



## Supplementary Materials for

### **Arthropod Diversity in a Tropical Forest**

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## Materials and Methods

### Field protocols and specimen processing

Field sampling was performed in the San Lorenzo Protected Area in Panama (9°16'N, 79°58'W, elevation ca 130 m). Annual rainfall in this lowland wet forest averages 3,139 mm and annual average air temperature is 26.0°C. Fifty percent of this area is a contiguous evergreen seasonal mixed forest (26) which contained our study area (hereafter SLPA, 6,000ha). SLPA is bounded by the Atlantic Ocean towards the North and a mosaic of pastures and coffee plantations towards the South (26). Twelve 20 x 20 m sites, all less than 2 km apart, were surveyed for plants and arthropods, from the ground to the upper canopy. At all sites, plants >10 mm dbh were tagged and identified before arthropod collections began. Access to the upper canopy was facilitated by fogging, single-rope climbing techniques and a variety of devices such as a canopy crane, canopy raft, canopy bubble and tree-platform (27). Arthropods were surveyed using 14 different protocols targeting the soil, litter, understorey, mid-canopy and upper canopy habitats, replicated across seasons in 2003 and 2004. These protocols included (27): Winkler sifting (item 1 in Fig. S1B); Berlese-Tullgren (2); hand-collecting of galls and social insects (3, 8); fogging (5); beating (6); wood-rearing (9); baits (7); and various types of traps such as pitfall (4), small and large flight-interception (11, 12), sticky (13), light (10), and Malaise traps (14). After an initial sampling period of 6 weeks during the late wet season, we replicated field work during three similar sampling periods targeting the dry, early wet and late wet seasons. During this extended sampling period, flight-interception, sticky and Malaise traps were ran for relatively long periods of time (flight-interception traps continuously from October 2003 to October 2004).

Focal arthropods were sorted to named species or morphospecies by taxonomists and grouped into 18 data sets including subsets of insect orders with similar feeding ecologies (Table S1). Singletons were defined as species represented by a single individual in all protocols combined together. Guild assignment for beetles was challenging since many species can be assigned into categories that mix up feeding relations and structural niches (28). Hence, we followed different authors (29-31) to assign beetle species to a modified guild system (32; Table S1).

### Estimates of species richness of focal taxa

As no sampling effort suffices to capture the full species richness of a larger area, various extrapolations were derived from the range of the empirical data collected. For each data set, we calculated six estimators (a1 to a6, hereafter called “models” for the sake of simplicity) using formulas and algorithms detailed elsewhere (33-36). These models account for incompleteness of surveys (model a1), larger sample size (a2), species-area relationship (a3), relationship to plant species (a4) and distance (a5), and species-abundance distribution (a6; Fig. S2).

a1. Non-parametric estimator of species richness. We calculated the Chao2 estimator (37) with EstimateS 8.20 (100 randomizations, 34). This estimator has performed well in a number of studies (38, 39). When Hortal *et al.* (40) reviewed the performance of 10

non-parametric estimators, they suggested considering the results of the six best: ACE, ICE, Chao1, Chao2, Jackknife1 and Jackknife2. All these metrics were calculated with EstimateS 8.20. For the sake of simplification, we then chose Chao2 as our non-parametric estimator since the difference between the arithmetic mean of the predictions of the six estimators calculated and that of the Chao2 was only 3.4% for all focal arthropods. The predictions of this estimator refer to an unspecified area, but it has the merit of providing a lower-bound estimate (41) against which the results of other models can be compared (Table S2).

a2. Species-accumulation curves based on sampling effort. To account for increasing species richness with larger sampling effort, we selected five functions: logarithmic (42), Michaelis-Menten (42), negative exponential (43), Weibull (36) and Beta-P (43). We fitted each of these functions to the number of sites surveyed and the cumulative average number of arthropod species per site based on randomized site order (obtained with EstimateS 8.20), choosing the best function with the lowest corrected Akaike's Information Criterion (AICc). To extrapolate to the whole area of SLPA, we considered  $6,000/0.04 = 150,000$  sites for the logarithmic function (which is non-asymptotic) and the asymptote value for all the other functions.

a3. Species-area relationships (SARs). The tendency of species to accumulate with increasing size of the area sampled has been studied for decades (44-46). Using the terminology of Smith (46), our census design used 12 disjunctive plots. Although a power function may often fit the data well, other functions may be better suited (33). We used the package mmSAR (33) to parameterize and select (based on AICc) the best fitting non-linear functional form (among eight: power, exponential, negative exponential, Monod, rational function, logistic, Lomolino, cumulative Weibull; all equations detailed in 33) for observed species-area data sets (i.e., cumulative area and cumulative average number of arthropod species per site based on randomized site order, computed by EstimateS 8.20). Model selection uncertainty arises when the data set supports several functions with a similar strength, but this was not the case for any of our data sets (one function was always identified as clearly superior to the others and was used for final SAR inference). Arthropod species richness was then extrapolated to our study area (6,000ha).

a4. Species-accumulation curves based on cumulative number of plant species surveyed ("plant model"). Many studies have documented relationships between species numbers of insects and plants (9, 17, 18, 47). We fitted a function describing the relationship between the cumulative average number of tree species per site (based on randomized site order; total number of tree species observed in the 12 plots = 162) and the cumulative average number of arthropod species per site (also based on randomized site order, both calculated with EstimateS 8.20). We chose the best functional form out of power (43), linear and Weibull (36) functions, based on AICc. We extrapolated the results to 328 tree species, the known number of tree species in SLPA (S. Lao, pers. comm.).

a5. Distance model. Species turnover along spatial environmental gradients produces a decrease of similarity with distance. Variation in distance decay rates among different taxa may arise if these taxa have different dispersal abilities (48). Hence, the cumulative number of species (cns) is expected to rise over increasing distance from a common origin. Our model considered the cns in aggregates of sites increasingly distant from origin, and extrapolated the results to a 8.74km distance gradient covering the whole of SLPA, by fitting either a linear or power relation between species richness, distance and number of sites. We first ordered the sites into cumulative aggregates increasingly distant from a common origin (each site,  $N = 12$ , hence 81 possible aggregates), thus preserving the spatial structure of the data, as opposed to pair-wise random calculations including all sites (49). The observed number of species in each aggregate depended on the distance from the source and the number of sites included in the aggregate. We fitted either a linear or power relation ( $y = a * \text{Distance}^b + c * \text{No.Sites}^d$ ) between species richness, distance and number of sites, depending on the lower AICc. We checked for spatial autocorrelation in the regression residuals with the software SAM, version 4.0 (50). For this purpose, barycenter aggregates were calculated as the sum of either x or y coordinates of each site in the aggregate, divided by the number of sites in the aggregate. Regressions were not fitted if significant spatial autocorrelation existed in model residuals (i.e., p-values of global Moran's I and Mantel tests  $< 0.05$ ). To estimate species richness in the whole of SLPA, we analyzed our model with distance = 8,740 m and number of sites in the aggregate = 54, the latter being proportional to the disposition of our sites in the study area (the 12 sites covered a distance gradient of 1,941 m).

a6. Species-abundance distribution (SAD). The SAD is one of the oldest patterns in ecology, characterized by few dominant and many rare species (51-53). An undersampled assemblage often produces a truncated log normal distribution and total species richness can be inferred by unveiling this distribution (7, 13, 54). We fitted relative species abundances to a truncated log normal distribution and calculated total richness with the Vegan R-package (function `prestondistr`, 55). The question of how to derive confidence limits for SADs has not been satisfactorily resolved as yet (53). The predictions of the SAD model refer to an unspecified area, probably not much larger than the total area of sites surveyed. SAD estimates for all arthropods are not available since many focal taxa did not fit SAD models.

In estimating species richness, different statistical models may sometimes fit the data equally well, but yield widely different estimates. Also, statistical models offering a good fit to the data does not necessarily result in a satisfactory species richness estimate. We therefore built our results on the explicit consideration of both biological and statistical criteria. For each data set, a "best estimate" was chosen according to biological and statistical arguments, with the former given greater weight. Biological arguments represented an extension of statistical arguments for arthropod groups for which studies with larger sampling effort were available (Table S2). Statistical arguments relied on the goodness of fit of the data (AICc, adjusted  $R^2$ ) and, between models, on the lowest log error of extrapolation (LEE, 35). We fitted each model to a randomized data set of 10 sites instead of 12 (a pragmatic compromise between

predictive power and loss of information) and then compared the predicted with the actual species richness observed within our 12 sites. Estimates of the number of species present in one ha were calculated with the SAR model. 95% *c.l.* of model parameters were estimated with algorithms provided by the main software used in the analyses (33, 34, 36).

Study sites were surveyed with different sampling effort, mainly because of unequal seasonal replication between sites (27). Unequal sampling effort among sites had no consequence for models a1, a2 and a6, but for models a3 and a4 randomization of sites with EstimateS 8.20 reduced spurious effects due to unequal sample size. Since the raw number of species observed was strongly correlated with the number of species rarefied with the smallest sample size in aggregates, we used the raw number of species for implementing model a5, with negligible differences in results. Since accumulation curves of species richness in samples (models a1 to a4) are defined as the average number of species under all possible permutations of these samples, samples are independent as they may occur anywhere in a random permutation (56). For the sake of consistency and comparison with other data sets, models related to termites and ants were calculated with abundance data rather than with presence-absence data (the latter an approach often adopted when studying social insects (57)).

#### Extrapolating results to non-focal taxa

Ratios between pairs of arthropod taxa in terms of numbers of species globally described (*I*) were assumed to be similar at the scale of SLPA (Table S4; Fig. S2; 21, 58-61). To estimate species richness for arthropod orders not surveyed by our protocols, we compared ratios including the more diverse Collembola for hexapodan taxa, Araneae for arachnid taxa and Coleoptera for insect and myriapod taxa.

We used global estimates of described species as opposed to global estimates of undescribed species, which are not readily available/agreed upon for most arthropod taxa (*I*). We preferred using global ratios ( $R_g$ ) of numbers of named species as opposed to local ratios of numbers of morphospecies (i.e. species not formally named) because (a) comprehensive local rainforest surveys targeting both the soil and canopy faunas are scarce, especially in the Neotropics; (b) taxonomic effort usually varies among taxa; and (c) relevant data are rarely available for all arthropod orders. As a result, an objective choice of one or a few landmark studies to derive local ratios of numbers of morphospecies appears currently to be a near impossible task. Nevertheless, we checked that calculations based on the local ratios available did not distort our best estimates (Fig. 1B, model B+Sloc; results were similar to model a1).

We also conducted a sensitivity analysis aimed at resolving how potential biases in the global taxon ratios ( $R_g$ ) used might affect our estimates. We examined the effect of shifting  $R_g$  up to 10% lower or up to 10% higher than actual  $R_g$  values (Table S4), for each of four arthropod orders that include hyperdiverse groups which are both poorly known taxonomically and were not surveyed here (Table S5). In the majority of cases, the effects on total arthropod species richness estimates in SLPA were moderate (i.e., estimates were well in the range of values reported in Fig. 1B), except for in one

scenario where the  $R_g$  for Diptera was reduced from 11.3% down to 1.3% (Table S5). In this case the sensitivity test is indicating that if the global species richness of Nematocera is grossly underestimated (see 62), then our estimate of total species richness in SLPA may be more than twice as high as the one reported here (Table S5).

#### Beta diversity and sample coverage

To examine the relative contribution of species turnover at different spatial scales, we partitioned overall species richness (63) within different arthropod guilds as  $\gamma_{SLPA} = \alpha + \beta_3 + \beta_6 + \beta_{12} + \beta_{ha} + \beta_{SLPA}$ , where  $\gamma_{SLPA}$  is the total species richness estimated for SLPA,  $\alpha$  is the average species richness within samples at the smallest spatial scale and  $\beta_3$ ,  $\beta_6$ ,  $\beta_{12}$ ,  $\beta_{ha}$ , and  $\beta_{SLPA}$  represent the number of species absent from a randomly selected sample at the immediately lower spatial scale (400 m<sup>2</sup>, 3, 6, 12 cumulative study sites and one ha).

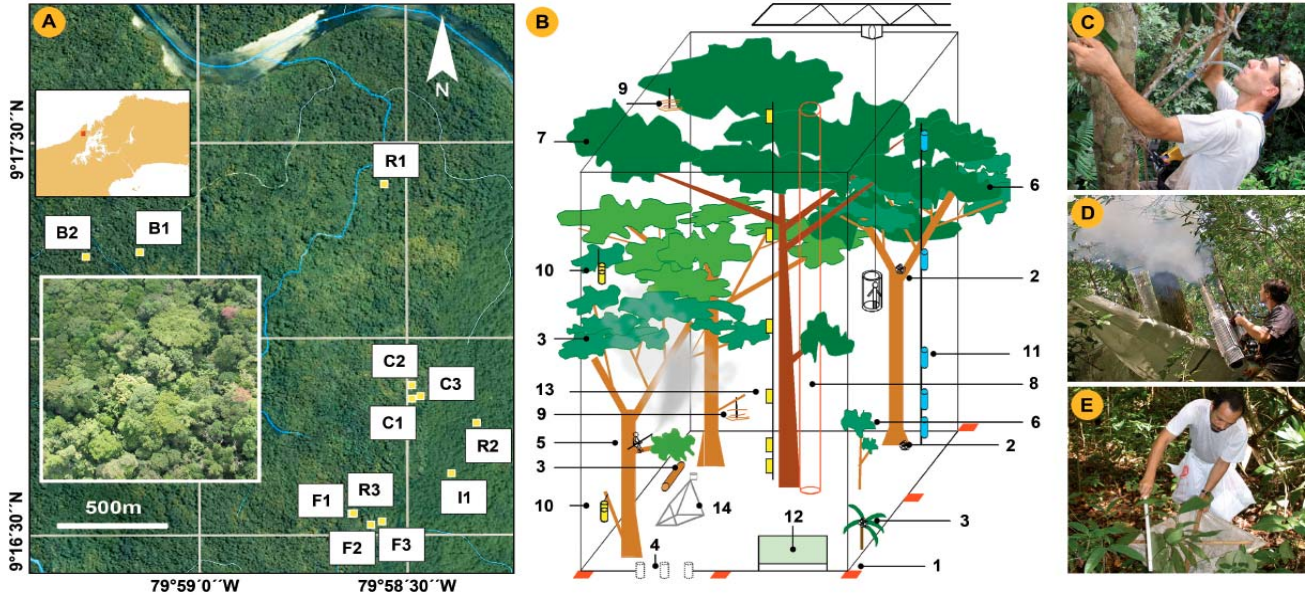
To make statistically reliable comparisons across arthropod guilds or taxa, we quantified the increase in sample completeness over the cumulative surveys of our 12 sites. We calculated an unbiased measure of sample completeness, i.e. sample coverage, which is the proportion of the total number of individuals in a community that belong to the species represented in the sample. The coverage deficit (= 1-sample coverage) represents the probability that the next individual collected belongs to a species not previously collected in the sample (64). If sample coverage is very high, then at least common species present in the community have likely been collected, whereas we will never be able to say with confidence whether the very rarest species have been observed or not (64). We estimated average sample coverage for all possible combinations of 1, 2, 3, ..., 12 sites, with a sample size of  $N = 12, 66, 220, 495, 792, 924, 792, 495, 220, 66, 11$  and 1 combination(s), respectively, for arthropod orders and guilds (Fig. 3). Sample coverage for the 18 data sets (12 sites) is indicated in Table S1.

#### **Supplementary Text**

Y.B. designed the study, analyzed data and wrote the paper. M.L. developed and managed the IBISCA database. T.R., M.L., L.C., P.C., R.K.D., V.N., F.Ø., J.S., A.K.T., N.N.W., D.W.R., L.L.F. and A.D. helped to write the paper. F.G. and O.M. helped with statistical analyses. B.C. and H.B. helped developing the study design. Y.B., L.C., P.C., R.K.D., F.Ø., J.S., A.K.T., N.N.W., H.-P.A., J.B., H.B., G.C., W.D.D., D.D., J.H.C.D., A.D., L.L.F., A.F., R.L.K., E.G.O., E.M., J.O., M.P., M.R., S.P.R., Y.R., D.W.R., J.B.S., L.S. and M.L. collected and/or contributed data. J.R.B. and S.E.M. contributed actively to the discussion of the ideas presented here. All authors discussed and commented on the results.

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**Fig. S1.**

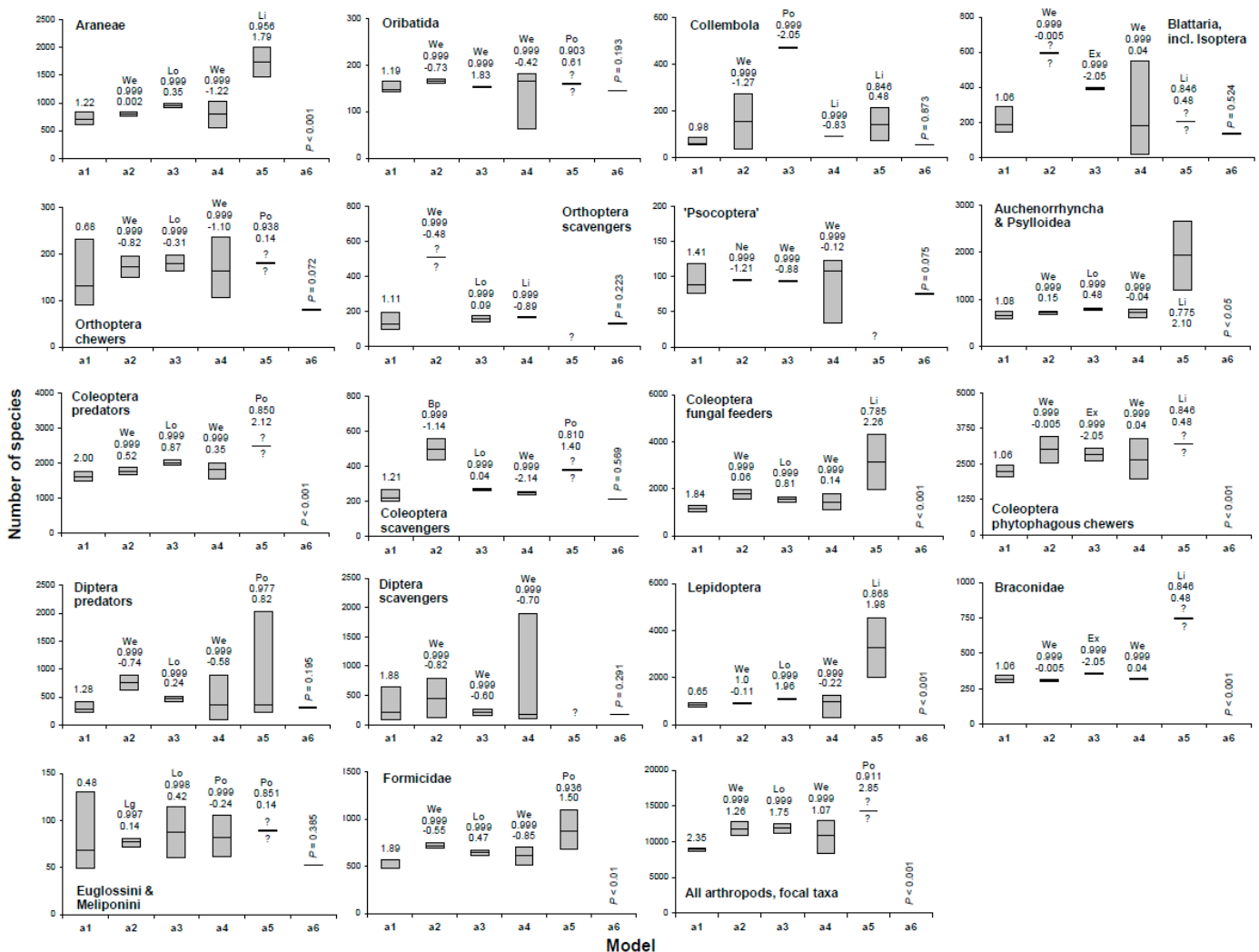
Study sites and field protocols. (A) Map of the lower Río Chagres, showing the 12 study sites. Upper inset: view of the Isthmus of Panama; lower inset: aerial view of the San Lorenzo forest. (B) Graphical summary of arthropod protocols used (27). (C) J. O. climbing into the canopy for hand collecting termites and ants. (D) J. S. performing canopy fogging. (E) H. B. beating shrubs in the understorey.

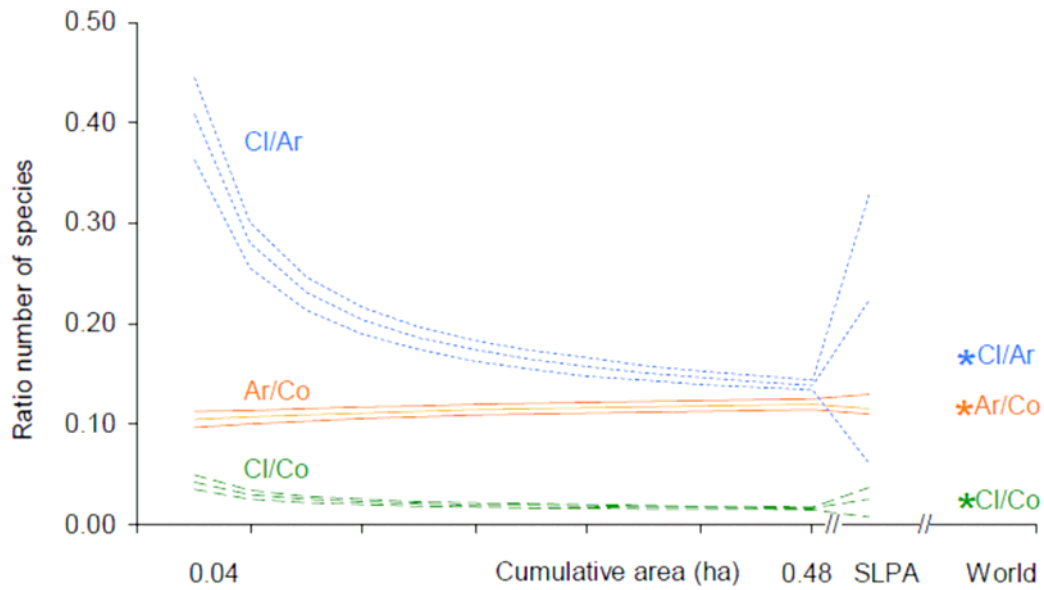


**Fig. S2**

Number of species estimated for SLPA for each data set and different models<sup>a</sup> (a1-a6, shaded boxes, means and 95% *c.l.*). Figures above each box represent (a) functions with lowest Akaike Information Criterion: Li= linear, Ne= negative exponential, We = Weibull (model a2) or cumulative Weibull (model a3)<sup>b</sup>, Bp = Beta-P, Ex = exponential; Lo = Lomolino; Po = power; Lg = logarithmic; (b) fit to models is assessed by adjusted  $R^2$  (when applicable, all models with at least  $P < 0.001$ ) and (c) log error of extrapolation (LEE) and Chi-square tests for SAD models. ? = Optimization algorithms did not converge to allow calculations of estimate and/or confidence limits.

<sup>a</sup>Estimates provided by models a2 to a4 are reasonably close to each other, those provided by a1 are lower, those provided by a5 are higher, and model a6 (SAD) could be fitted to only about half of our data sets. Sampling intensity for many of these data sets was probably too low to fit SAD. <sup>b</sup>SAR models were mainly fitted by sigmoid functions (cumulative Weibull, Lomolino), suggesting that estimates of species richness may be scale-dependent (45) and that the power law may not be necessarily the best model for SAR (33).





**Fig. S3**

Plot of pairwise ratios of species richness among three arthropod orders against cumulative area of study sites, SLPA and the world (mean and 95% *c.l.* when available): Collembola to Araneae (dotted blue line, CI/Ar), Araneae to Coleoptera (solid orange line, Ar/Co) and Collembola to Coleoptera (broken green line, CI/Co). Ratios of Collembola to Araneae appear less stable than other ratios, with rather large confidence limits. Ratios involving at least one species-rich taxon, such as Coleoptera (as in our template, Table S4) appear more stable with increasing area, but precision is low.

**Table S1.**

Taxonomic details of focal taxa studied at San Lorenzo (same data sets and ordering as in Fig 1A). SC = Sample coverage for 12 study sites. % G, % S = percentage of species identified to named genera and species, respectively. TK = Taxonomic knowledge (1=most species identified; 2=mixed identified species and morphospecies not identified; 3= mostly morphospecies not identified). Supervisors were entomologists responsible in the field for a particular sampling protocol and the study of one or several focal taxa. Entomology students facilitated initial sorting at the ordinal or familial level of the material. The supervisors then collaborated with taxonomic authorities for the formal study of the material, first pre-sorting adult arthropods into morphospecies, then identifying them as far as current knowledge allowed.

Data set	SC %	% G	% S	TK	Guild	Supervisors	Taxonomic authorities
1. Araneae	92.0	22.8	3.6	2	Pre	J. Schmidl	L. Sørensen, D. De Bakker, B.A. Huber, W. Fannes, G. Ruiz, A. Bolando, J.B. Schmidt
2. Oribatida	99.9	97.8	32.4	2	Mix	N. Winchester	V. Behan-Pelletier
3. Collembola	99.9	98.0	4.0	2	Sca	G. Castaño-Meneses	J. Palacios-Vargas
4. Blattaria, including Isoptera	99.6	44.4	23.1	2	Sca	Y. Roisin, M. Leponce, J. Schmidl	Y. Roisin, T. Bourguignon, I. Fritzsche
5. Acrididae, Tettigoniidae, Tetrigidae & Phasmatodea	80.3	0	0	3	Chw	J. Bail	O.Conle, F. Hennemann, C. Schwarz
6. Gryllidae	98.0	0	0	3	Sca	J. Bail	C.F. Sperber
7. Non parasitic Psocodea (ex 'Psocoptera')	85.4	40.9	1.5	2	Sca	P. Cuénoud	P. Cuénoud
8. Auchenorrhyncha & Psylloidea	98.1	71.0	29.0	2	Sap	Y. Basset	S. McKamey, M. Webb, J. Bonfils, D. Burckhardt, J. Sanborn, L. O'Brien, G. Goemans, V. Gnezdilov
9. Coleoptera predators *	97.2	75.6	11.6	2	Pre	F. Ødegaard, G. Curletti, A. Tishechkin, J. Schmidl, L. Cizek, N. Winchester	F. Cassola, C. Carlton, J. Klimaszewski, R. Gerstmeier
10. Coleoptera scavengers **	98.1	78.0	48.0	2	Sca	F. Ødegaard, J. Schmidl, L. Cizek	J. Ferrer, H. Fuchs
11. Coleoptera fungal feeders ***	98.2	28.0	10.6	2	Fun	A. Tishechkin, F. Ødegaard, J. Schmidl, L. Cizek	P. Prudek, A. Cline
12. Coleoptera phytophagous chewers ****	97.9	78.2	28.0	2	Chw	F. Ødegaard, G. Curletti, J. Schmidl, L. Cizek, H. Barrios, A. Floren	P. Cate, L. Borowiec, M. Daccordi, B. Anderson, L. Bartolozzi, L. Kirkendale
13. Dolichopodidae & Asilidae	97.6	98.0	7.0	2	Pre	R. Didham, L. Fagan	M. Pollet, M. Rapp
14. Scatopsidae & Stratiomyidae	85.7	98.3	39.7	2	Sca	M. Rapp	J.-P. Haenni
15. Pyraloidea, Geometridae & Arctiidae	91.3	50.6	39.8	2	Chw	R. Kitching	B. Poole
16. Braconidae *****	95.6	0	0	3	Par	E. Medianero	E. Medianero
17. Euglossini & Meliponini	99.0	100	97.7	1	Chw	D. Roubik/D. Frame	D. Roubik
18. Formicidae	99.3	100	61.9	2	Ant	J. Orivel, A. Dejean, B. Corbara, M. Leponce	J. Delabie, W. DaRocha
All focal arthropods	98.3	62.3	23.7	2	-	All above	All above

\$ Ant = ants; Chw = phytophagous chewers; Fun = fungal feeders; Mix = mixed; Par = parasitoids; Pre = predators; Sap = Sap suckers; Sca = Scavengers. \* Cantharidae, Carabidae (part, #), Cleridae, Coccinellidae (part, #), Elateridae (part, #), Histeridae, Lampyridae, Lycidae, Rhizophagidae, Salpingidae, Scydmaenidae, Staphylinidae (part, #). \*\* Dermestidae, Scarabaeidae (part, #), Scirtidae, Sphindidae, Staphylinidae (part, #), Tenebrionidae (part, #), Throscidae. \*\*\* Aderidae, Anthribidae, Biphyllidae, Bothrideridae, Ceratocanthidae, Cerylonidae, Ciidae, Colydiidae, Corylophidae, Cryptophagidae, Endomychidae, Erotylidae, Eucnemidae, Laemophloidae, Lathridiidae, Melandryidae, Mycetophagidae, Nitidulidae (part, #), Phalacridae, Silvanidae, Tenebrionidae (part, #), Trogossitidae. \*\*\*\* Alleculidae, Anobiidae, Anthicidae, Apionidae, Atteblidae, Brentidae, Buprestidae, Cerambycidae, Chelonariidae, Chrysomelidae, Curculionidae, Elateridae (part, #), Languriidae, Oedemeridae, Passalidae, Scarabaeidae (part, #), Scaptiidae. \*\*\*\*\* In analyses of the parasitoid guild, we also included a few additional parasitoid species belonging to Diptera and Coleoptera. # Subfamilial or generic guild assignment. Note: beetle families not listed here were not surveyed.

**Table S2.**

Biological and statistical arguments for the choice of the best estimate of the number of species occurring in SLPA, detailed for each data set (Sobs = number of species observed at SLPA). Biological arguments list relevant studies with the number of species (spp.) observed, statistical arguments (statistics) show the model (a1-a6) with the lowest LEE and its number of species estimated, and Decision indicates the model chosen as best estimate along with the number of species estimated. BCI = Barro Colorado Island (Panama), LAS = La Selva (Costa Rica).

Data set	Sobs	Biological arguments *				Statistics	Decision	
		Spp	Location	References	Rationale <sup>#</sup>			
Araneae	394	700 <sup>S</sup>	Guyana	7, 65	SLPA ca or > BCI	a4/807	a1/699	
Oribatida	139	379	BCI	66-71	SLPA < Guyana	a2/166	a2/166	
		264	LAS		Moss/litter habitats in ground and			
		134	Panama		canopy less developed in SLPA than			
Collembola	50	193	Ecuador	70, 71	in LAS. SLPA ca or < LAS	a3/471	a2/156	
		196	Peru		Comprehensive surveys of ground			
		< 50	Mexico, Australia		and canopy faunas far lower than			
Blattaria, incl. Isoptera	114	79	BCI	72	Blatt. represent 58 spp. at SLPA	a3/200	a4/92	
		Blatt.			(50.9%).			Blatt.
					SLPA ca or > BCI			
Orthoptera chew.	59	-	-	-	-	a4/163	a4/163	
Orthoptera scav.	81	-	-	-	-	a4/165	a4/165	
'Psocoptera'	66	178 <sup>S</sup>	BCI	73	SLPA ca or > BCI	a2/94	a4/108	
'Homoptera'	449	779	BCI	74	SLPA ca or > BCI	a4/1811	a3/786	
Coleoptera pred.	1070	300 <sup>S</sup>	Ecuador	28	Psel. represent 142 spp. at SLPA	a4/244	a4/244	
		Psel.			(13.5%). SLPA < Ecuador			Psel.
Coleoptera scavengers	173	43	Neotropical sites	75	Scar. represent 43 spp. at SLPA	a4/62	a1/55	
		Scar.			(24.9%)			Scar.
					SLPA ca Neotropical sites			
Coleoptera fungal feeders	719	-	-	-	-	a2/1765	a2/1765	
Coleoptera phyto. chewers	1254	2961 <sup>S</sup>	SLPA	12, 76	SLPA: estimates should be similar;	a4/2647-	a4/2647-	
		1239	BCI		Curc. represent 763 spp. at SLPA			1609
					(60.8%); SLPA ca or > BCI			
Diptera predators	153	97	Peru	77	Asil. represent 21 spp. at SLPA	a2/104	a4/48	
		Asil.			(13.7%). SLPA < Peru			Asil.
Diptera scavengers	40	197	Neotropics	78	Scat. represent 16 spp. at SLPA	a2/181	a4/70	
		70	Central America		(40.0%). SLPA < Central America or			Scat.
					Neotropics			
Lepidoptera	533	162	LAS	79-81	Arctiidae represent 118 spp. at SLPA	a4/215	a3/238	
		250	BCI		(22.1%)			Arct.
					SLPA > LAS or BCI			
Braconidae	272	-	-	-	-	a4/314	a4/314	
Euglossini & Meliponini	42	99	SLPA	82,83	Near complete inventory	a4/82	a3/87	
Formicidae	417	437	LAS	13, 84, 85	SLPA ca > LAS, BCI	a4/617	a1/481	
		384	BCI		D. Donoso,			SLPA << Ecuador
		692 <sup>S</sup>	Ecuador		pers.			SLPA < Brazil
		429	Brazil	comm.				
All focal arthropods	6144	-	-	-	-	a4/10871	a4/10871	

\*Abbreviations for taxa: Blatt. = Blattaria *sensu stricto*; Psel. = Pselaphinae; Scar. = Scarabaeinae; Curc. = Curculionidae; Asil. = Asilidae; Scat. = Scatopsidae; Arct. = Arctiidae.

<sup>§</sup>Estimated no. of species <sup>§</sup>Mid-point of estimate <sup>#</sup>Two recurrent biological arguments are worth emphasizing: (a) all things being equal, we expect Panamanian sites to be more species-rich than Costa Rican sites, because of the influx of South American species (86). (b) Since SLPA is wetter for a similar mean air temperature than the drier BCI (27), we expect, on the basis of broad-scale geographic patterns of species richness (87), higher species richness at SLPA than at BCI. This is confirmed by different taxa, including trees (88) and herbivorous beetles (12).

**Table S3.**

A comparison of estimates of species richness derived for tropical and temperate forests. Ratios refer to the number of arthropod species (estimated) for each vascular plant, breeding bird and mammal species.

Location & forest type	Area (ha)	Study*	Arthropod spp. (taxa)	Plant – bird - mammal spp.	Ratios	References & notes
<i>Tropical forests</i>						
San Lorenzo, Panama lowland evergreen forest	6,000	S, V	25,246 <sup>est</sup> (all arthropods)	1,294 <sup>s</sup> -306-81	20:83:312	This study, 26, 89 G. Angehr, pers. comm.
Volcán Barva-La Selva, Costa Rica, lowland to montane forests	7,689	S	13,783 <sup>obs</sup> (large fraction of arthropods)	-	-	90 Altitudinal transect from 50 m to 2,900 m
Madang Province, Papua New Guinea mosaic of secondary and primary lowland forest	1	S, P	1,490 <sup>obs</sup> 9,600 <sup>est</sup> (all herbivores)	200-?-?	48 : ? : ?	11
San Lorenzo, Panama lowland evergreen forest	1	S, S	6,100 <sup>est</sup> (all herbivores)	>211-?-?	>29 : ? : ?	This study
Sulawesi, Indonesia lowland evergreen forest	500	U, G	4,532 <sup>obs</sup> 6,200 <sup>est</sup> (all beetles)	-	-	29
San Lorenzo, Panama lowland evergreen forest	6,000	S, V	6,030 <sup>est</sup> (all beetles)	-	-	This study
San Lorenzo, Panama lowland evergreen forest	6,000	S, P	2,961 <sup>est</sup> (beetle herbivores)	-	-	12 F. Ødegaard & O. Diserud, unpubl. data
Yasuni National Park, Ecuador, lowland evergreen forest	1964	U, R	24,665 to 35,255 <sup>est</sup> (all insects)	-	-	60 Estimates derived from Histeridae & Pselaphinae, representing 3.9% of all beetle species
<i>Temperate forests</i>						
Païolive, France <i>Quercus pubescens</i> forest	5,300	U, G	1,670 <sup>obs</sup> 7,400 <sup>est</sup> (all arthropods)	1,400-150-41	5:49:180	91
Bosco della Fontana, Italy meso-xerophilous <i>Quercus</i> spp.	233	U, G	1,963 <sup>obs</sup> 3,000 <sup>est</sup> (all arthropods)	481-102-24	6:29:125	92-95 Canopy surveyed
Monks Wood, U. K. ancient ash-oak woodland	157	U	3,317 <sup>obs</sup> (all arthropods)	1,084-158-37	3:21:90	96,97 Surveyed nearly completely
Paláva Biosphere Reserve, Czech Republic mixed forest	8,300	U	11,727 <sup>obs</sup> (all arthropods)	1450 <sup>#</sup> -306-65	8:38:180	98-99 Include mixed forests and meadows
Santa Barbara, Azores Azorean native forest	1,347	S, S	183 <sup>obs</sup> 509 <sup>est</sup> (large fraction of arthropods)	78-12-5	7:42:102	100 P.A.V. Borges, pers. comm

\* Type of study: U = unstructured, S = structured inventory. Model for arthropod estimations: V = various models, P = plant-based, S = species-area relationship, R = ratios of local to global species richness, G = informed guess.  
obs = observed, est = estimated. <sup>s</sup> Estimated from (101, 102); <sup>#</sup> J. Danihelka, pers. comm.

**Table S4.**

Template used for estimating the species richness of non-focal taxa. Greyed cells indicate the entry data (species observed, Sobs). The number of additional estimated species (Sest) are calculated with either global ratios ( $R_g$ ) or local ratios ( $R_l$ ).  $R_g$  is the ratio of number of named species world-wide.  $R_l$  is an average of local tropical and subtropical studies ( $N$  = number of studies; may be lower than the number of associated references, Ref.). Assuming a constant ratio between taxa (Ratio A : B), the number of additional estimated species calculated for orders partly surveyed (ii) are  $Sest_{g,l} = ((Sobs \times 100) / R_{g,l}) - Sobs$ , using global and local ratios. For orders not surveyed (iii) these two estimates are  $Sest_{g,l} A = ((Sobs B + Sest_{g,l} B) \times R_{g,l}) / 100$ . In this example entry data are the number of species observed in 0.48 ha of SLPA. The same template was used to calculate best estimates, models a1 to a6 and their *c.l.*, as well as the number of species occurring in one ha. There is a strong correlation between global and local ratios and there is no significant difference between them, even if only ratios > 10% are considered (in the later case  $r = 0.979$ ,  $P < 0.001$ , paired t-test,  $t = -1.307$ ,  $P = 0.233$ , *d.f.* = 8).

Taxa	Sobs	Sest <sub>g</sub>	Sest <sub>l</sub>	Ratio * A : B	R <sub>g</sub> (%)	R <sub>l</sub> (%)	Ref. R <sub>g</sub>	N	Ref. R <sub>l</sub>
<b>(i) Orders wholly surveyed</b>									
Araneae	394								
Blattaria, including Isoptera	114								
Collembola	50								
'Psocoptera'	66								
<b>(ii) Orders partly surveyed</b>									
Coleoptera									
Surveyed Coleoptera	3279								
Non-surveyed Coleoptera		425	443	Surv. Col : Col	88.5	88.1	103	9	29,104-111
Diptera									
Diptera surveyed	198								
Diptera not surveyed		1556	1231	Surv. Dip : Dip	11.3	13.9	112	6	90,106,113-116
Hemiptera									
Surveyed Hemiptera	449								
Non-surveyed Hemiptera		535	368	Surv. Hem : Hem	45.6	55.0	117-119	6	58,106,114,116,120,121
Hymenoptera									
Surveyed Hymenoptera	731								
Non-surveyed Hymenoptera		2616	1546	Surv. Hym : Hym	21.8	32.1	117,122-125	6	90,113-116,126
Lepidoptera									
Surveyed Lepidoptera	533								
Non-surveyed Lepidoptera		1325	1079	Surv. Lep : Lep	28.7	33.1	117,127-129	10	80,81,90,114-116,130-137
"Orthopteroids"									
Surveyed orthopteroids	140								
Non-surveyed orthopteroids		33	22	Surv. Ort : Ort	81.0	86.5	138,139	7	90,106,114-116,120,140
Acarina									
Oribatida	139								
Non-Oribatida		320	299	Ori : Aca	30.3	31.8	1	9	66,90,113,114,116,141-145
<b>(iii) Orders not surveyed</b>									
Trichoptera		133	63	Tri : Col	3.7	1.8	1	6	106,113,114,116,120,146
Diplopoda		72	53	Dio : Col	2.0	1.5	1	6	106,113,114,116,120,146
Odonata		54	52	Odo : Col	1.5	1.4	1	6	106,113,114,116,120,146
Thysanoptera		54	288	Thy : Col	1.5	8.0	1	6	106,113,114,116,120,146
Neuroptera	4	50	124	Neu : Col	1.5	3.6	1	6	106,113,114,116,120,146
Phthiraptera		47	1	Pht : Col	1.3	0.02	1	6	106,113,114,116,120,146

Oniscidea		36	50	Oni : Col	1.0	1.4	1, 147	6	106,113,114,116,120,146
Opiliones	34	26	0	Opi : Ara	15.3	5.5	1	7	106,114-116,120,148,149
Plecoptera		35	3	Ple : Col	1.0	0.07	1	6	106,113,114,116,120,146
Pseudoscorpionida		32	32	Pse : Ara	8.1	8.0	1	7	106,114-116,120,148,149
Ephemeroptera		30	8	Eph : Col	0.8	0.2	1	6	106,113,114,116,120,146
Chilopoda		29	42	Chi : Col	0.8	1.2	1	6	106,113,114,116,120,146
Siphonaptera		19	0	Sip : Col	0.5	0.00	1	6	106,113,114,116,120,146
Dermaptera		18	13	Der : Col	0.5	0.4	1	6	106,113,114,116,120,146
Mantodea	5	17	28	Man : Col	0.6	0.9	1	6	106,113,114,116,120,146
Scorpionida	2	16	6	Sco : Ara	4.6	2.1	1	7	106,114-116,120,148,149
Paupoda		8	3	Pau : Col	0.2	0.07	1	6	106,113,114,116,120,146
Mecoptera		7	0	Mec : Col	0.2	0.00	1	6	106,113,114,116,120,146
Strepsiptera		6	4	Str : Col	0.2	0.1	1	6	106,113,114,116,120,146
Diplura		5	3	Diu : Cll	9.8	6.5	1	4	106,114,115,148
Protura		5	0	Pro : Cll	9.9	0.00	1	4	106,114,115,148
Archaeognatha		5	25	Arc : Col	0.1	0.7	1	6	106,113,114,116,120,146
Zygentoma		5	0	Zyg : Col	0.1	0.00	1	6	106,113,114,116,120,146
Megaloptera		3	0	Meg : Col	0.1	0.00	1	6	106,113,114,116,120,146
Symphyla		2	0	Sym : Col	0.05	0.00	1	6	106,113,114,116,120,146
Amblypygi		1	4	Amb : Ara	0.4	1.1	1	7	106,114-116,120,148,149
Palpigradi		1	0	Pal : Ara	0.2	0.00	1	7	106,114-116,120,148,149
<b>(iv) Orders with too few species</b>									
Ricinulei	2								
Embioptera	1								
Zoraptera	1								
Schizomida	1								
Onychophora	1								
Notoptera	0								
Solifugae	0								
Uropygi	0								
<b>Total</b>	<b>6144</b>	<b>7549</b>	<b>5817</b>						
<b>Grand total</b>		<b>13693</b>	<b>11961</b>						

\* Aca = Acarina; Amb = Amblypygi; Ara = Araneae; Arc = Archaeognatha; Chi = Chilopoda; Cll = Collembola; Col = Coleoptera; Der = Dermaptera; Dio = Diplopoda; Dip = Diptera; Diu = Diplura; Eph = Ephemeroptera; Hem = Hemiptera; Hym = Hymenoptera; Lep = Lepidoptera; Man = Mantodea; Mec = Mecoptera; Meg = Megaloptera; Neu = Neuroptera; Odo = Odonata; Oni = Oniscidea; Opi = Opiliones; Ori = Oribatida; Ort = Orthopteroids; Pal = Palpigradi; Pau = Paupoda; Pht = Phthiraptera; Ple = Plecoptera; Pro = Protura; Pse = Pseudoscorpionida; Sco = Scorpionida; Sip = Siphonaptera; Str = Strepsiptera; Surv. = Surveyed; Sym = Symphyla; Thy = Thysanoptera; Tri = Trichoptera; Zyg = Zygentoma.



**Table S5.**

Sensitivity analysis of the impact of global taxon ratios ( $R_g$ , see Table S4) on estimates of total arthropod species richness for SLPA. For arthropod orders including hyperdiverse groups omitted from our focal taxa, we shifted the  $R_g$  values used in the main analyses by up to 10% lower or up to 10% higher. For reference, calculations with the original  $R_g$  values yield 25,246 species (95% *c.l.* = 19721, 33181) as our best estimate for SLPA (see main text).

<b>Order</b>	<b><math>R_g</math> (%)</b>	<b>Spp. <math>R_g</math> 10% lower</b> (95% <i>c.l.</i> )	<b>Spp. <math>R_g</math> 10% higher</b> (95% <i>c.l.</i> )	<b>Hyperdiverse group</b> (% of total spp. in order)	<b>Ref.</b>
Acari	30.3	25517 (19988, 33450)	25110 (19595, 33030)	Non-oribatids (30.3)	<i>1</i>
Diptera	11.3	61912 (33323, 106846)	23025 (18904, 28707)	Nematocera (34.8)	<i>112</i>
Hymenoptera	21.8	28658 (22992, 37050)	23979 (18514, 31729)	Chalcidoidea (18.0)	<i>125</i>
Lepidoptera	28.7	27257 (21671, 35246)	24276 (18789, 32168)	Microlepidoptera <sup>s</sup> (27.8)	<i>151</i>

<sup>s</sup> Sensu (*150*)

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