Supplementary Material

Appendix 1. Flea traits: explanations and details of calculations

Abundance: To estimate characteristic abundance, we calculated the mean number of individuals of a flea species collected per host individual within each region (we did this for the principal host species for a flea species, that is the host in which a given flea attained the highest abundance), and then we averaged the highest regional abundances of each flea species across all regions (Krasnov et al., 2015). The values of mean abundance were log+1-transformed prior to the main analyses.

Numerical host specificity: The number of host species on which a flea was recorded in a region (i.e., the size of flea’s host spectrum) was weakly, but significantly correlated with the number of host individuals examined (*r*2 = 0.03, *F* = 28.3, *P* < 0.001). Consequently, we substituted the original values of this number with the residuals of the regression of their values against the number of hosts examined within a region in a log-log space and then averaged these across regions.

Phylogenetic host specificity: Phylogenetic relatedness among host species exploited by a parasite necessitates an estimation of the phylogenetic aspect of its host specificity (Poulin *et al.*, 2011). We estimated phylogenetic host specificity of a flea (PHS) within a region using the average phylogenetic distinctness between all pairs of host species used by this flea (Poulin and Mouillot, 2003) measured as the Δ+ index of Clarke and Warwick (1999) and Warwick and Clarke (2001) modified to take into account phylogenetic rather than taxonomic distances and calculated using the package “vegan” (Oksanen *et al.*, 2018) implemented in R Statistical Environment (R Core Team, 2018). This metric was independent of the number of species in a host spectrum. The phylogenetic distances between hosts were based on patristic distances calculated using the R package “adephylo” (Jombart and Dray, 2010). We used the phylogenetic supertree for mammals by Bininda-Emonds *et al.* (2007) as a backbone for host phylogeny, modified as described by Krasnov *et al.* (2011). For each flea species, values of PHS were averaged across all regions in which this flea was recorded.

Microhabitat preference: Microhabitat preference is determined by the proportion of time fleas spend on either a body of a host or its burrow/nest. This proportion is a species-specific trait and so-called “body” fleas and “nest” fleas are distinguished (see details in Krasnov, 2008). We considered a flea species to being a “body” or “nest” or “both body and nest” based on literature sources (see references in Krasnov, 2008).

Seasonality: We characterized seasonal preferences of a flea species based on a season of their main reproduction period and distinguished between fleas reproducing during the warm season, the cold season or year round. The seasonal characteristics of flea reproduction were drawn from the literature (see Krasnov, 2008 and references therein).

Armament: Fleas possess sclerotinized tools (helmets, ctenidia, spines, setae, bristles) with which they anchor themselves in the host’s hairs and thus resist the host’s grooming (Traub, 1980). The most noticeable structures of flea armament are ctenidia (=combs), that are rows of highly scletorinized thick spines below the head (genal comb) or at the back of the pronotum (pronotal comb). We characterised each flea species as lacking combs, having only a pronotal comb or both combs (no species has a genal comb only). These data were taken from our earlier study (Krasnov *et al.*, 2016). Body size was measured on flea specimens (stored on permanent slides) from the entomological collections of the Zoological Museum at Moscow State University (Moscow, Russia), Zoological Institute of the Russian Academy of Sciences (Saint Petersburg, Russia) and Stavropolsky Antiplague Scientific Research Institute (Stavropol, Russia). Measurement procedures are described in details elsewhere (Surkova *et al.*, 2018*a,b*). Due to female-biased sexual size dimorphism in fleas, we used the median of the average male and average female body size as a single value characterizing body size of a species and log-transformed these values prior to analyses. The degree of sexual size dimorphism was estimated as *ln*(*f*/*m*), where *f* is female size and *m* is male size (Smith, 1999; see justification in Surkova *et al.,* 2018*b*). Sexual size dimorphism in fleas is allometric and decreases with an increase in male size (Surkova *et al.*, 2018*b*). Consequently, we regressed values of sexual size dimorphism against values of the ln-transformed male size and substituted the original values with their residual deviations. Data on body size and sexual size dimorphism were available for 194 of 202 species.

Size and latitude of the center of geographic range: these data were taken from our recent studies (see Krasnov *et al.*, 2018*a*,*b* for details of calculations). Values of geographic range size were log-transformed prior to analyses. These data were available for 119 of 202 flea species.

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**Table S1.** Summary of principal coordinate analysis of quantitative morphobionomic traits. MBV1 and MBV2 – the first and the second vectors, respectively. SSD – sexual size dimorphism (controlled for male body size); *r* - Spearman correlation between a vector and the original trait variables

|  |  |  |
| --- | --- | --- |
| Principal component | MBV1 | MBV2 |
| Eigenvalue | 9.15 | 6.68 |
| Explained variance | 0.51 | 0.37 |
| Cumulative proportion of total variance | 0.51 | 0.88 |
| *r* | Body size | -0.21 | 0.10 |
| SSD | 0.14 | -0.23 |

**Table S2.** Summary of Kruskal-Wallis ANOVAs for the relationships between morphobionomic trait vectors (MBTV1 and MBTV2) produced by principal coordinate analysis of morphobionomic trait variables and original ordinal (armament) and nominal (microhabitat preference and seasonality) variables.

|  |  |  |  |
| --- | --- | --- | --- |
| Trait variable | Trait vector | Kruskal-Wallis *H* | *P* |
| Microhabitat preference | MBTV1 | 145.33 | < 0.001 |
|  | MBTV2 | 55.09 | < 0.001 |
| Seasonality | MBTV1 | 75.96 | < 0.001 |
|  | MBTV2 | 148.94 | < 0.001 |
| Armament | MBTV1 | 105.22 | < 0.001 |
|  | MBTV2 | 22.63 | < 0.001 |

**Fig. S1.** Relationships between morphobionomic trait vectors (1 and 2) and ordinal and nominal morphobionomic trait variables (see text for explanations). Columns – mean, whiskers - ±S.E., points – median.



Appendix 2. Environmental (off-host) predictors

**Table S2.** Summary of principal component analysis of environmental variables. PC1, PC2, and PC3 – the first, the second and the third principal component, respectively. NDVIa, NDVIsp, NDVIsu, and NDVIw - Normalized Difference Vegetation Indices for autumn, spring, summer and winter, respectively; Pa, Psp, Psu, and Pw – mean precipitation in autumn, spring, summer and winter, respectively; Ta and Tm – annual and mean monthly air temperature ranges. Tmax, Tmin and Tmean – maximal, minimal and mean annual air temperature; Alt – mean altitude. *r* - Pearson correlation between a principal component and an environmental variable

|  |  |  |  |
| --- | --- | --- | --- |
| Principal component | PC1 | PC2 | PC3 |
| Eigenvalue | 5.36 | 3.39 | 2.31 |
| Explained variance | 5.36 | 3.39 | 2.31 |
| Cumulative proportion of total variance | 0.38 | 0.24 | 0.17 |
| *r* | NDVIa | -0.88 | 0.27 | -0.29 |
| NDVIsp | -0.81 | -0.25 | -0.31 |
| NDVIsu | -0.64 | 0.63 | -0.32 |
| NDVIw | -0.70 | -0.24 | -0.21 |
| Pa | -0.76 | 0.47 | 0.20 |
| Psp | -0.45 | -0.03 | 0.72 |
| Psu | -0.54 | 0.69 | -0.29 |
| Pw | -0.58 | 0.04 | 0.67 |
| Ta | 0.71 | 0.31 | -0.47 |
| Tm | 0.56 | -0.29 | -0.13 |
| Tmax | -0.08 | -0.82 | -0.44 |
| Tmean | -0.50 | -0.84 | -0.12 |
| Tmin | -0.64 | -0.72 | 0.15 |
|  | Alt | 0.38 | 0.01 | 0.66 |

Appendix 3. Environmental (host-associated) predictors

**Table S3.** Main phylogenetic/ecological clades of small mammalian hosts (in alphabetical order).

|  |  |  |
| --- | --- | --- |
| Clade | Abbreviation | Genera |
| Bank voles | BV | *Myodes, Craseomys* |
| Birch mice | BM | *Sicista* |
| Chipmunk | CH | *Tamias* |
| Crocidurine shrews | CS | *Crocidura*, *Diplomesodon* |
| Dormice | DM | *Muscardinus*, *Myoxus*, *Dryomys* |
| Gerbils | GB | *Meriones, Rhombomys* |
| Hamsters | HM | *Allocricetulus*, *Cricetus*, *Mesocricetus*, *Tscherskia, Phodopus, Cricetulus* |
| Jerboas | JB | *Allactaga*, *Pygeretmus, Dipus*, *Eremodipus*, *Stylodipus* |
| Lemmings | LM | *Myopus*, *Lemmus* |
| Marmotines | MM | *Spermophilus, Spermophilopsis, Marmota* |
| Meadow voles, mole-voles and water vole | MV | *Microtus*, *Blanfordimys*, *Lasiopodomys*, *Chionomys, Protheomys, Ellobius, Arvicola* |
| Mole-rats | MR | *Spalax*, *Myospalax* |
| Moles | ML | *Talpa* |
| Mountain voles | MTV | *Alticola* |
| Pikas | PK | *Ochotona* |
| Rats and house mouse | RM | *Mus, Rattus, Nesokia* |
| Soricine shrews | SS | *Sorex*, *Neomys* |
| Steppe lemmings | SL | *Eolagurus*, *Laguru*s |
| Woodmice and harvest mouse | WM | *Apodemus, Micromys* |

**Table S4.** Summary of principal coordinate analysis of the number of host species belonging to main phylogenetic/ecological clades per region. HCV1, HCV2, and HCV3 – the first, the second and the third vectors, respectively. See Table S2 for full names and genera of host phylogenetic clades. *r* - Spearman correlation between a vector and an original host composition variable

|  |  |  |  |
| --- | --- | --- | --- |
| Principal component | PC1 | PC2 | PC3 |
| Eigenvalue | 3249.25 | 1439.54 | 874.44 |
| Explained variance | 0.48 | 0.21 | 0.13 |
| Cumulative proportion of total variance | 0.48 | 0.69 | 0.82 |
| *r* | BV | -0.70 | 0.17 | -0.54 |
| BM | -0.43 | -0.32 | -0.44 |
| CH | -0.34 | 0.14 | -0.39 |
| CS | -0.04 | -0.08 | 0.62 |
| DM | -0.09 | -0.32 | 0.35 |
| GB | 0.69 | -0.19 | 0.25 |
| HM | 0.42 | -0.74 | -0.21 |
| JB | 0.62 | -0.43 | -0.13 |
| LM | -0.45 | 0.35 | -0.38 |
| MM | 0.55 | -0.53 | -0.29 |
| MV | -0.49 | -0.71 | 0.05 |
| MR | 0.01 | -0.40 | -0.17 |
| ML | -0.69 | -0.16 | -0.01 |
| MTV | 0.40 | 0.08 | -0.43 |
| PK | 0.23 | 0.26 | -0.53 |
| RM | -0.01 | -0.35 | 0.29 |
| SS | -0.89 | -0.04 | -0.09 |
| SL | 0.03 | -0.41 | -0.36 |
|  | WM | -0.60 | -0.46 | 0.36 |

Appendix 4.

Flea species contribution to total beta-diversity (SCBD). Values of SCBD are in parentheses and those higher than average are in bold.

*Palaeopsylla soricis* (**0.0189**), *Rhadinopsylla integella* (**0.0184**), *Amalaraeus penicilliger* (**0.018**), *Corrodopsylla birulai* (**0.0173**), *Hystrichopsylla talpae* (**0.0172**), *Megabothris turbidus* (**0.0171**), *Leptopsylla segnis* (**0.0166**), *Megabothris rectangulatus* (**0.0165**), *Ctenophthalmus assimilis* (**0.0164**), *Frontopsylla elata* (**0.0155**), *Nosopsyllus fasciatus* (**0.0151**), *Peromyscopsylla bidentata* (**0.015**), *Amphipsylla rossica* (**0.0143**), *Catallagia dacenkoi* (**0.014**), *Amphipsylla sibirica* (**0.0139**), *Neopsylla pleskei* (**0.0131**), *Neopsylla mana* (**0.0128**), *Peromyscopsylla silvatica* (**0.0125**), *Ctenophthalmus uncinatus* (**0.0115**), *Megabothris calcarifer* (**0.0115**), *Megabothris walkeri* (**0.0115**), *Leptopsylla taschenbergi* (**0.0115**), *Megabothris advenarius* (**0.0113**), *Ceratophyllus indages* (**0.0112**), *Callopsylla caspia* (**0.011**), *Hystrichopsylla microti* (**0.0105**), *Nosopsyllus consimilis* (**0.0105**), *Ceratophyllus sciurorum* (**0.0102**), *Doratopsylla dasycnema* (**0.0101**), *Oropsylla silantiewi* (**0.0099**), *Amphipsylla primaris* (**0.0097**), *Ctenophthalmus agyrtes* (**0.0094**), *Catallagia ioffi* (**0.0092**), *Amphipsylla kuznetzovi* (**0.0091**), *Citellophilus tesquorum* (**0.009**), *Neopsylla setosa* (**0.0089**), *Nosopsyllus mokrzeckyi* (**0.0089**), *Oropsylla ilovaiskii* (**0.0088**), *Neopsylla acanthina* (**0.0087**), *Ctenophthalmus breviatus* (**0.0085**), *Amphalius runatus* (**0.0085**), *Peromyscopsylla ostsibirica* (**0.0084**), *Amphipsylla schelkovnikovi* (**0.0081**), *Rhadinopsylla li* (**0.008**), *Mesopsylla hebes* (**0.0077**), *Amphipsylla marikovskii* (**0.0077**), *Amphipsylla vinogradovi* (**0.0076**), *Pectinoctenus nemorosa* (**0.0074**), *Palaeopsylla kohauti* (**0.0071**), *Neopsylla bidentatiformis* (**0.0069**), *Nosopsyllus laeviceps* (**0.0068**), *Ctenophthalmus congeneroides* (**0.0067**), *Oropsylla alaskensis* (**0.0066**), *Xenopsylla conformis* (**0.0065**), *Amphipsylla dumalis* (**0.0065**), *Ctenophthalmus pisticus* (**0.0063**), *Frontopsylla elatoides* (**0.0062**), *Ctenophyllus armatus* (**0.0062**), *Frontopsylla ornata* (**0.0061**), *Ctenophthalmus proximus* (**0.0061**), *Frontopsylla protera* (**0.0061**), *Rhadinopsylla rothschildi* (**0.006**), *Neopsylla teratura* (**0.006**), *Ctenophthalmus bisoctodentatus* (**0.0059**), *Leptopsylla nana* (**0.0058**), *Rhadinopsylla cedestis* (**0.0057**), *Ctenophthalmus wagneri* (**0.0056**), *Rhadinopsylla pseudodahurica* (**0.0056**), *Frontopsylla luculenta* (**0.0055**), *Echidnophaga oschanini* (**0.0053**), *Paraneopsylla ioffi* (**0.005**), *Rhadinopsylla dahurica* (0.0049), *Ctenophthalmus arvalis* (0.0049), *Nosopsyllus fidus* (0.0049), *Amphipsylla anceps* (0.0048), *Ceratophyllus anisus* (0.0048), *Stenoponia montana* (0.0048), *Pectinoctenus pavlovskii* (0.0046), *Coptopsylla lamellifer* (0.0045), *Ctenophthalmus dolichus* (0.0045), *Paradoxopsyllus repandus* (0.0045), *Stenoponia ivanovi* (0.0045), *Amphipsylla kalabukhovi* (0.0043), *Citellophilus lebedewi* (0.0043), *Paradoxopsyllus scorodumovi* (0.0043), *Pectinoctenus pectiniceps* (0.0042), *Mesopsylla lenis* (0.0041), *Citellophilus trispinus* (0.0041), *Ophthalmopsylla volgensis* (0.004), *Ophthalmopsylla praefecta* (0.0038), *Ctenophthalmus orientalis* (0.0038), *Ctenophthalmus golovi* (0.0038), *Rhadinopsylla angusta* (0.0037), *Amphipsylla phaiomydis* (0.0036), *Stenoponia sidimi* (0.0036), *Ctenophthalmus bogatschevi* (0.0036), *Nosopsyllus tersus* (0.0035), *Xenopsylla gerbilli* (0.0035), *Xenopsylla hirtipes* (0.0035), *Myoxopsylla jordani* (0.0035), *Mesopsylla tuschkan* (0.0034), *Frontopsylla semura* (0.0034), *Amphipsylla prima* (0.0034), *Neopsylla meridiana* (0.0034), *Ctenophthalmus secundus* (0.0033), *Rhadinopsylla ucrainica* (0.0033), *Stenoponia conspecta* (0.0033), *Mesopsylla eucta* (0.0031), *Frontopsylla ambigua* (0.003), *Frontopsylla hetera* (0.0029), *Ochotonobius hirticrus* (0.0029), *Paramonopsyllus scalonae* (0.0029), *Nosopsyllus turkmenicus* (0.0028), *Stenoponia vlasovi* (0.0028), *Xenopsylla skrjabini* (0.0028), *Leptopsylla sicistae* (0.0028), *Ctenophthalmus dilatatus* (0.0027), *Amphipsylla montana* (0.0026), *Stenoponia suknevi* (0.0026), *Atyphloceras nuperus* (0.0025), *Ctenophthalmus obtusus* (0.0025), *Ctenophthalmus solutus* (0.0025), *Hystrichopsylla orientalis* (0.0025), *Rhadinopsylla pentacantha* (0.0025), *Rhadinopsylla insolita* (0.0023), *Frontopsylla macrophthalma* (0.0023), *Amalaraeus dissimilis* (0.0022), *Megabothris asio* (0.0022), *Pectinoctenus lauta* (0.0021), *Ctenophthalmus acuminatus* (0.0021), *Paradoxopsyllus hesperius* (0.0021), *Mesopsylla apscheronica* (0.002), *Nosopsyllus iranus* (0.002), *Stenoponia tripectinata* (0.002), *Megabothris beljaevi* (0.002), *Paradoxopsyllus teretifrons* (0.002), *Ctenophthalmus dux* (0.0019), *Citellophilus transcaucasicus* (0.0018), *Rhadinopsylla altaica* (0.0018), *Amphipsylla asiatica* (0.0017), *Nosopsyllus aralis* (0.0017), *Citellophilus ullus* (0.0017), *Ctenophthalmus wladimiri* (0.0017), *Amphipsylla longispina* (0.0017), *Frontopsylla wagneri* (0.0017), *Paradoxopsyllus dashidorzhii* (0.0017), *Rhadinopsylla bivirgis* (0.0016), *Desertopsylla rothschildi* (0.0016), *Rostropsylla daca* (0.0016), *Amphipsylla georgica* (0.0016), *Ctenophthalmus euxinicus* (0.0016), *Ctenophthalmus hypanis* (0.0016), *Ctenophthalmus inornatus* (0.0016), *Ctenophthalmus shovi* (0.0016), *Hystrichopsylla satunini* (0.0016), *Palaeopsylla caucasica* (0.0016), *Paradoxopsyllus naryni* (0.0015), *Pectinoctenus pamirensis* (0.0015), *Wagnerina schelkovnikovi* (0.0014), *Ctenophthalmus chionomydis* (0.0014), *Rhadinopsylla isacantha* (0.0014), *Amalaraeus ioffi* (0.0013), *Catallagia striata* (0.0013), *Megabothris bispinosa* (0.0013), *Callopsylla lagomys* (0.0012), *Ceratophyllus sinicus* (0.0012), *Nosopsyllus simla* (0.0012), *Rhadinopsylla altifrons* (0.0012), *Ctenophthalmus congener* (0.0012), *Peromyscopsylla fallax* (0.0012), *Catallagia fetisovi* (0.0011), *Ctenophyllus subarmatus* (0.0011), *Ophthalmopsylla kukuschkini* (0.001), *Wagnerina tuvensis* (0.001), *Paraneopsylla tiflovi* (0.0009), *Synosternus longispinus* (0.0009), *Neopsylla democratica* (0.0009), *Rhadinopsylla ioffi* (0.0009), *Rhadinopsylla socia* (0.0009), *Xenopsylla magdalinae* (0.0009), *Callopsylla saxatilis* (0.0007), *Coptopsylla arax* (0.0007), *Ctenophthalmus teres* (0.0007), *Xenopsylla cheopis* (0.0007), *Amphipsylla argoi* (0.0007), *Amphipsylla parthiana* (0.0007), *Coptopsylla bairamalensis* (0.0007), *Coptopsylla olgae* (0.0007), *Nosopsyllus philippovi* (0.0007), *Ophthalmopsylla karakum* (0.0007), *Paradoxopsyllus microphthalmus* (0.0007), *Peromyscopsylla tikhomirovae* (0.0007), *Phaenopsylla kopetdag* (0.0007), *Phaenopsylla tiflovi* (0.0007), *Xenopsylla nuttalli* (0.0007), *Xenopsylla persica* (0.0007), *Neopsylla abagaitui* (0.0007), *Neopsylla galea* (0.0007), *Ophthalmopsylla kiritschenkovi* (0.0007), *Paradoxopsyllus integer* (0.0007), *Paradoxopsyllus kalabukhovi* (0.0007), *Wagnerina longicauda* (0.0007).

Appendix 5.

**Fig. S2.** Map of contributions of flea assemblages to total beta diversity (LCBD). Sizes of squares are proportional to LCBD values.

