Supplementary Methods
Details of the GMPD

The Global Mammal Parasite Database 2.0 (GMPD) [1] contains host-parasite

association records reported from literature for free-ranging populations from the mammalian

orders Artiodactyla, Perissodactyla, Carnivora, and Primates. The database includes both positive

and negative records (i.e., cases where a parasite was sampled for but not found in a given host).

In this study, we limited our data analysis to ungulate species and excluded primarily domestic

species (e.g., camels). We also included only populations sampled in their native ranges

(following [2] and [3]). The GMPD uses the taxonomy of Wilson & Reeder [4], but to harmonize

these data with the PanTHERIA database used in some analyses [5], we collapsed two pairs of

species together where taxonomies disagreed (*Alces americanus* was included within *Alces alces*

and *Alcelaphus liechtensteinii* was included within *Alcelaphus buselaphus*).

Calculations of parasite species richness

We used the parasite taxonomy provided in the GMPD to identify unique parasite

operational taxonomic units (OTUs); we refer to these unique parasite OTUs as "species"

throughout the manuscript, even though some parasite types (e.g. viruses) are not identified as

species. We defined parasite species richness as the number of parasite species detected in all

native, free-ranging populations of a host species [2,6,7]. For parasites that were identified only

to the genus level, we included these in the richness measure only if no other species from that

genus was also present in a given host species (e.g. *Strongyloides sp.* was counted as a unique

parasite only if no other species of *Strongyloides* had been detected in that host). We excluded

any records that were identified to the family level or above.

We used the Chao2 estimator to account for uneven sampling effort. The Chao2 estimator

is based on the ratio of singletons to doubletons in the dataset; we selected it for this study

because it has been shown to accurately predict species richness when data is in the form of presence-absence records and sample sizes for some sites or species are low [8–10]; it also performs better than other diversity estimators on the GMPD data [7].

Prevalence data were recorded for 89% of entries included in this analysis. These prevalence data are based either on direct detection of pathogens (by visible stages or using genetic markers) or detection of host antibodies (e.g., seroprevalence), and thus can represent either active infection or previous exposure to a given parasite.

Movement data compilation

To gather data on the movement strategy of each ungulate host species, we first searched for species reports in the journal Mammalian Species, which provides descriptions of species' ecology. If no Mammalian Species report was available for a given ungulate host or the movement strategy was not clear from the report, we searched Google Scholar for the species' binomial name along with "movement OR seasonal OR migration OR 'home range' OR nomadic OR nomadism OR sedentary OR resident", using synonyms from all known taxonomies (e.g. [4,11]). If there was no movement description in either Mammalian Species or in these articles, we searched the online databases Animal Diversity Web and Ultimate Ungulate for description of movement patterns.

To categorize populations' movement patterns, we used the following definitions, based on those by Mueller *et al.* [12,13]: a population was considered *migratory* if it showed seasonal and typically long-distance differences in location but little inter-annual variability in seasonal range use. *Nomadic* populations were those whose location was described as differing across the year but in an irregular and/or resource-driven manner. Most often, these descriptions included phrases such as "may travel long distances in search of food," "migrates to [location] in some years and elsewhere in others," and "has unpredictable movements." Last, *resident* populations

were characterized by limited seasonal differences in location or home range. Most often, these assessments came from descriptions of high home range overlap between seasons or year-round territorial maintenance. In addition, any species where no migration are nomadism was described in any available source were considered resident. Under our hierarchical classifications of movement behavior, we did not consider partial migration or partial nomadism explicitly because of the difficulty in accurately defining these behaviors [14], and because our questions revolve around overall effects of migration on the species level, meaning that we consider any degree of migratory behavior as having a potential effect on infection.

Life-history and geographic range data

In PanTHERIA, adult body mass is the average mass of non-pregnant adult specimens of either sex from captive, wild, or provisioned populations. Population group size is the average number of individuals in a non-captive population that spends the majority of their time in a day together and is roughly equivalent to herd size for ungulates [5]. PanTHERIA also provides other measures of group size, but we considered population group size the most relevant to parasite transmission.

We gathered geographic data from species distribution maps downloaded from the IUCN Red List [11], from which we calculated the range area (in km^2) and the mid-range latitude of each ungulate species. We also quantified the diversity of habitats used by each species using WWF's definitions of ecoregions, which are geographic areas defined by characteristic biotic assemblages and abiotic conditions [15]. For each species, we counted the number of unique ecoregions that overlapped with the species' geographic range (from IUCN range maps) as a measure of habitat diversity.

Data analysis

During our model selection process, we excluded any models that included both geographic range area and number of ecoregions to increase the accuracy of our parameter estimates (following [16]). Model averaging performs well when predictor variables are moderately collinear, but still results in biased parameter estimates when predictor variables are highly collinear, as is the case here (r=0.90 after log transformation) [17].

In our models that explicitly accounted for sampling effort, we used the number of hits for a species' Latin binomial on Web of Science as our measure of sampling effort, following other studies using similar datasets [2,18,6,7]. WOS citation count reflects the overall effort spent on studying the biology of a species. In this model set, we used log-transformed observed parasite species richness as the response variable; included log-transformed sampling effort as an additional explanatory variable; and a weighting scheme based on the number of individuals sampled per species in the GMPD (weight = 1/(log(number of individuals) + 1).

In our models that examined different parasite groups separately, we first estimated parasite richness of each parasite group in each host species using the Chao2 estimator. Because of the smaller sample sizes for these subsetted data, we included only variables with importance >0.5 in the full model set as candidate explanatory variables, which were movement strategy, number of ecoregions, and body mass.
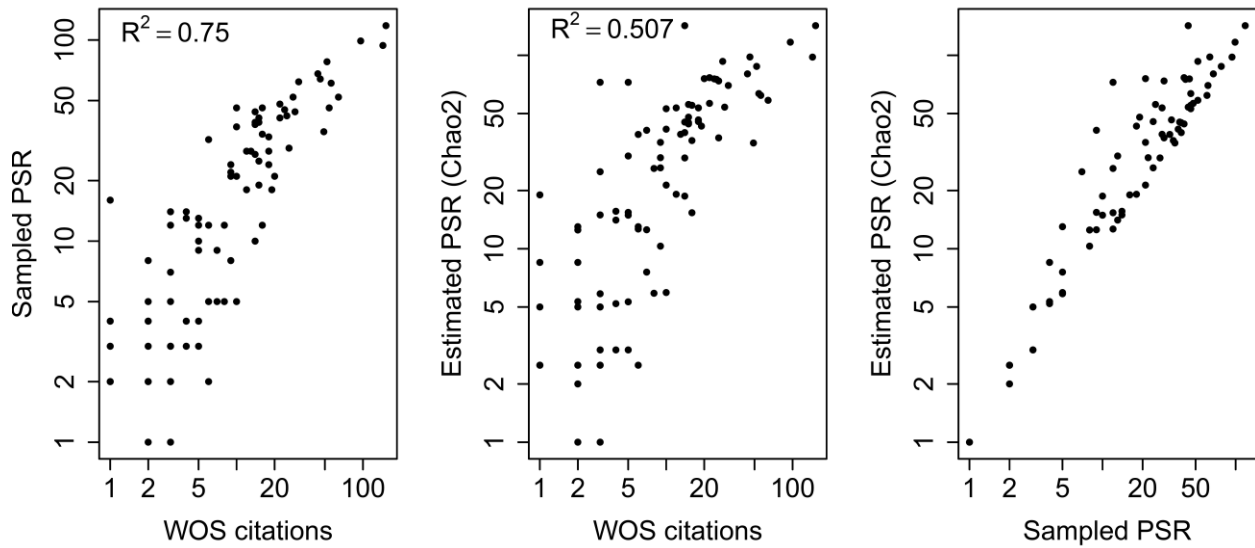
In our analysis of prevalence data, for each positive host-parasite interaction where at least five host individuals were sampled, we estimated the average prevalence of each parasite in each host species, (following [19] and [20]). Then, for each parasite species, we calculated the average prevalence in migratory and resident hosts separately, and found the difference between these values. A positive value indicates that the average migratory species has higher prevalence than the average resident species for a given parasite.
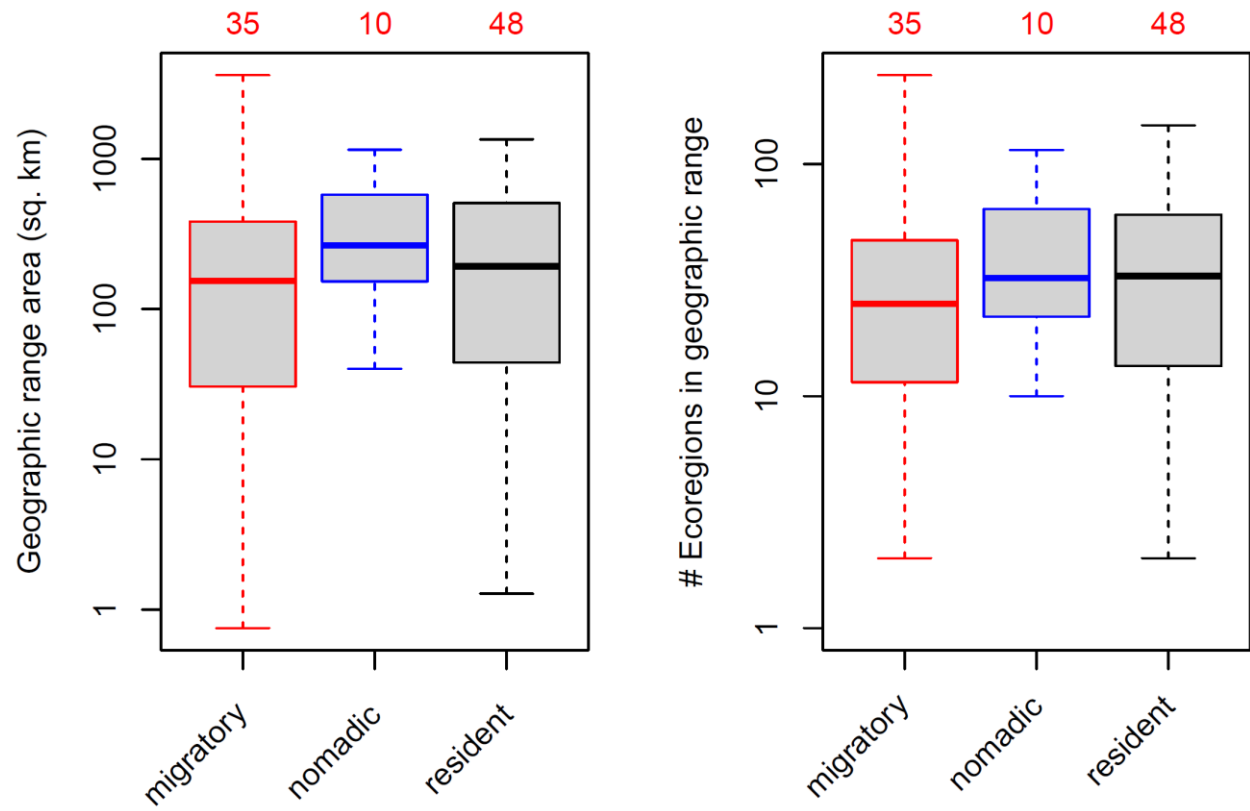
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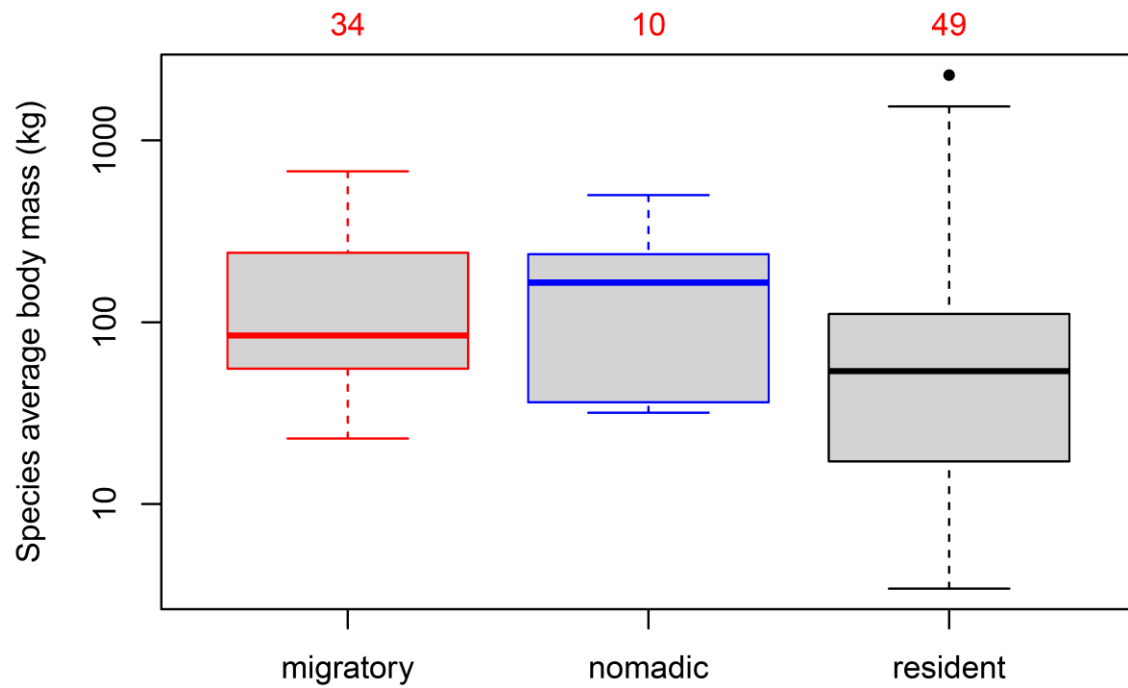
Supplementary figures and tables

Figure S1: Effects of sampling effort on sampled and estimated parasite species richness (PSR) in the Global Mammal Parasite Database (GMPD). Sampled PSR is closely related to sampling effort, measured as the number of studies of a given host species in the GMPD (R^2=0.750, A). The bias-corrected Chao2 estimator reduces the strength of this relationship (R^2=0.507, B). Estimated PSR is always equal to or greater than sampled PSR (C).

Figure S2: Geographic range size and habitat diversity of ungulate species with different movement strategies. No differences between groups were statistically significant (Tukey test, α=0.05).

Figure S3: Average body mass of species with different movement modes. Resident species had, on average, marginally lower body mass than migratory species (Tukey test, p=0.050); nomadic species were not statistically distinguishable from either other group.

Table S1: Model results from the averaged model of the four best models predicting parasite species richness using an alternative classification of movement, where we excluded species categorized as both migratory and nomadic (N=12 species excluded). Results are quantitatively and qualitatively similar to the hierarchical classification method (Table 1). As in the main model, geographic range area was included as a possible predictor but was not present in any of the top models.

	Estimate	**Lower**	**Upper**
Intercept	1.780	0.388	3.173
nomadic	-1.326	-2.211	-0.44
resident	-0.788	-1.377	-0.199
Habitat diversity	0.362	0.094	0.629
Body mass	0.083	-0.125	0.291
Mid-range latitude	0.004	-0.01	0.018

Table S2: Model results from the averaged model of the four best models predicting parasite species richness using an alternative classification of movement, where we included "migratory/nomadic" as a fourth movement category. Results are quantitatively and qualitatively similar to the hierarchical classification method (Table 1). As in the main model, geographic range area was included as a possible predictor but was not present in any of the top models.

	Estimate	Lower	Upper
Intercept	1.878	0.449	3.307
migratory and nomadic	-0.152	-1.016	0.712
nomadic	-1.387	-2.328	-0.446
resident	-0.847	-1.516	-0.178
Habitat diversity	0.324	-0.008	0.657
Body mass	0.088	-0.124	0.3
Mid-range latitude	0.004	-0.01	0.017
Geographic range area	0.015	-0.083	0.113

Table S3: AICc values for all candidate models predicting total parasite species richness. ΔAICc is the difference in AICc between a given model and the top model; models where ΔAICc<2 (in bold) are considered competitive.

Model	AICc	ΔAICc	weight
movementMode + log(nEcoregions) + log(bodyMass)	**305.953**	**0**	**0.221**
movementMode + log(nEcoregions) + log(bodyMass) + abs(midLat)	**306.215**	**0.262**	**0.194**
movementMode + log(nEcoregions)	**306.555**	**0.602**	**0.163**
movementMode + log(nEcoregions) + abs(midLat)	**306.877**	**0.924**	**0.139**
movementMode + log(geoAreaIUCN) + log(bodyMass)	308.044	2.091	0.078
movementMode + log(geoAreaIUCN) + log(bodyMass) + abs(midLat)	308.945	2.992	0.049
movementMode + log(geoAreaIUCN)	309.427	3.474	0.039
movementMode + log(bodyMass)	310.168	4.215	0.027
movementMode + log(geoAreaIUCN) + abs(midLat)	310.43	4.477	0.024
log(nEcoregions) + log(bodyMass) + abs(midLat)	311.167	5.214	0.016
movementMode	311.607	5.654	0.013
movementMode + log(bodyMass) + abs(midLat)	311.885	5.932	0.011
movementMode + abs(midLat)	312.649	6.696	0.008
log(nEcoregions) + abs(midLat)	313.413	7.46	0.005
log(nEcoregions) + log(bodyMass)	314.374	8.421	0.003
log(geoAreaIUCN) + log(bodyMass) + abs(midLat)	314.913	8.96	0.003
log(bodyMass) + abs(midLat)	315.285	9.332	0.002
log(bodyMass)	316.658	10.705	0.001
log(geoAreaIUCN) + log(bodyMass)	316.707	10.754	0.001
log(nEcoregions)	316.745	10.792	0.001
log(geoAreaIUCN) + abs(midLat)	316.92	10.967	0.001
log(geoAreaIUCN)	318.161	12.208	0
abs(midLat)	319.39	13.437	0

Table S4: Model results from the best average model of parasite species richness explicitly considering sampling effort. The model predicted raw parasite species richness (log); candidate independent variables were WOS citations (log), movement strategy, habitat diversity (log), body mass (log), absolute mid-range latitude, and geographic range area (log).

	Estimate	Lower	Upper
Intercept	0.878	-0.147	1.904
nomadic	-1.74	-2.408	-1.071
resident	-0.724	-1.271	-0.176
Habitat diversity	0.131	-0.156	0.419
Sampling effort	0.33	0.141	0.519
Mid-range latitude	-0.002	-0.012	0.008
Body mass	0.012	-0.074	0.098

Table S5: Model results from models predicting estimated species richness of parasites transmitted by close contact and environmentally separately, using the same predictors as the top-ranked model for total parasite species richness. Transmission modes were based on assignments in the GMPD; environmental transmission is assigned as "nonclose" in the GMPD.

	Environmental			Contact		
	Estimate	**Lower**	**Upper**	**Estimate**	**Lower**	**Upper**
(Intercept)	1.906	0.781	3.031	0.013	-1.274	1.3
nomadic	-1.832	-2.697	-0.968	-0.848	-1.672	-0.025
resident	-0.402	-0.93	0.127	-0.573	-1.069	-0.078
Habitat diversity	0.183	-0.144	0.509	0.293	0.044	0.542
Body mass	-	-	-	0.132	-0.094	0.358