxy for sampling effort: $F_{2,10} = 8.87$, $R^2 = 0.64$, $P = 0.0061$; partial regression
396 coefficient for latitude = -0.023 , $P =$
397 0.0046 ; coefficient for rearing records
398 = 0.062 , $P = 0.69$. Results are
399 essentially identical with different
400 covariates: the area of sites, the
401 number of years that records have been
402 taken at each site, the number of
403 records, or the number of herbivore
404 species (years, records, area and
405 number of species are not individually
406 significant, but the overall model and
407 the effect of latitude are always
408 significant; in all cases covariates
409 conform to assumptions of standard
410 linear models). Although α changes
411 with latitude, the goodness of fit of the
412 Pareto distribution does not change
413 with latitude, as can be seen for
414 family-level diet breadth in Fig. S4A.

415 The shape of the discrete,
416 truncated Pareto for species-level diet
417 breadth also changes with latitude
418 (Fig. S4B): the associated partial
419 regression coefficient for latitude is $-$
420 0.015 ($P = 0.035$); results for the
421 whole model as follows: $F_{2,10} = 3.65$,
422 $R^2 = 0.42$, $P = 0.065$.

423 Phylogenetic diet breadth (PD)
424 similarly changes with latitude (Fig.
425 2C, main text). Using the number of
426 rearing records from each site as a
427 covariate for sampling effort, results
428 from the full model relating latitude to
429 PD are as follows: $F_{2,10} = 11.58$, $R^2 =$
430 0.70 , $P = 0.0025$; for the latitude term:

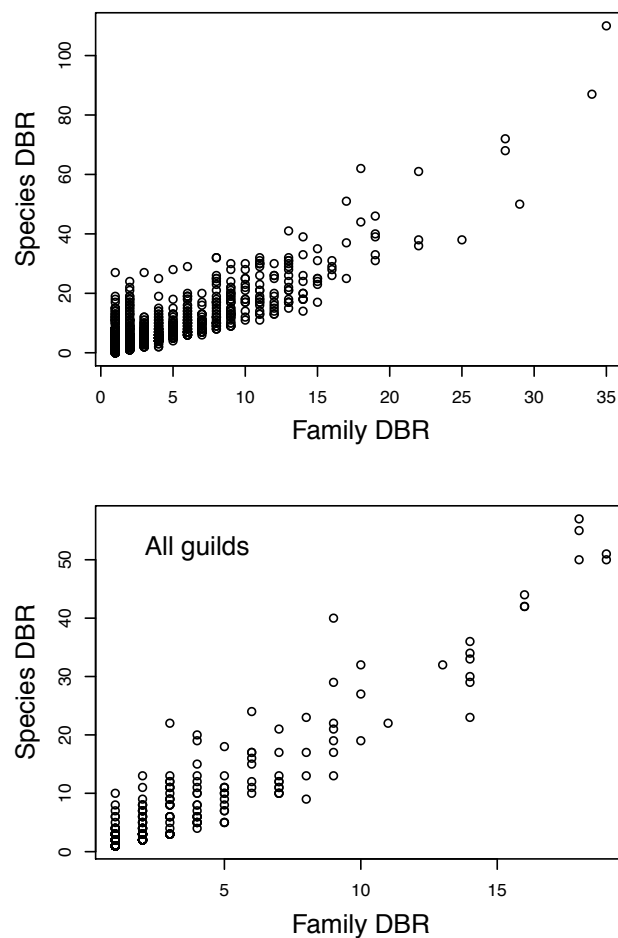


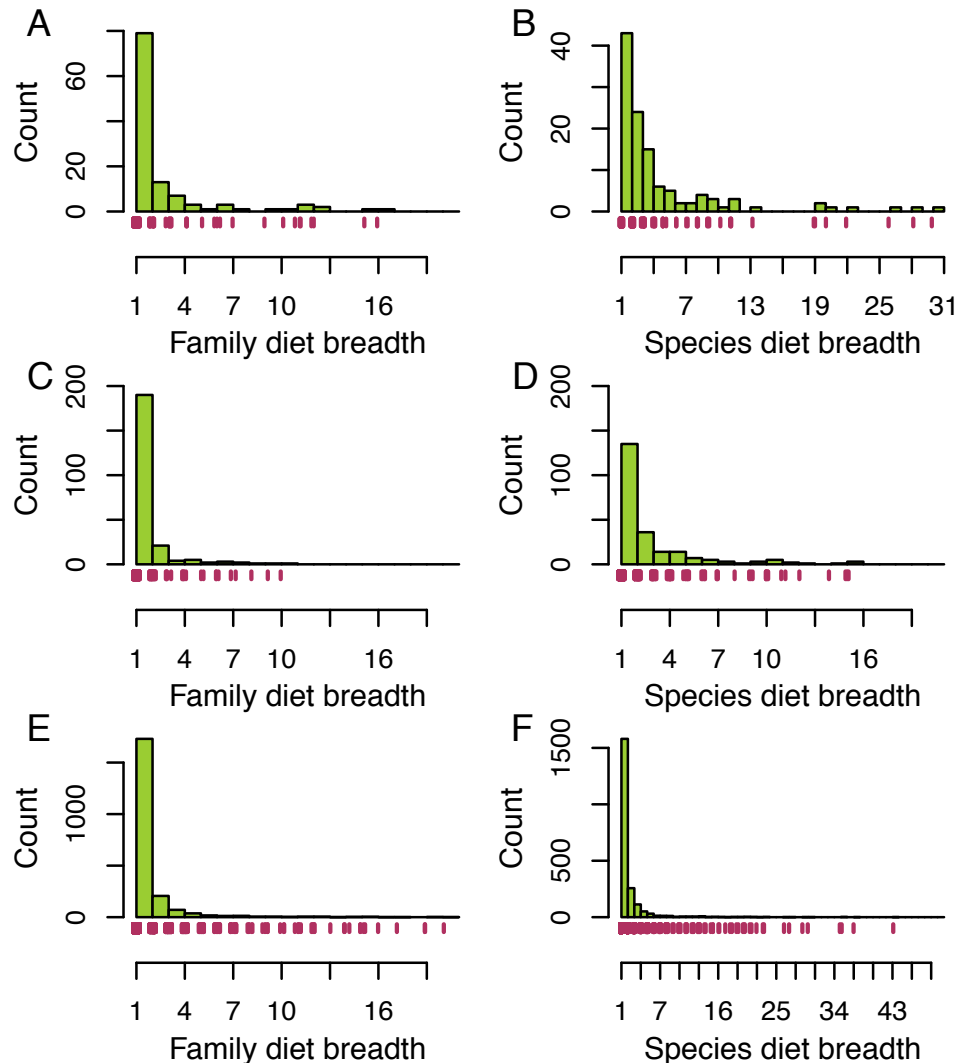
Fig. S1. Species-level diet breadth against family-level diet breadth for the two major subset of the data: all Lepidoptera, and all guilds (excluding Lepidoptera). Each point illustrates species and family-level diet breadth for a single herbivore species.

431 2.35 partial regression coefficient, $P < 0.001$; for the sampling records term: 22.40 coefficient, P
432 $= 0.088$.

433 Finally, both species-level and family-level diet breadth were investigated for taxonomic
434 and geographic subsets of the data. Results for analyses of the Pareto distribution for subsets of
435 the data are shown in Table S3, including focal sites for Lepidoptera, and for species within the
436 top ten most frequently occurring families of Lepidoptera in our data. Also shown in Table S3
437 are the Pareto statistics for different herbivore guilds and for the diet breadth of Lepidoptera
438 associated with

439 the top ten most
440 frequently-
441 studied plant
442 families.
443 Finally, fit is
444 shown for
445 parasitoids from
446 one New and
447 one Old World
448 site.

449 For
450 Pareto fit
451 associated with
452 the top ten most
453 frequently
454 studied plant
455 families (Table
456 S3), the species
457 count is the
458 number of
459 associated
460 herbivores not
461 the number of
462 plant species.
463 With respect to
464 the Pareto fit to
465 parasitoid diet
466 breadth (the last
467 two rows), only
468 family-level
469 records were
470 available.
471 Included in
472 Table S3 is a
473 test statistic
474 from a χ^2 test for
475 goodness of fit
476 and associated P values.



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Fig. S2. Examples of the distribution of family and species-level diet breadth from three sites, from high to low latitude: Connecticut (A and B), Papua New Guinea (C and D), and Ecuador (E and F). Tick marks under plots mark individual observations for ease of visualization in the thin tail of the distribution. Note that the y axes differ in scale among plots as the number of Lepidoptera species differs among sites.

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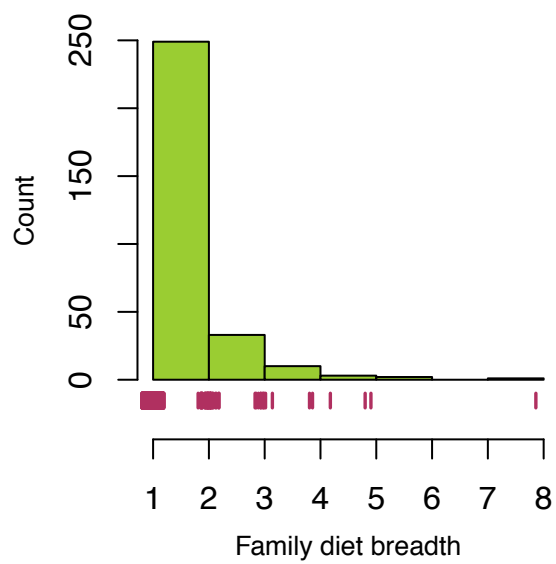


Fig. S3. Distribution of diet breadth for tachinid flies, Ecuador. These are parasitoids that attack caterpillars.

Table S3. Pareto statistics for species-level and family-level diet breadth (DBR): alpha (the shape parameter) and the upper truncation parameter (the maximum observation) are shown, as well as the goodness of fit test statistic and associated *P* value (values less than 0.05 reject the fit of the Pareto distribution). Also shown is richness (“Sp.”) for each site or taxon. For focal sites, percentages after site names are the percentages of species found in association with a single host species and a single host family as calculated from raw data (first and second values shown, respectively). The same values are reported for feeding guilds.

Site or taxon	Sp.	α	species-level DBR			family-level DBR			
			max.	test stat.	<i>P</i>	α	max.	test stat.	<i>P</i>
All Lepidoptera									
World	6,388	1.53	110	57.60	0.06	1.85	35	6.37	1.00
New world	5,565	1.50	110	47.78	0.19	1.82	35	6.90	1.00
Old world	679	1.11	31	3.70	1.00	1.45	16	13.29	0.58
Focal sites									
Canada (22%, 43%)	671	0.90	46	93.52	<0.01	1.32	15	18.42	0.19
Japan (63%, 67%)	174	1.10	14	4.50	0.98	0.98	7	2.13	0.91
Czech Republic (51%, 58%)	74	1.03	13	9.72	0.96	1.18	9	5.11	0.75
Connecticut (37%, 68%)	116	0.58	30	3.06	1.00	0.86	16	9.26	0.86
Ohio (45%, 58%)	173	1.02	26	5.76	0.95	0.99	15	3.42	1.00
Great Basin (56%, 60%)	25	0.29	9	6.19	0.62	0.49	9	2.29	0.97
Arizona (53%, 64%)	186	1.11	53	4.01	0.98	1.31	24	2.25	0.97
Louisiana (53%, 60%)	328	1.07	67	1.41	1.00	1.24	36	3.39	1.00
Brazil (67%, 77%)	568	1.33	33	3.23	1.00	1.46	19	16.44	0.56
La Selva (71%, 81%)	1321	1.62	61	20.47	0.77	1.95	28	6.36	0.96
Panama (78%, 92%)	400	1.72	18	0.78	1.00	2.39	10	9.35	0.41
Papua New Guinea (59%, 83%)	229	0.88	15	4.92	0.99	1.69	10	1.19	1.00
Ecuador (74%, 82%)	2122	1.52	43	8.05	1.00	1.79	20	5.99	1.00
Ten most frequently-studied Lepidoptera families									
Geometridae	1293	1.25	41	14.78	1.00	1.67	17	3.07	1.00
Noctuidae	826	1.23	45	23.09	0.88	1.67	19	6.22	0.99
Erebidae	419	1.03	109	18.90	0.59	1.28	35	5.63	1.00
Pyalidae	608	1.69	25	2.27	1.00	2.00	17	3.13	0.99
Tortricidae	256	0.70	33	4.26	1.00	1.20	19	1.78	1.00
Saturniidae	189	0.71	40	10.70	0.91	0.86	22	9.65	0.79
Nymphalidae	363	1.44	20	1.87	1.00	2.60	7	4.61	0.60
Notodontidae	328	1.16	33	3.13	1.00	1.56	11	1.08	0.98
Hesperiidae	317	1.66	27	2.82	0.99	2.31	5	0.56	0.97
Lymantriidae	47	0.48	60	12.61	0.32	0.66	22	11.49	0.18
Ten most frequently-studied plant families (as Lepidoptera hosts)									
Pinaceae	291	0.52	23	8.96	0.99	-	-	-	-
Betulaceae	484	1.52	11	5.27	0.88	-	-	-	-
Fabaceae	672	2.06	18	2.86	1.00	-	-	-	-
Salicaceae	455	1.77	9	5.74	0.68	-	-	-	-
Piperaceae	513	1.79	27	2.55	1.00	-	-	-	-
Asteraceae	448	1.66	16	5.83	1.00	-	-	-	-
Rosaceae	403	1.52	9	0.98	1.00	-	-	-	-
Fagaceae	320	1.56	13	4.01	0.95	-	-	-	-
Sapindaceae	356	1.90	7	2.69	0.85	-	-	-	-
Rubiaceae	384	1.87	8	0.71	1.00	-	-	-	-

Guilds

Leaf miners, Belize (89%, 99%)	81	2.08	8	1.20	0.88	6.22	2	7.88 $\times 10^{-13}$	1.00
Leaf miners, Papua New Guinea (89%, 99%)	124	2.03	9	1.85	0.93	4.96	3	3.13	0.21
Leaf miners, UK (77%, 97%)	31	1.96	5	0.52	0.77	4.73	2	4.82 $\times 10^{-13}$	1.00
Leaf miners, Poland (82%, 97%)	34	2.53	3	0.094	0.95	3.44	3	2.08	0.35
Leaf suckers, Papua New Guinea (83%, 94%)	36	2.60	3	0.079	0.96	3.17	3	0.68	0.71
Leaf suckers, UK (59%, 76%)	55	0.58	17	2.03	0.96	1.32	7	2.82	0.83
Leaf suckers, Germany (NA, 70%)	81	-	-	-	-	1.31	7	2.20	0.90
Larval leaf chewers, Papua New Guinea (61%, 83%)	326	1.07	25	8.77	0.98	1.57	15	12.68	0.55
Larval leaf chewers, Czech Republic (56%, 66%)	94	1.19	13	1.60	1.00	1.39	9	2.48	0.96
Xylem chewers, Papua New Guinea (33%, 35%)	40	0.45	16	5.69	0.93	0.60	10	4.21	0.90
Xylem chewers, Panama (64%, 77%)	22	1.08	6	1.68	0.89	1.43	3	0.096	0.95
Xylem chewers, Czech Republic (35%, 48%)	46	0.69	19	20.89	0.035	0.91	9	4.69	0.79
Phloem suckers, Papua New Guinea (45%, 45%)	29	-	-	-	-	0.20	8	1.24	0.99
Phloem suckers, Germany (NA, 70%)	84	-	-	-	-	1.33	12	3.42	0.91
Adult leaf chewers, Papua New Guinea (43%, 55%)	245	0.46	57	5.02	1.00	0.68	19	8.63	0.97
Adult leaf chewers, Czech Republic (55%, 55%)	20	0.14	13	9.42	0.67	0.31	8	0.78	0.94
Gallers, Papua New Guinea (99%, 100%)	76	6.12	2	3.91 $\times 10^{-14}$	1.00	-	-	-	-
Gallers, Czech Republic (86%, 100%)	43	2.22	2	1.74 $\times 10^{-15}$	1.00	-	-	-	-

Parasitoids

Ecuador, Tachinidae	309	-	-	-	-	2.56	8	4.44	0.73
Papua New Guinea, wasps and flies	58	-	-	-	-	3.49	2	9.98 $\times 10^{-14}$	1.00

534

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537 **Appendix S3, Change among sites in the distribution of diet breadth**

538

539 The shape parameter (α) of the
 540 discrete, truncated Pareto
 541 distribution is a useful
 542 summary statistic for
 543 investigating change in the
 544 distribution of diet breadth (e.g.
 545 Fig. 2A, main text), but change
 546 in diet breadth can also be
 547 visualized with the maximum
 548 observation (the upper
 549 truncation parameter from the
 550 Pareto distribution) and
 551 quantiles (as in Fig. 2B). In Fig.
 552 S5, we show examples of the
 553 distribution of family-level diet
 554 breadth at a subset of sites in
 555 order to visualize the behavior
 556 of summary statistics including
 557 quantiles.

558 Specifically, five
 559 parameters are shown in Fig.
 560 S5: α (the shape parameter
 561 from the discrete, truncated
 562 Pareto), β (the upper truncation
 563 parameter), and a selection of
 564 quantiles (the 99th, the 95th,
 565 and the 90th). Quantiles are a useful
 566 way to measure change in
 567 density throughout the tail as
 568 the frequency of relatively-
 569 specialized herbivores
 570 increases at lower latitudes. In
 571 the main text and Fig. 2B,
 572 change in the 90th quantile is
 573 presented ($F_{1,11} = 0.79$, $R^2 = 0.68$, $P < 0.001$). Dynamics for the 95th and 99th quantile are shown
 574 in Fig. S6. The former (95th) changes significantly with latitude ($F_{1,11} = 17.43$, $R^2 = 0.61$, $P =$
 575 0.0016), while the 99th does not ($F_{1,11} = 0.79$, $R^2 = 0.067$, $P = 0.39$). The latter result (for the 99th
 576 quantile) is consistent with the static nature of the far reach of the tail of the distribution (see also
 577 the maximum observations in Fig. 2B, which do not change with latitude).

578

579

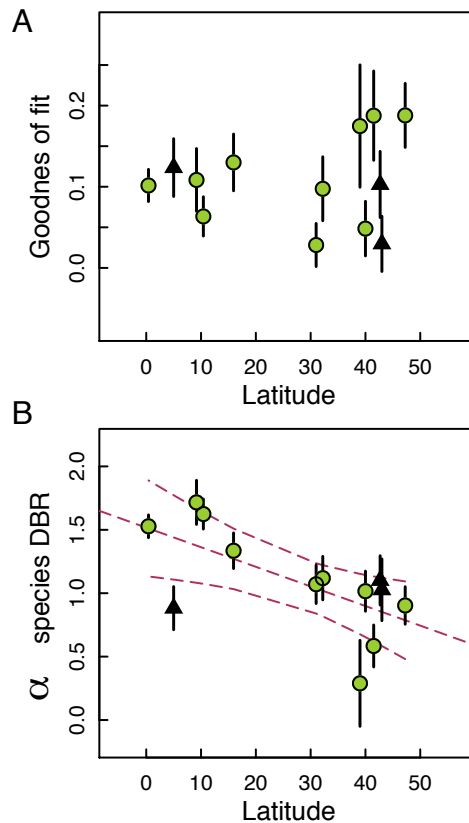


Fig. S4. (A) Goodness of fit of the Pareto distribution to family-level diet breadth (DBR) against latitude, with standard errors from 1000 bootstrap resamples. (B) Latitudinal trend in the shape parameter for species-level diet breadth (DBR). Greater values of the shape parameter indicate distributions of diet breadth at individual sites that include a greater portion of relatively specialized herbivores. Standard errors for individual sites (points) are shown based on 1000 bootstrap resamples, and 95% confidence limits are shown around the regression line. Green circle are New World sites, dark triangles are Old World in both panels.

579 **Appendix S4, Plant diversity and specialization**

580
 581 Multiple regression and path
 582 analysis were used to
 583 investigate relationships among
 584 plant diversity, diet breadth and
 585 relevant variables. First, we
 586 asked if there is a relationship
 587 between the species richness of
 588 plant families and the diet
 589 breadth of insects that attack
 590 those families. Table S4 shows
 591 results associated with
 592 particular factors in regression
 593 models, as described in the
 594 main text. Details for full
 595 models as follows: $F_{4,24} =$
 596 7.73 , $R^2 = 0.56$, $P < 0.001$ (for
 597 the model with all herbivores);
 598 $F_{4,21} = 2.01$, $R^2 = 0.28$, $P =$
 599 0.13 (for the model with only
 600 herbivores occurring at sites \leq
 601 25 degrees of latitude); and
 602 $F_{4,21} = 3.67$, $R^2 = 0.41$, $P =$
 603 0.020 (for herbivores occurring
 604 at sites >25 degrees of
 605 latitude). In these analyses, we
 606 included plant families from
 607 which caterpillars had been
 608 reared at least 100 times.
 609 Qualitatively similar results
 610 were obtained for all
 611 herbivores as well as for
 612 herbivores at lower latitudes
 613 (Table S4); much lower power
 614 was available for the higher
 615 latitude subset.

616 Finally, path analysis
 617 was used to address
 618 relationships among plant
 619 richness, latitude and dietary
 620 specialization for the thirteen
 621 Lepidoptera sites (dietary
 622 specialization was represented
 623 by α , the shape parameter from
 624 the Pareto distribution; higher

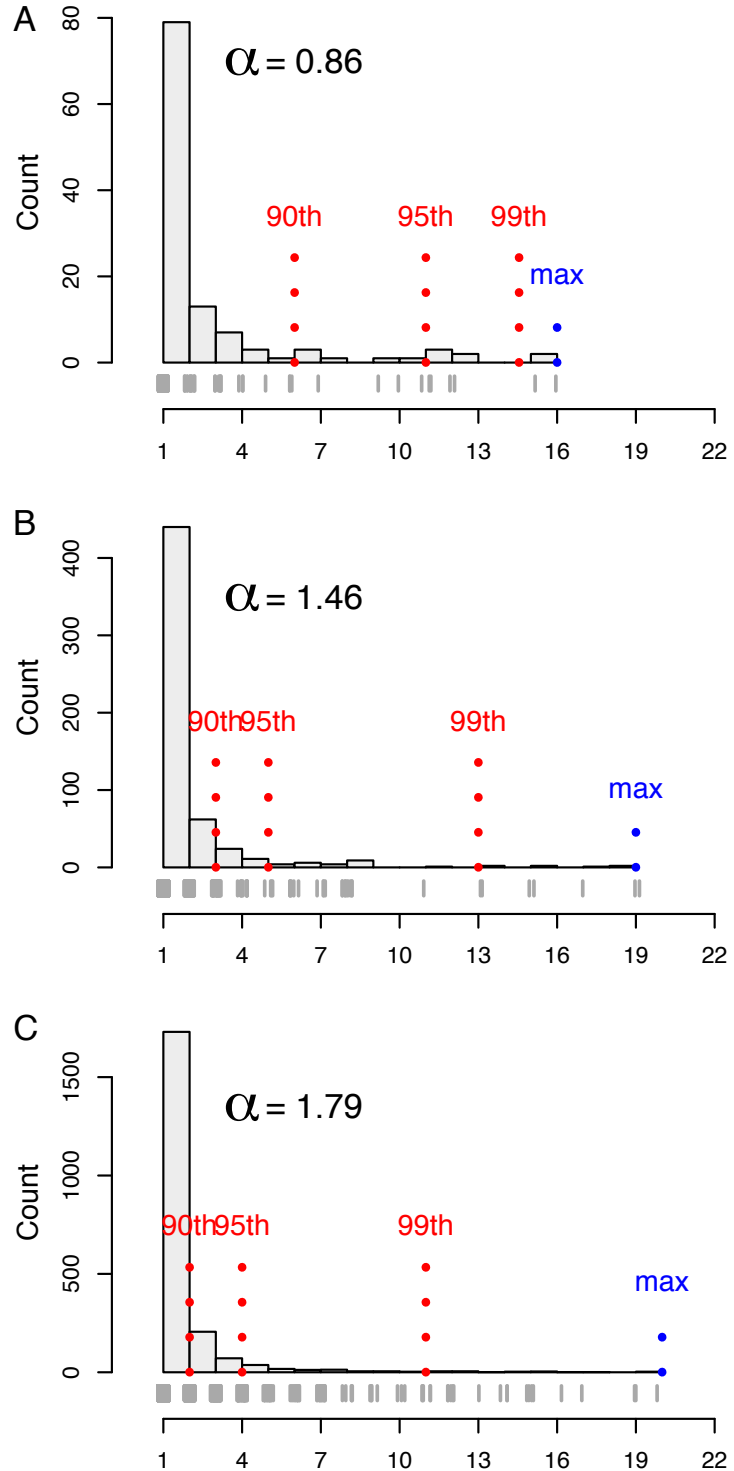


Fig. S5. Illustration of descriptive statistics associated with family-level diet breadth distributions from three sites: Connecticut (A), Brazil (B), and Ecuador (C).

625 values of α correspond to a greater fraction of specialized herbivores). Plant richness in these
 626 analyses refers to the numbers of plant families and species encompassed by insect sampling at
 627 each site. Results from analyses
 628 are summarized in Fig. S7 for
 629 two models, one in which plant
 630 richness refers to plant species
 631 ($\chi^2 = 1.62$, d.f. = 2, $P = 0.44$),
 632 and another in which plant
 633 richness refers to plant families
 634 ($\chi^2 = 1.61$, d.f. = 2, $P = 0.45$).
 635 Both models fit the data: P
 636 values did not reject the null
 637 hypothesis of fit. Multiplying
 638 standardized path coefficients,
 639 we see that the indirect effect
 640 of latitude on specialization via
 641 plant richness (in the model
 642 with plant species richness) is -
 643 $0.70 * 0.22 = -0.15$. Thus the
 644 contribution of plant richness
 645 to the latitudinal gradient in
 646 specialization is approximately
 647 1/4 the direct effect of latitude
 648 on specialization (-0.65).
 649 Analyses shown in Fig. S7 only
 650 involved α calculated for
 651 family-level diet breadth.
 652 Analyses are not shown for
 653 species-level α , for which
 654 results were qualitatively
 655 identical to the results in Fig.
 656 S7.
 657

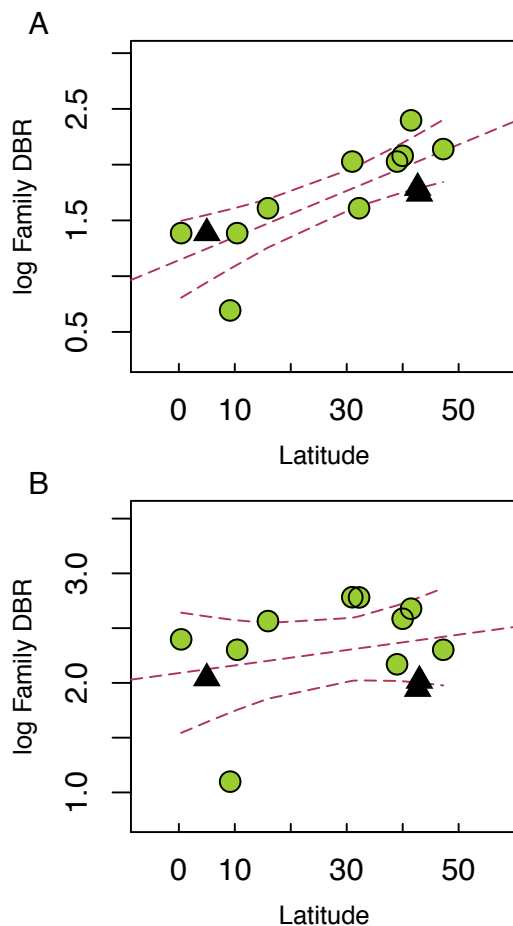


Fig. S6. 95th (A) and 99th (B) quantiles versus latitude; see main text and Fig. 2B for 90th quantile. 95% confidence limits are shown. As in other plots, green circles are New World, black triangles Old World.

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Table S4. Results from three multiple regression models with independent variables as shown below, and the dependent variable of median species-level diet breadth for insects associated with different host plant families. The three analyses are for all insect herbivores, herbivores at and below 25 degrees of latitude, and herbivores at sites greater than 25 degrees.

Factor	Estimate	Std. error	T
All herbivores			
Richness	-0.36	0.067	-5.42 ***
Range	0.0076	0.0030	2.49 *
Age	0.49	0.30	1.61
Sample size	0.067	0.14	0.47
Tropical			
Richness	-0.14	0.059	-2.37 *
Range	0.0035	0.0027	1.30
Age	0.28	0.27	1.07
Sample size	-0.09	0.26	-0.74
Temperate			
Richness	-0.040	0.069	-0.59
Range	-0.0022	0.0032	-0.67
Age	0.17	0.32	0.54
Sample size	-0.37	0.15	-2.53*

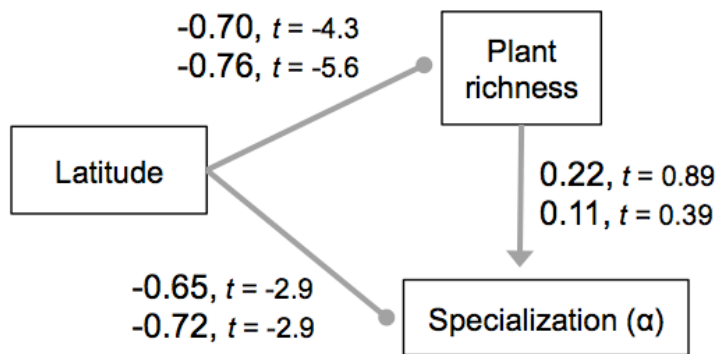


Fig. S7. Path analyses of latitude, plant richness and dietary specializations across all 13 focal sites; specialization is represented by α , the shape parameter from the Pareto distribution fit to family-level diet breadth. Next to each path, two sets of coefficients and test statistics are reported: the first value is for models that included plant species richness, and the second value is for models that included plant family richness. R^2 from both models as follows: 0.49 and 0.57 for plant richness in models with plant species richness and plant family richness, respectively; 0.68 and 0.66 for diet breadth, similarly for models with plant species and plant family richness.

```

727 Appendix S5, R code for fit of the discrete, truncated Pareto
728
729 ## To accompany Forister et al. "The global distribution of diet breadth in insect herbivores"
730 ## 11 June 2014
731 ## Two blocks of code below, one for estimation of Pareto fit,
732 ## and one for graphing a survival plot (as in Fig 1D and E of main text).
733
734 ## The Pareto fit works on a simple vector of diet breadth values (positive integers),
735 ## Usage:
736 ## dtparlogest(exampleData$sdb,0,10)
737 ## where sdb is the vector of diet breadth values, and 0 and 10 set bounds on
738 ## estimation of the shape parameter alpha.
739
740 ## The survival plotting function works on a data frame with two columns:
741 ## one with site identifier (collection locale, for example), and the second
742 ## with diet breadth values (each row being comprised of the diet breadth
743 ## for one herbivore species). Usage:
744 ## Pfit2("sdb",exampleData,"siteName",-35,10,0,5)
745 ## where the first term specifies the diet breadth column,
746 ## the second term is the name of the data frame,
747 ## the third term is the name of the site (or rows within the data frame to be analyzed),
748 ## and the last terms set x and y limits for survival plot.
749
750 ##### main Pareto estimation #####
751
752 ## Function computing least squares distance between logs of sample and
753 ## model cdf
754 lslogdist.dtpar<-function(x, a)
755 {
756   n <- length(x)
757   x <- sort(x)
758   xmin<-min(x)
759   xmax<-max(x)
760   xval<-seq(from=xmin, to=xmax, by=1)
761   nxval<-length(xval)
762   cdf<-rep(0, times=nxval)
763   for (i in 1:nxval){
764     cdf[i]<-length(x[x<=xval[i]])/n
765   }
766
767 g<-xmin
768 nu<-xmax
769 values=seq(from=g, to=nu, length=nu-g+1)
770 den=(1/g)^a - (1/(nu+1))^a
771 numvalues<-nu-g+1
772 numterm1=1/values^a

```

```

773 numterm2<-rep(0, times=numvalues)
774 numterm2[1:numvalues-1]<-numterm1[2:numvalues]
775 numterm2[numvalues]<-1/(nu+1)^a
776 numterm2<-1/(values+1)^a
777 numterm2
778 num=numterm1-numterm2
779 probs<-num/den
780 sum(probs)
781 cprobs<-cumsum(probs)
782
783 ## survival function
784 surv<-1-cprobs
785 emp.surv<-1-cdf
786 lsurv<-length(surv)
787 lsurvm1<-lsurv-1
788 logsurv<-log(surv[1:lsurvm1])
789 logemp.surv<-log(emp.surv[1:lsurvm1])
790 lslogdist<-sum((logsurv-logemp.surv)^2)
791 lslogdist
792 }
793
794 dtparlogest<-function(y, int1, int2)
795 {
796     gamma <- min(y)
797     nu <- max(y)
798     out <- optimize(lslogdist.dtpar, interval = c(int1, int2), maximum = F,
799         tol = 1e-005, x = y)
800     alpha <- out$minimum
801     cat("gamma=", gamma, "nu=", nu, "alpha=", alpha, "\n")
802     alpha
803 }
804
805 ##### survival plot #####
806
807 Pfit2 <- function(type,data,where,ylim1,ylim2,xlim1,xlim2){
808     new<-subset(data,site==where)
809     x<-new[,type]
810     n <- length(x)
811     x <- sort(x)
812     xmin<-min(x)
813     xmax<-max(x)
814     xval<-sort(unique(x))
815     nxval<-length(xval)
816     nxvalm1<-nxval-1
817     surv<-rep(0, times=nxval)
818     for (i in 1:nxval){

```



```

819         surv[i]<-length(x[x>xval[i]])/n
820     }
821     a<-dtparlogest(x, 0.1, 10)
822     g<-xmin
823     nu<-xmax
824     values=seq(from=g, to=nu, length=nu-g+1)
825     xs<-1/(xval+1)^a
826     xs1<-xs -1/(nu+1)^a
827     num<-xs1[1:nxvalm1]
828     den<-1/g^a
829     den<-den-1/(nu+1)^a
830     surv.th<-num/den
831     xcoord<-log(xval[1:nxvalm1])
832     survth<-log(surv.th[1:nxvalm1])
833     survdata<-log(surv[1:nxvalm1])
834     plot(xcoord, survdata, col=c(1), pch=20,cex=1.5, xlim=c(xlim1, xlim2), ylim=c(ylim1,
835     ylim2),ylab="",xlab="")
836     points(log(xval[1:nxvalm1]), survth,pch=1,cex=2)
837     lpois<-mean(x)
838     cdf.pois<-ppois(xval, lpois)
839     surv.pois<-1-cdf.pois
840     log.surv.pois<-log(surv.pois[1:nxvalm1])
841     points(log(xval[1:nxvalm1]), log.surv.pois, col=1, pch=0,cex=1.5, xlab="", ylab="")
842     geo.mean<-1/mean(x)
843     xvalm1<-xval-1
844     cdf.geom<-pgeom(xvalm1, geo.mean)
845     surv.geom<-1-cdf.geom
846     log.surv.geom<-log(surv.geom[1:nxvalm1])
847     points(log(xval[1:nxvalm1]), log.surv.geom, cex=1.5,col=1, pch=2, xlab="", ylab="")
848     }
849
850

```

850 *Appendix S6, Additional acknowledgements*

851
852 Acknowledgements below to supplement those in the main text, alphabetically by last name of
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901

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