Consistent covariation of dispersal, life history and thermal niches across terrestrial arthropods

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Abstract

Arthropods, as ectotherms, are experiencing global declines, with many species facing the need to either acclimate or disperse in response to climate change. To generate general insights into such responses, a framework integrating traits on life history, dispersal and thermal niche is currently lacking. In light of this, understanding to which degree these traits covary and are organised into syndromes are key to improve distribution forecasting under climate change. We quantified life history, dispersal and thermal range covariation among 4000 Western European arthropod species spanning eight orders, considering phylogenetic relationships to account for shared ancestry. We demonstrate the existence of two independent axes of life history variation: the fast-slow continuum and the reproductive strategy axis. Notably, species at the fast end of the continuum tend to have higher dispersal capacities and broader thermal niches than slower species. The resulting syndromes were surprisingly consistent across orders, indicating a relatively uniform pattern of trait covariations across arthropod groups. These trait combinations, which generally enhance range-shifting potential, point to the emergence of two distinct groups of arthropods: those well-suited and those less equipped to mitigate the effects of future climate change.

Main

Climate change is an escalating global problem, threatening numerous species across various taxonomic groups[1–3]. Species may cope with changing climatic conditions by acclimatisation and/or adaptation to the experienced novel conditions, or by tracking their climate window through dispersal[4]. The pace at which species expand or shift their distribution will critically depend on their life histories—such as survival, reproduction and development—that determine population growth rate and overall demography. Furthermore, this rate of range shifts will be shaped by their dispersal capacity and ability to acclimate to novel conditions[4]. Forecasting biodiversity under climate change[5,6], therefore, relies on our ability to incorporate accurate trait data into extinction risk projections[7,8], thereby informing vulnerability assessments[9,10]and refining predictions of emerging community assemblages[11,12]. For arthropods, such an approach seems to be most urgent since any detailed species-specific assessment will fail to provide the needed insights in light of their steep global decline[13], which potentially jeopardizes the crucial ecosystem services these organisms provide[14].

Species are expected to show intrinsic life history trade-offs, positioning them along a “slow-fast” continuum[15–17]. Slow-living species have longer development times and lifespans, prioritizing resource allocation toward offspring survival rather than fecundity, while fast-living species adopt the opposite strategy[18]. In theory, slow-living species are better adapted to stable environments and have, therefore, greater difficulty recovering from stochastic mortality events[19]. Due to similar evolutionary pressures stemming from environmental instability, dispersal rates are expected to be lower in species with slow life histories[20,21]. Body size, however, may have contrasting effects. While smaller body sizes are typically linked to a fast-paced lifestyle, larger body sizes are often positively correlated with greater dispersal ability[4,22–24]. Predicted relationships between species’ dispersal and life history traits are therefore highly variable, both among and within species[25].

Both dispersing towards new areas and staying within a changing environment comes with certain costs, such as the risk of staying or settling in environments where conditions may be unfavourable[26].

Such limitations should be especially pronounced in ecological specialists, as they will suffer most from local environmental changes and/or experience greater challenges in establishing populations within unfamiliar habitats[27–30]. In the context of climate change, thermal tolerance is a particularly important niche component in shaping distribution patterns. Species with narrow thermal niche breadths are generally expected to be more vulnerable to climate change[31,32] and will have to face greater risks during dispersal into new environments in order to track their optimal temperature. Given this pivotal role of a species' thermal niche in determining both distribution ranges and dispersal costs, it can be expected to have shaped the evolution of both life histories[33,34] and dispersal[35,36].

Traits underlying life history variation can show complex covariation and are integrated into so-called syndromes[37–39]. Similarly, dispersal syndromes notify covariations between dispersal and other traits, and have been documented across various taxonomic groups[20,21,40–42]. Understanding the organisation of trait syndromes not only allows us to estimate missing trait data[21,43] in understudied taxa, but also allows more accurate forecasting of species distributions under environmental change[44]. Given the urgency to understand and predict arthropod distributions under future climate change, we aim to identify covariations between dispersal, life history and thermal niche widths across a wide range of Western European species. If dispersal and thermal range are independent of life history traits, they should form separate axes of variation alongside the fast-slow continuum. Conversely, if dispersal and thermal range covary with life history traits, their inclusion will reshape the existing life history axes. Given the vast diversity in arthropod morphology, lifestyles and dispersal modes, we expect different taxa to exhibit significant variation in both the direction and strength of these trait covariations. Additionally, we explore whether these syndromes are phylogenetically conserved, as shared evolutionary history may drive similar trait associations in closely related species, eventually shaping their responses to environmental changes and range shifts.

Results

Data on dispersal capacity, life history traits and thermal niche were obtained from an existing dataset described by Logghe et al. (2024). From this dataset, we selected eight arthropod orders with sufficiently high data quality, resulting in a refined dataset comprising over 4000 species and nine functional traits. As a first exploration of these data, we conducted a phylogenetically corrected PCA on a subset of species with complete data for all traits. This analysis revealed no distinct separation among orders, suggesting that covariations may be consistent across taxonomic groups (Figure 1). PC1 shows a strong positive relationship with voltinism and dispersal, while it is also strongly negatively correlates with development time (Appendix S.1). Additionally, it exhibits a positive correlation with thermal mean and range, though this relationship is not as strong as with the other traits. In contrast, PC2 is strongly positively correlated with fecundity and size. These results indicate the existence of covariations between dispersal, life history, body size and thermal niche across arthropod orders.

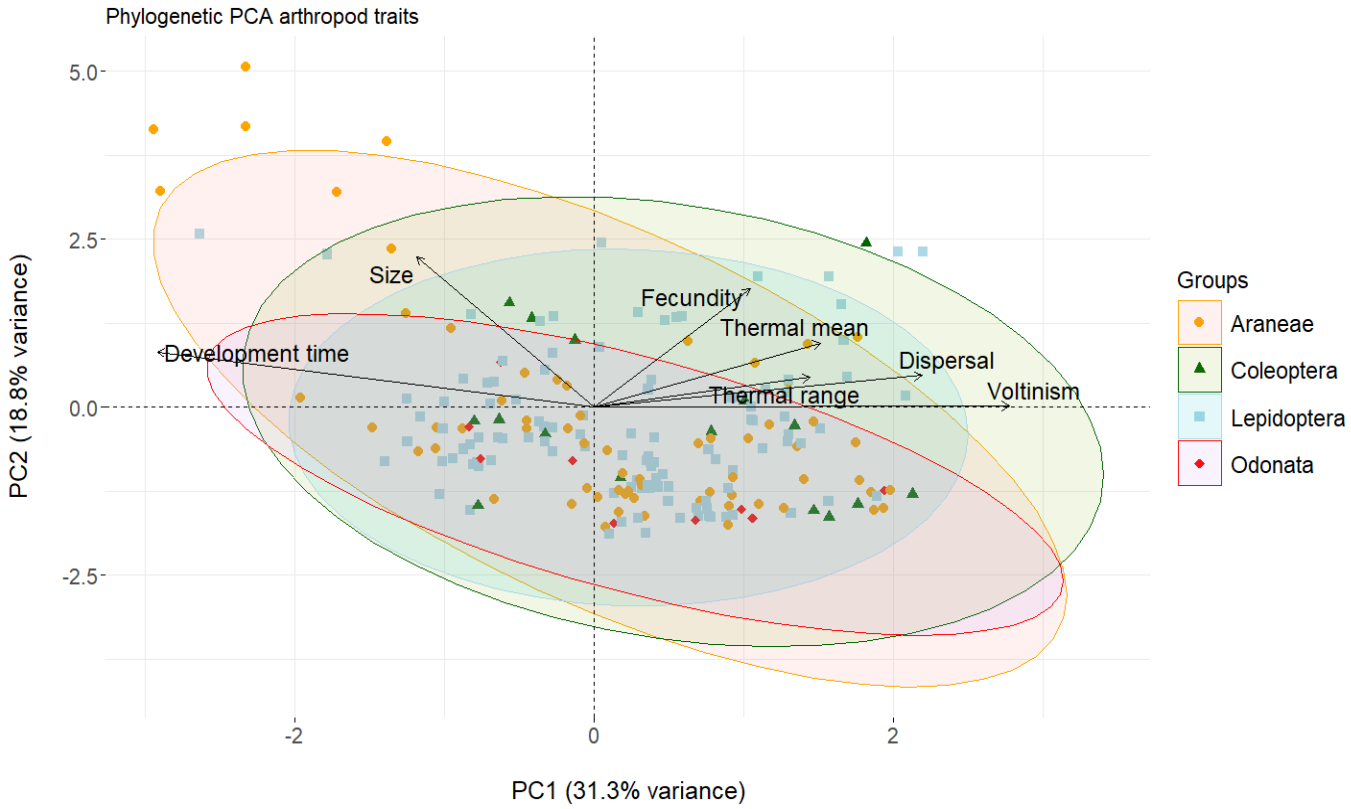

Figure 1: PCA results for arthropod species for which data on all traits was available (n=200). Dots represent species with symbol colour and shape according to their taxonomic order. Arrows represent the direction and magnitude of each variable's contribution to the principal components.

Next, we employed Bayesian Generalized Linear models to identify trait covariations within each of the eight arthropod orders. These models accounted for phylogenetic relatedness between species, ensuring that observed relationships reflect ecological and evolutionary patterns. Our results reveal multiple trait syndromes within various arthropod orders (Figure 2 for an example, all in Appendix S.2). In most orders, there is a clear positive relationship between fast development, voltinism and dispersal (Figure 3). Additionally, temperature niche components tend to covary positively with dispersal capacity, fecundity and size in the majority of orders. Covariations between other trait combinations are always present within at least one order. However, these are highly order specific and, therefore, not generalizable across arthropod orders.

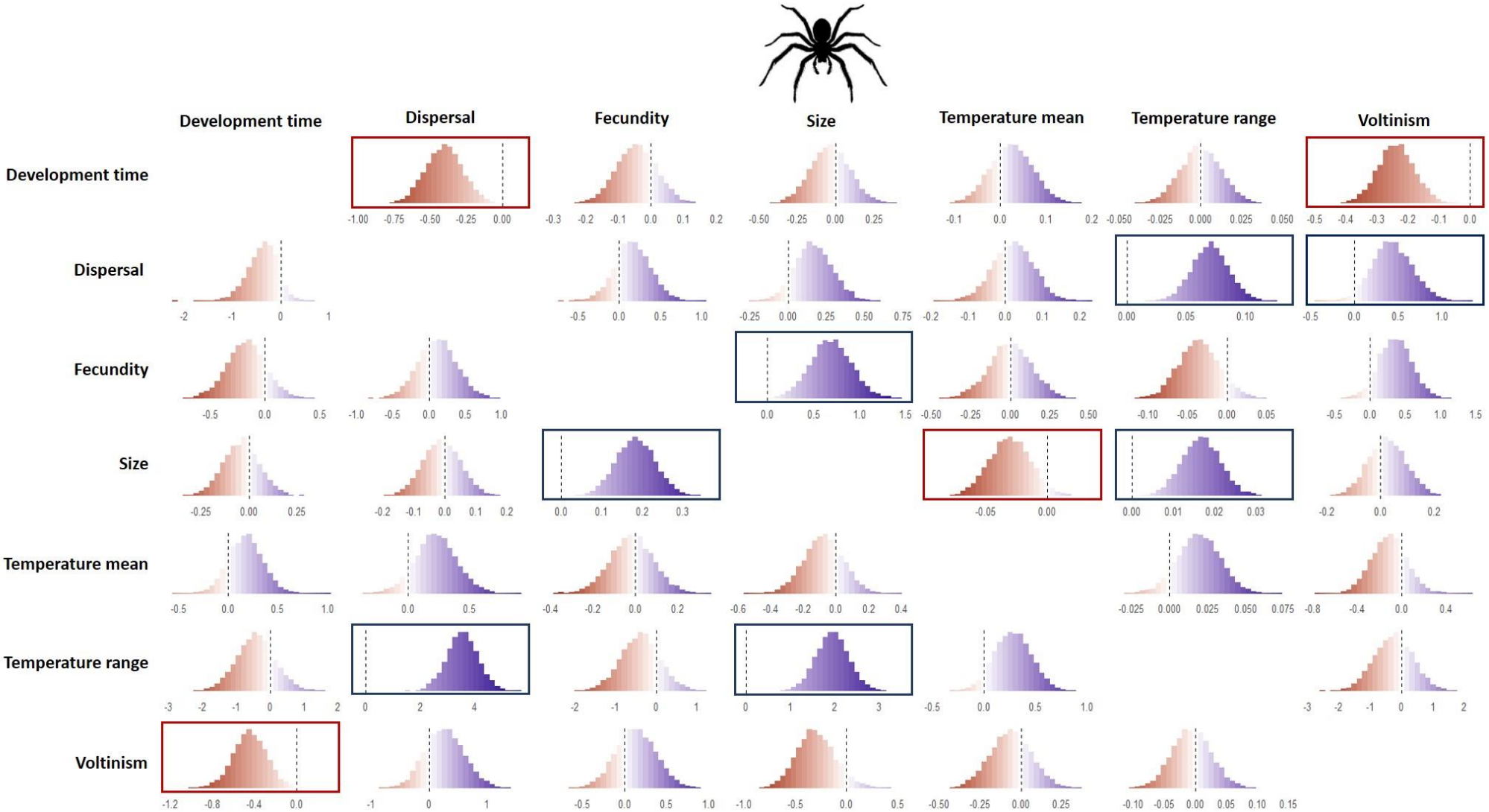

Figure 2: Pairwise posterior distributions for trait covariations (slopes of the linear regressions) within Araneae. Column names represent independent variables, while row names denote dependent variables. Negative covariations are highlighted in red and positive covariations in blue. Effect sizes that are clearly determined (i.e. the 95% interval does not include zero) are outlined in the corresponding colour.

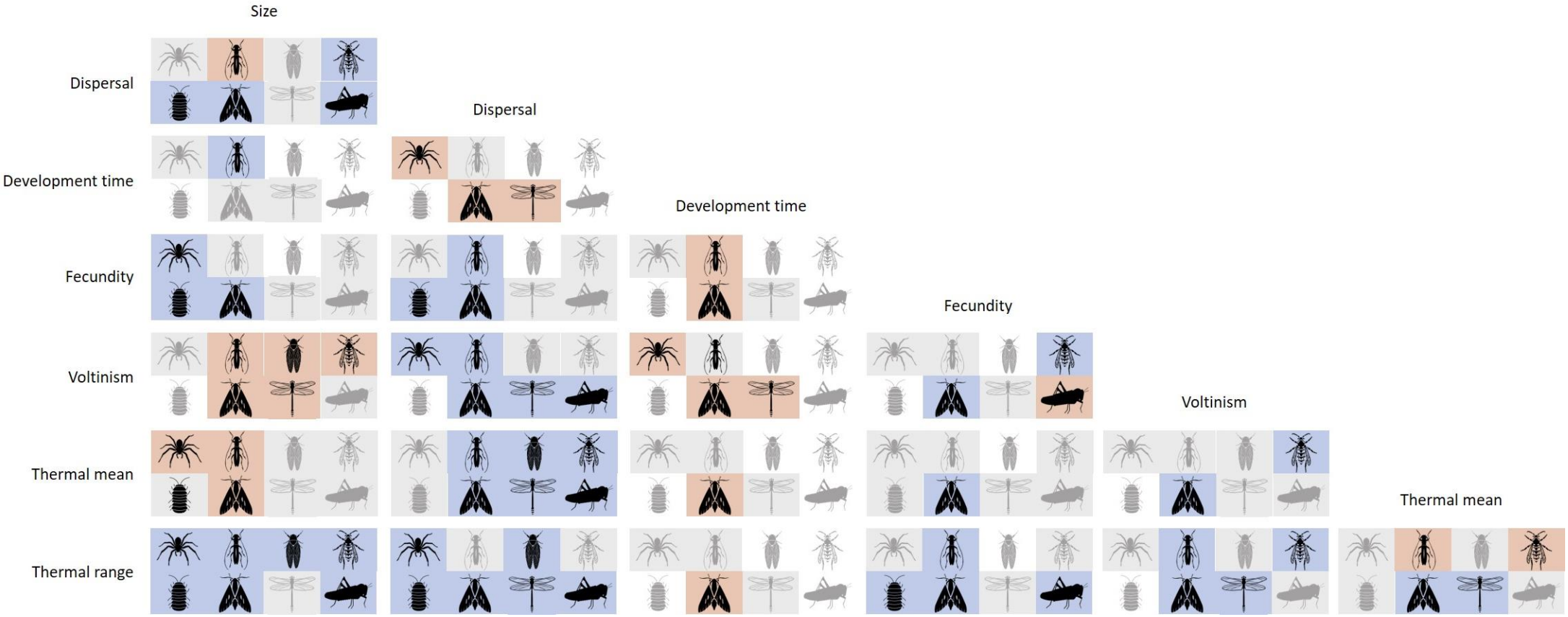

Figure 3: Overview of trait covariations across each order, represented as a correlation matrix. Each grid of the matrix is divided into eight cells, with each cell representing one order. The taxa are, from left to right and top to bottom: Araneae, Coleoptera, Hemiptera, Hymenoptera, Isopoda, Lepidoptera, Odonata and Orthoptera. Red cells indicate a clearly determined (0 not included in the 95 credibility interval) negative relationship, blue cells indicate a clearly determined positive relationship, and grey cells show that the relationship was not clearly determined. White cells denote that this trait combination was not assessed for the given order, due to either an absence of data for one of the traits or convergence issues.

In order to estimate how much trait values are determined by shared ancestry between species, we calculated the phylogenetic signal for every trait and arthropod order (Figure 4). On average, body size and development time showed very strong phylogenetic signals, suggesting these traits are generally strongly influenced by phylogeny. In contrast, thermal niche and fecundity appeared largely independent of phylogeny in most arthropod orders. Finally, the phylogenetic signal for dispersal displayed considerable variation, indicating that the influence of phylogenetic relationships differs substantially between orders (Appendix S.3).

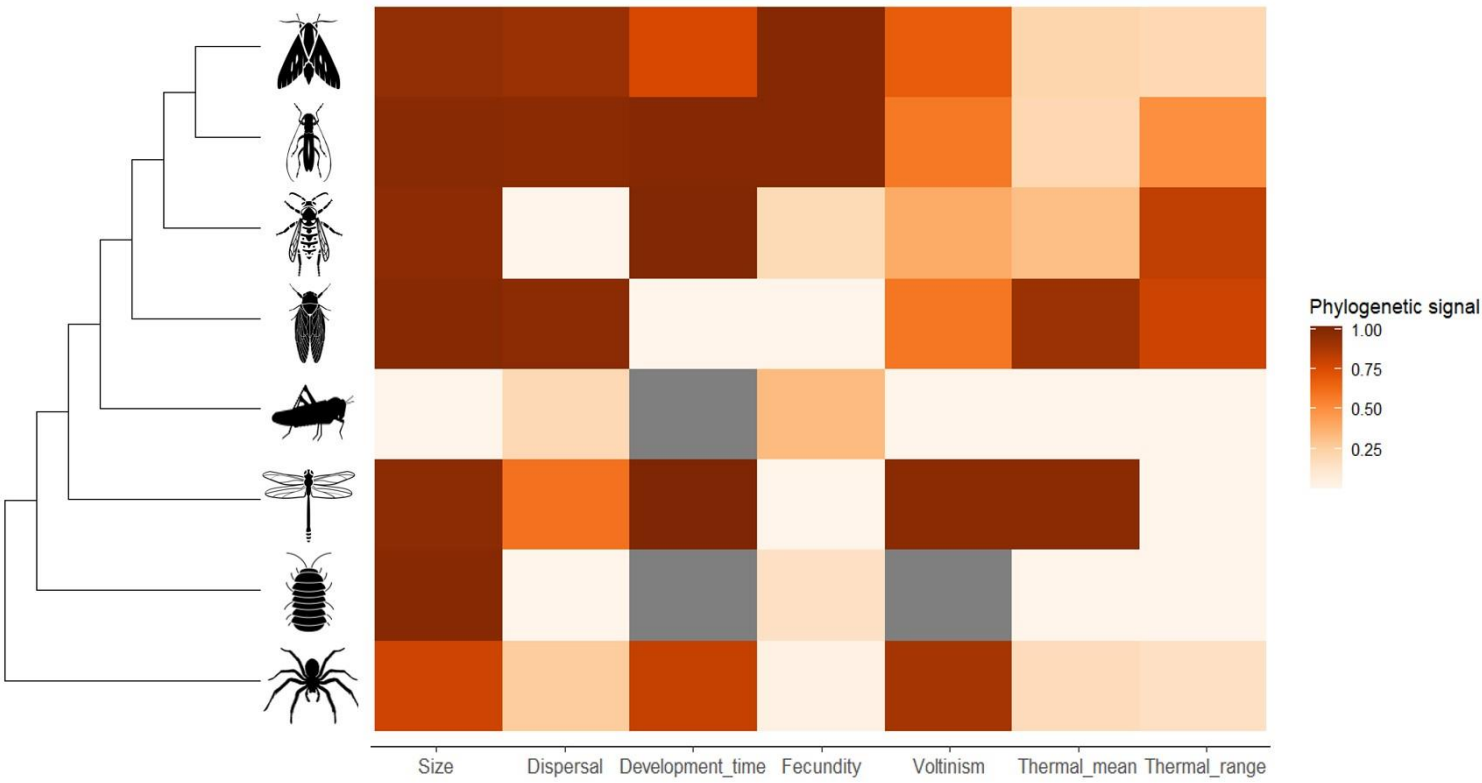

Figure 4: Overview of the phylogenetic signal (Pagel's Lambda) for every assessed trait for each arthropod order. Arthropod orders are from top to bottom: Lepidoptera, Coleoptera, Hymenoptera, Hemiptera, Orthoptera, Odonata, Isopoda and Araneae. Colours represent the strength of phylogenetic signal, with higher values (darker red) indicating that trait values are more explained by phylogenetic relationships. The grey squares indicate that the phylogenetic signal was not calculated for that trait and order due to a lack of data.

Discussion

Our quantitative synthesis across a wide range of Western European arthropods indicates that dispersal, life history and thermal niche are tightly connected, implying similar evolutionary pressures on these traits. While there are notable differences between orders, these relationships remain largely

consistent across taxa, suggesting that trait covariations can be generalized to a broad range of arthropod species.

A considerable amount of interspecific life history trait variation in arthropods can be attributed to the slow-fast continuum, with a clear distinction between species with fast and slow lifecycles. Interestingly, development time appears closely tied to dispersal capacity, as we observed clear covariations between development time, voltinism and dispersal across various orders. Previous research has shown similar patterns, with high dispersal ability often linked with fast life history strategies[20,21,45]. Given that most insects disperse only in their winged adult stages, this dispersal-life history syndrome may have evolved as a bet-hedging strategy in response to unstable environments, allowing for rapid relocation when conditions become unfavourable[46,47]. Interestingly, we found limited evidence to suggest that fast-living species produce more offspring, a pattern that would typically be anticipated within the slow-fast continuum framework[18]. While Lepidoptera and Coleoptera did show a clear negative relationship between fecundity and development time, our analyses suggest that the reproductive axis of variation is as good as independent from the developmental axis. We thus show that the independence of these two distinct axes of life history variation is rather a rule than an exception, as was previously reported for plants[48] and vertebrates[16,49,50].

Our results suggest that thermal niche breadth has played a role in shaping the evolution of dispersal in arthropods, with most orders showing a positive relationship between realised thermal niche breadth and dispersal ability. This relationship likely arises from the costs associated with dispersing to new environments, where the risk of encountering unfavourable climatic conditions is high[26]. A broader thermal niche breadth reduces this risk by increasing the chances that newly colonised areas fall within the species' tolerable thermal range. However, the causal relationship could also work in reverse, as limited dispersal capacity may constrain a species' realised thermal niche by restricting access to potentially suitable regions, despite physiological tolerance to those climates[51]. In other

153 words, the realised thermal niche, as considered in this study, would be narrower than the
154 fundamental thermal niche, simply because of dispersal limitations. Implementation of other niche
155 components such as diet or habitat specialisation could have provided a more holistic view on the
156 relationship between dispersal and ecological generalisation. It is worthwhile to notice that the
157 retrieved thermal niche-body size relationships were predominantly negative, which aligns with
158 experimentally derived patterns of lower thermal tolerance in large-bodied animals[52].

159 Besides thermal niche breadth, thermal optima also covary with dispersal ability. Across nearly all
160 assessed arthropod orders, species adapted to warmer climates exhibit higher dispersal capacities.
161 Although cold-adapted species may face greater risks from climate change and thus might benefit
162 more from range shifting as a mitigation strategy, their generally lower dispersal capacities make
163 spreading a less viable option[53]. Furthermore, our findings indicate that low dispersal capacity often
164 covaries with slower life histories, which hampers colonization success due to slower population
165 growth rates and, therefore, elevated vulnerability to stochastic extinction[54]. Consequently, the
166 arthropod species most at risk from temperature changes due to climate change are also those least
167 equipped to mitigate its effects through range shifts - a trend also noted in European mammals[55].

168 Phylogenetic signals were highly variable and strongly influenced by both the specific trait and
169 arthropod order being assessed. Body size and development time showed strong phylogenetic
170 conservation in most orders, while thermal niche was largely independent of shared ancestry.
171 Dispersal and fecundity present an interesting pattern, being strongly conserved in some orders but
172 showing minimal phylogenetic influence in others. A strong phylogenetic signal in body size was
173 expected, as closely related species often share a similar morphology. Development time is typically
174 linked to size, as larger species require more time to accumulate tissue[56,57]. However, our data do not
175 fully support the idea that larger arthropod species develop more slowly, as only Coleoptera showed
176 a clear positive relationship between body size and development time. Instead, it appears that closely
177 related arthropod species have evolved similar pace-of-life strategies due to comparable life cycle

178 characteristics[58]. The weak phylogenetic signal in thermal traits aligns nicely with earlier findings
179 suggesting directional selection driven by physiological constraints and experienced thermal
180 conditions within species' range over evolutionary history[59]. The variable phylogenetic signal for
181 dispersal capacity likely reflects the diverse dispersal mechanisms across arthropod orders. For
182 example, dispersal in flying insects like Lepidoptera and Odonata tends to be body size-dependent,
183 with larger species typically showing higher mobility[24,60,61]. In Coleoptera and Hemiptera, dispersal
184 capacity is closely tied to hind wing development, a trait that is also strongly phylogenetically
185 conserved[62–64]. For taxa with more passive dispersal mechanisms, a lower phylogenetic signal in
186 dispersal capacity is expected, as dispersal is less directly linked to specific morphological traits. In
187 Araneae, for instance, nearly all species show ballooning behaviour regardless of size, with larger
188 species typically ballooning as juveniles. Dispersal propensity in spiders is thus more strongly
189 correlated with habitat stability and specialization, factors that are generally independent of
190 phylogenetic lineage[65].

191 One of the most unexpected findings of this study was the remarkable consistency across arthropod
192 orders in terms of covariations between dispersal, life history and thermal niche. Given the
193 extraordinary diversity within this phylum, we expected significant differences in these covariations
194 between groups. Although all trait combinations had at least one order that lacked a clearly
195 determined relationship, the overall consistency across orders remains noteworthy. This uniformity
196 could have important implications for modelling the future effects of climate change, suggesting that
197 detailed trait information for every species might not be as necessary as previously suggested[66].
198 Instead, many missing trait values could potentially be inferred from accessible trait data, facilitating
199 broader, more efficient predictions.

Methods

Data description

The data used for this study was sourced from the dataset described by Logghe et al. (2024), which contains information on 28 life history and ecological traits for 4874 terrestrial arthropod species. We focused on eight arthropod orders for which data on both dispersal and life history was available: Araneae, Coleoptera, Hemiptera, Hymenoptera, Isopoda, Lepidoptera, Odonata and Orthoptera. Two orders, Diptera and Opiliones, were excluded due to lacking data. This resulted in a dataset containing 4343 species. From this dataset, we selected nine traits deemed particularly relevant for predicting range shifts under climate change[66,68]. These included four life history traits (development time, dispersal, fecundity and voltinism), four thermal traits (mean, maximum, minimum and range of temperatures), and body size, which is often correlated with both life history and thermal limits (e.g. Berger et al., 2008; Hillaert et al., 2018; Klockmann et al., 2017). Appendix S.4 shows the data coverage of traits for each order.

As a measure for body size, adult arthropod's body length in millimetres is used. Development time is defined as the duration between egg laying and adult emergence, expressed in days. Fecundity is defined as the number of offspring a female could produce during her lifetime, while voltinism refers to the maximum number of generations a species could complete in a single year. Note that the maximum value for voltinism is used, as the number of generations can vary annually and across regions. Dispersal is defined as the movement of a species from its place of birth to their location of reproduction[71], with significant variation in modes and proxies both across and within orders. To enable comparison, Logghe et al. (2024) rescaled dispersal capacity on a relative scale from 0.1 to 1 within each order, where 0.1 represented the least dispersive species and 1 the most dispersive. Thermal mean, minimum and maximum represent the average, minimum and maximum annual temperatures (in °C) across the species' geographic range (see Logghe et al., 2024 for details on the

224 calculation of these metrics). Finally, thermal range was calculated as the difference between thermal
225 minimum and maximum.

226 Statistical analysis

227 To account for the shared evolutionary history among species, which can influence trait similarities,
228 we controlled for phylogenetic relatedness in all our analyses. This approach ensured that observed
229 relationships between traits reflected ecological or evolutionary patterns, rather than being influenced
230 by shared ancestry. To achieve this, we constructed a phylogenetic tree including all species in the
231 dataset, which served as the basis for subsequent analyses. The tree was built by linking species names
232 to the Open Tree Taxonomy database, which contains data on known phylogenetic relationships ("rotl"
233 package)[72]. Branch lengths were added to the tree using the "ape" package[73] and calculated with the
234 "Grafen" method[74].

235 To examine how life history and thermal traits are distributed across arthropod orders, we performed
236 a phylogenetic principal component analysis (PCA) using the "phyl.pca" function from the "phytools"
237 package[75]. Unlike standard PCA, this method incorporates phylogenetic relationships, correcting for
238 the lack of independence between species due to shared ancestry. The analysis was conducted on a
239 subset of the dataset that included only the 145 species for which complete data on all traits were
240 available.

241 Bayesian Generalized Linear models were employed to assess whether covariations were present
242 between the selected traits ("brms" package)[76]. Given the strong phylogenetic signal across the tree
243 of life, the variation in data quantity and quality among orders, and our aim to detect and understand
244 potential divergence in the covariations across arthropod orders, we analysed every order separately.
245 Trait data on body size, fecundity and development time underwent log transformation before analysis
246 to reduce skewness of the data. For every order, each trait combination was run two times, with the
247 dependent and independent variable interchanged. Each model was fitted with a distribution
248 depending on the independent variable: zero-one-inflated beta for voltinism, binomial for dispersal

249 and Gaussian for the remaining variables. The models were run using 4 chains and 4000 iterations,
250 with a burn-in period of 1000. Non-informative flat priors were used for the model parameters.
251 Phylogenetic distances between species were derived from a phylogenetic distance matrix derived
252 from the previously mentioned phylogenetic tree ("geiger" package)[77]. These distances were
253 incorporated into every Bayesian model as blocking factors, to ensure that phylogenetic relationships
254 were considered when the covariation between traits is estimated. Convergence of the models was
255 checked by examining the effective sample size (>1000) for each chain as well as Gelman-Rubin statistic
256 (Rhat < 1.1) among chains. Effect sizes were deemed clearly determined when 0 was not included in
257 the 95% credibility intervals of the posteriors.

258 Finally, we assessed the phylogenetic signal using Pagel's Lambda for each considered trait and
259 arthropod order[78]. This is a metric that estimates how much closely related species resemble each
260 other compared to expectations under a Brownian motion model of evolution. Pagel's Lambda
261 typically ranges from 0 (indicating no influence of phylogenetic relationships on trait values) to 1
262 (indicating trait values are entirely explained by phylogenetic relationships). We calculated this metric
263 using the "phylosig" function from the "phytools" package[75].

264 R version 4.0.4[79] was used to perform all data analyses.

265 Data availability

266 The complete dataset on arthropod life histories and ecological traits can be found on GBIF:
267 https://doi.org/10.15468/75g5z9. The filtered dataset specific to this study can be accessed on
268 Zenodo: 10.5281/zenodo.14527806.

269 References

270 1. Bellard, C., Bertelsmeier, C., Leadley, P., Thuiller, W. & Courchamp, F. Impacts of climate change
271 on the future of biodiversity. *Ecology Letters* **15**, 365–377 (2012).

2. Habibullah, M. S., Din, B. H., Tan, S.-H. & Zahid, H. Impact of climate change on biodiversity loss: global evidence. *Environmental Science and Pollution Research* **29**, 1073–1086 (2022).
3. Maxwell, S. L. *et al.* Conservation implications of ecological responses to extreme weather and climate events. *Diversity and Distributions* **25**, 613–625 (2019).
4. MacLean, S. A. & Beissinger, S. R. Species' traits as predictors of range shifts under contemporary climate change: A review and meta-analysis. *Global Change Biology* **23**, 4094–4105 (2017).
5. Settele, J. *et al.* Terrestrial and inland water systems. in *Climate change 2014: Impacts, adaptation, and vulnerability. Fifth assessment report of the Intergovernmental Panel of Climate Change* 1–153 (Cambridge University Press, New York, NY, 2014).
6. Urban, M. C. Projecting biological impacts from climate change like a climate scientist. *WIREs Climate Change* **10**, e585 (2019).
7. La Sorte, F. A. & Jetz, W. Projected range contractions of montane biodiversity under global warming. *Proceedings of the Royal Society B.* **277**, 3401–3410 (2010).
8. Thomas, C. D. *et al.* Extinction risk from climate change. *Nature* **427**, 145-148 (2004).
9. Foden, W. B. *et al.* Identifying the World's Most Climate Change Vulnerable Species: A Systematic Trait-Based Assessment of all Birds, Amphibians and Corals. *PLoS ONE* **8**, e65427 (2013).
10. Foden, W. B. & Young, B. E. *IUCN SSC Guidelines for Assessing Species' Vulnerability to Climate Change. Version 1.0*. (IUCN Species Survival Commission, Cambridge, England, 2016).
11. Stralberg, D. *et al.* Re-Shuffling of Species with Climate Disruption: A No-Analog Future for California Birds? *PLoS ONE* **4**, e6825 (2009).
12. Williams, W. W. & Jackson, S. T. Novel climates, no-analog communities, and ecological surprises. *Frontiers in Ecology and the Environment* **5**, 475–482 (2007).
13. Wagner, D. L. Insect Declines in the Anthropocene. *Annual Review of Entomology.* **65**, 457–480 (2020).

14. Yang, L. H. & Gratton, C. Insects as drivers of ecosystem processes. *Current Opinion in Insect Science* **2**, 26–32 (2014).
15. Beukhof, E. *et al.* Marine fish traits follow fast-slow continuum across oceans. *Scientific Reports* **9**, 17878 (2019).
16. Gaillard, J.-M. *et al.* An Analysis of Demographic Tactics in Birds and Mammals. *Oikos* **56**, 59 (1989).
17. Promislow, D. E. L. & Harvey, P. H. Living fast and dying young: A comparative analysis of life-history variation among mammals. *Journal of Zoology* **220**, 417–437 (1990).
18. Reynolds, J. D. Life histories and extinction risk. in *Macroecology* 195–217 (Blackwell Publishing, Oxford, 2003).
19. Pianka, E. R. On r- and K-Selection. *The American Naturalist* **104**, 592–597 (1970).
20. Beckman, N. G., Bullock, J. M. & Salguero-Gómez, R. High dispersal ability is related to fast life-history strategies. *Journal of Ecology* **106**, 1349–1362 (2018).
21. Stevens, V. M. *et al.* Dispersal syndromes and the use of life-histories to predict dispersal. *Evolutionary Applications* **6**, 630–642 (2013).
22. Hillaert, J., Hovestadt, T., Vandegehuchte, M. L. & Bonte, D. Size-dependent movement explains why bigger is better in fragmented landscapes. *Ecology and Evolution* **8**, 10754–10767 (2018).
23. Jenkins, D. G. *et al.* Does size matter for dispersal distance? *Global Ecology and Biogeography* **16**, 415–425 (2007).
24. Sekar, S. A meta-analysis of the traits affecting dispersal ability in butterflies: can wingspan be used as a proxy?: Factors affecting dispersal ability in butterflies. *Journal of Animal Ecology* **81**, 174–184 (2012).
25. Bonte, D. Integrating dispersal in life history. in *Life history evolution: Traits, Interactions, and Applications* (eds. Segoli, M. & Wajnberg, E.) 175–185 (Wiley, Hoboken, NJ, 2025).
26. Bonte, D. *et al.* Costs of dispersal. *Biological Reviews* **87**, 290–312 (2012).

27. Gilman, S. E., Urban, M. C., Tewksbury, J., Gilchrist, G. W. & Holt, R. D. A framework for community interactions under climate change. *Trends in Ecology & Evolution* **25**, 325–331 (2010).

28. Hill, J. K., Thomas, C. D. & Huntley, B. Climate and recent range changes in butterflies. in *'Fingerprints' of Climate Change* (eds. Walther, GR., Burga, C. A. & Edwards, P. J.) 77–88 (Springer, Boston, 2001).

29. Pöyry, J., Luoto, M., Heikkinen, R. K., Kuussaari, M. & Saarinen, K. Species traits explain recent range shifts of Finnish butterflies. *Global Change Biology* **15**, 732–743 (2009).

30. Warren, M. S. *et al.* Rapid responses of British butterflies to opposing forces of climate and habitat change. *Nature* **414**, 65-69 (2001).

31. Grinder, R. M. & Wiens, J. J. Niche width predicts extinction from climate change and vulnerability of tropical species. *Global Change Biology* **29**, 618–630 (2023).

32. Saupe, E. E. *et al.* Niche breadth and geographic range size as determinants of species survival on geological time scales. *Global Ecology and Biogeography* **24**, 1159–1169 (2015).

33. Carbonell, J. A. & Stoks, R. Thermal evolution of life history and heat tolerance during range expansions toward warmer and cooler regions. *Ecology* **101**, e03134 (2020).

34. Hampe, A. & Jump, A. A. Climate relicts: Past, Present, Future. *Annual Review of Ecology, Evolution, and Systematics* **42**, 313–333 (2011).

35. Hillaert, J., Boeye, J., Stoks, R. & Bonte, D. The evolution of thermal performance can constrain dispersal during range shifting. *Journal of Biological Dynamics* **9**, 317–335 (2015).

36. Travis, J. M. J. *et al.* Modelling dispersal: an eco-evolutionary framework incorporating emigration, movement, settlement behaviour and the multiple costs involved. *Methods in Ecology and Evolution* **3**, 628–641 (2012).

37. Dammhahn, M., Dingemanse, N. J., Niemelä, P. T. & Réale, D. Pace-of-life syndromes: a framework for the adaptive integration of behaviour, physiology and life history. *Behavioral Ecology and Sociobiology* **72**, 62, s00265-018-2473-y (2018).

38. Polverino, G., Santostefano, F., Díaz-Gil, C. & Mehner, T. Ecological conditions drive pace-of-life syndromes by shaping relationships between life history, physiology and behaviour in two populations of Eastern mosquitofish. *Scientific Reports* **8**, 14673 (2018).
39. Wright, J., Bolstad, G. H., Araya-Ajoy, Y. G. & Dingemanse, N. J. Life-history evolution under fluctuating density-dependent selection and the adaptive alignment of pace-of-life syndromes. *Biological Reviews* **94**, 230–247 (2019).
40. Buoro, M. & Carlson, S. M. Life-history syndromes: Integrating dispersal through space and time. *Ecology Letters* **17**, 756–767 (2014).
41. Ronce, O. & Clobert, J. Dispersal syndromes. in *Dispersal Ecology and Evolution* 119–138 (Oxford University Press, Oxford, 2012).
42. Stevens, V. M. *et al.* A comparative analysis of dispersal syndromes in terrestrial and semi-terrestrial animals. *Ecology Letters* **17**, 1039–1052 (2014).
43. Whitmee, S. & Orme, C. D. L. Predicting dispersal distance in mammals: a trait-based approach. *Journal of Animal Ecology* **82**, 211–221 (2013).
44. Weil, S.-S. *et al.* Body size and life history shape the historical biogeography of tetrapods. *Nature Ecology & Evolution* **7**, 1467–1479 (2023).
45. Weil, S. *et al.* Chameleon biogeographic dispersal is associated with extreme life history strategies. *Ecography* **2022**, e06323 (2022).
46. Snyder, R. E. Leaving home ain't easy: non-local seed dispersal is only evolutionarily stable in highly unpredictable environments. *Proceedings of the Royal Society B* **278**, 739–744 (2011).
47. Southwood, T. R. E. Habitat, the Templet for Ecological Strategies? *The Journal of Animal Ecology* **46**, 336 (1977).
48. Salguero-Gómez, R. *et al.* Fast–slow continuum and reproductive strategies structure plant life-history variation worldwide. *Proceedings of the National Academy of Sciences U.S.A.* **113**, 230–235 (2016).

49. Sæther, B.-E. The Influence of Body Weight on the Covariation between Reproductive Traits in European Birds. *Oikos* **48**, 79 (1987).
50. Stearns, S. C. The Influence of Size and Phylogeny on Patterns of Covariation among Life-History Traits in the Mammals. *Oikos* **41**, 173 (1983).
51. Sax, D. F., Early, R. & Bellemare, J. Niche syndromes, species extinction risks, and management under climate change. *Trends in Ecology & Evolution* **28**, 517–523 (2013).
52. Gunderson, A. R. Disentangling physiological and physical explanations for body size-dependent thermal tolerance. *Journal of Experimental Biology* **227**, jeb245645 (2024).
53. Tayleur, C. M. *et al.* Regional variation in climate change winners and losers highlights the rapid loss of cold-dwelling species. *Diversity and Distributions* **22**, 468–480 (2016).
54. Caswell, H. & Hastings, A. Fecundity, developmental time, and population growth rate: An analytical solution. *Theoretical Population Biology* **17**, 71–79 (1980).
55. Morrison, L., Estrada, A. & Early, R. Species traits suggest European mammals facing the greatest climate change are also least able to colonize new locations. *Diversity and Distributions* **24**, 1321–1332 (2018).
56. Blueweiss, L. *et al.* Relationships between body size and some life history parameters. *Oecologia* **37**, 257–272 (1978).
57. Calder, W. A. *Size, Function, and Life History*. (Dover Publications, New York, 1996).
58. Taylor, F. & Karban, R. *The Evolution of Insect Life Cycles*. (Springer New York, New York, 1986).
59. Bennett, J. M. *et al.* The evolution of critical thermal limits of life on Earth. *Nature Communications* **12**, 1198 (2021).
60. Kuussaari, M., Saarinen, M., Korpela, E., Pöyry, J. & Hyvönen, T. Higher mobility of butterflies than moths connected to habitat suitability and body size in a release experiment. *Ecology and Evolution* **4**, 3800–3811 (2014).
61. Wootton, R. Dragonfly flight: morphology, performance and behaviour. *International Journal of Odonatology* **23**, 31–39 (2020).

62. Braendle, C., Davis, G. K., Brisson, J. A. & Stern, D. L. Wing dimorphism in aphids. *Heredity* **97**, 192–199 (2006).

63. Roff, D. A. The Evolution of Wing Dimorphism in Insects. *Evolution* **40**, 1009–1020 (1986).

64. Roff, D. A. The evolution of flightlessness: Is history important? *Evolutionary Ecology* **8**, 639–657 (1994).

65. Bonte, D., Vanden Borre, J., Lens, L. & Maelfait, J.-P. Geographical variation in wolf spider dispersal behaviour is related to landscape structure. *Animal Behaviour* **72**, 655–662 (2006).

66. Urban, M. C. *et al.* Improving the forecast for biodiversity under climate change. *Science* **353**, aad8466 (2016).

67. Logghe, G. *et al.* An in-depth dataset of northwestern European arthropod life histories and ecological traits. Preprint at bioRxiv 2024.12.17.628846 (2024).

68. Estrada, A., Morales-Castilla, I., Caplat, P. & Early, R. Usefulness of Species Traits in Predicting Range Shifts. *Trends in Ecology & Evolution* **31**, 190–203 (2016).

69. Berger, D., Walters, R. & Gotthard, K. What limits insect fecundity? Body size- and temperature-dependent egg maturation and oviposition in a butterfly. *Functional Ecology* **22**, 523–529 (2008).

70. Klockmann, M., Günter, F. & Fischer, K. Heat resistance throughout ontogeny: body size constrains thermal tolerance. *Global Change Biology* **23**, 686–696 (2017).

71. Clobert, J., Le Galliard, J.-F., Cote, J., Meylan, S. & Massot, M. Informed dispersal, heterogeneity in animal dispersal syndromes and the dynamics of spatially structured populations. *Ecology Letters* **12**, 197–209 (2009).

72. Michonneau, F., Brown, J. W. & Winter, D. J. rotl: an R package to interact with the Open Tree of Life data. *Methods in Ecology and Evolution* **7**, 1476–1481 (2016).

73. Paradis, E. & Schliep, K. ape 5.0: an environment for modern phylogenetics and evolutionary analyses in R. *Bioinformatics* **35**, 526–528 (2019).

74. Grafen, A. The phylogenetic regression. *Philosophical Transactions of the Royal society of London* **326**, 119–157 (1989).

75. Revell, L. J. phytools: An R package for phylogenetic comparative biology (and other things). *Methods in Ecology and Evolution* **3**, 217–223 (2012).
76. Bürkner, P.-C. Bayesian Item Response Modeling in R with brms and Stan. *Journal of Statistical Software* **100**, 1–54 (2021).
77. Matthew, P. *et al.* geiger v2.0: an expanded suite of methods for fitting macroevolutionary models to phylogenetic trees. *Bioinformatics* **30**, 2216–2218 (2014).
78. Pagel, M. Inferring the historical patterns of biological evolution. *Nature* **401**, 877–884 (1999).
79. R Core Team. R: A language and environment for statistical computing. (2021).

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Author contributions

Garben Logghe, Femke Batsleer, Dirk Maes and Dries Bonte conceived the framework of the study. Garben Logghe collected the trait data. Guillermo Fandos and Garben Logghe developed the statistical

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Ethics declarations

The authors declare that they have no competing interests.