Article:
Mair, L, Thomas , C D, Anderson, B J et al. (3 more authors) (2012) Temporal variation in responses of species to four decades of climate warming. Global Change Biology, 18. pp. 2439-2447. ISSN 1354-1013

Abundance changes and habitat availability drive species' responses to climate change

Louise Mair[1], Jane K. Hill[1], Richard Fox[2], Marc Botham[3], Tom Brereton[2] & Chris D. Thomas[1]

[1]Department of Biology, University of York, Wentworth Way, York, YO10 5DD, UK.

[2]Butterfly Conservation, Manor Yard, East Lulworth, Wareham, BH20 5QP, Dorset, UK.

[3]Centre for Ecology & Hydrology, Maclean Building, Benson Lane, Crowmarsh Gifford, Wallingford, Oxfordshire, OX10 8BB, UK.

Supplementary Information

Supplementary methods

Determinants of change in distribution area

The availability of distribution data was determined by the occurrence of national recording efforts used to produce butterfly distribution atlases[14,27]. Due to the vast spatial extent of data collection, annual data did not achieve sufficient spatial coverage for robust analyses and so data were necessarily grouped into periods of several years. Choice of study periods were this selected as 1970-82 to 1995-99 (first study period) and 1995-99 to 2005-09 (second study period) corresponding to national atlas recording periods. Change in species' distribution area was calculated as the percentage change in the number of 10 km Ordnance Survey grid squares with records. Sub-sampling was carried out on the distribution dataset prior to analysis, to account for the large increase in recording effort over time. For example, there was an increase from 185,649 records in 1970-82 to 1,710,586 records in 1995-99[27]. Sub-sampling was carried out per 10 km grid square using an established method[27], and aimed to achieve a spatially and temporally consistent recording effort across Britain over time. Thus for each 10 km grid square, sub-samples were taken to produce a consistent number of records of each temporal resolution (records can be collected over a day, month or year) over time. Sub-sampling was carried out 100 times per time period and the mean values of distribution change per species obtained were used in analyses.

A mobility score[17] was used to represent species' dispersal ability. The mobility score was determined by expert opinion from surveys[17]. This score was correlated with species' wingspan (linear regression $R^2 = 0.47$, $P<0.001$ taken from publication[29]) and another movement index[30] created using a composite of mobility variables, including some of the distribution data used in this analysis (linear regression, $F_{1,31}=47.78$, $R^2=0.59$, $P<0.001$). These relationships suggest that the mobility score from expert opinion is relatively robust.

Habitat availability for each species was quantified as the proportion of each species' breeding habitat in the landscape using LCM2000[19] (for the first study period; 1970-82 to 1995-99) and LCM2007[18] (for the second study period; 1995-99 to 2005-09) 25m resolution raster data. Land cover categories considered to be species' breeding habitat were identified using expert opinion[14], and their importance was weighted based on the frequency with which species' distribution records were from grid squares containing that land cover type. Weighting was based by computing the total number of 100 m grid square records containing both the species of interest and its breeding land cover type; this value was then divided by the total number of 100 m grid records of any butterfly species containing the focal species' habitat land cover type. This gives a metric for the frequency of a given butterfly species in a particular land cover category, relative to records of all butterfly species. Only grid cells within the Ordnance Survey 100 km grid squares of the focal species' distribution were included to control for other factors limiting species' ranges such as dispersal and climate. This provided a method for weighting each land cover type in relation to the focal species' use of the habitat (Table S2). The proportion of habitat available at the species' distribution leading edge (defined as the 10 km grid squares which were unoccupied at the start of the study period, but colonised by the end of the study period) was estimated from land cover datasets and multiplied by the species' habitat weighting, to give an index of habitat availability for each species. For species breeding in more than one habitat type, values were summed across all breeding habitats to produce the index. The habitat availability index was then transformed (log_{10}) to give a normalised distribution.

Change in abundance was calculated using only continuously-occupied transect sites in order to exclude population increases that occur following colonisation. Thus for 1995-99 to 2005-09, sites had to be continuously occupied by a species since 1990 to be included (1-31 transects per species, median = 7.6). For 1970-82 to 1995-99, the lack of early data (UKBMS started in 1976[16]) meant that sites had to be continuously occupied from 1982 to be included (1-25 transects per species, median = 5). For each species, abundance trends were computed from fitting mixed models by regressing log_{10} abundance index against year, with transect site as a random variable.

We employed an information-theoretic approach to identify the best models for explaining distribution changes in relation to abundance trends, habitat availability and dispersal ability. For each of the two study periods (1970-82 to 1995-99 and 1995-99 to 2005-09), we constructed general linear models to assess distribution change against all three explanatory variables (habitat availability, dispersal ability and abundance change) and their interactions (the literature provided evidence for linear relationships between distribution change and change in abundance[5], dispersal ability[1] and habitat availability[31], as did initial data exploration). Interactions between habitat availability and dispersal might be expected if the effect of habitat availability on expansion depended on the dispersal rate. Also, we might expect that if abundance trends were related to change in distribution area, then positive effects of habitat availability and dispersal ability might be contingent on stable or increasing abundance trends. Thus all interactions between variables were explored in our analyses. Explanatory variables were standardized using the function standardize in the package arm (in the statistical program R[28]) and the function dredge in the package MuMIn was used to rank models based on AICc values and Akaikes weights. Where Δ AICc < 2, model averaging was used (only models with Δ AICc < 2 relative to the top-ranked model were included in model averaging), otherwise the model with the lowest AICc value was considered the best fit. Change in abundance was calculated from a different number of transect sites for each species, and therefore our confidence in the estimates of this variable differed among species, so we weighted species abundance trend data by the inverse of the standard error of change in abundance. These analyses with weighting were then evaluated against models which did not include weights, and weighting was found to be the better model for distribution change in the second study period (both when species' change in abundance was computed from continuously-occupied transect sites and when it was computed across all transect sites, Table S4b and d).

Colonisation distance distributions

Distributions of colonisation distances were extracted from the BNM dataset for the second study period (1995-99 to 2005-09; data from the earlier period 1970-82 were of too low spatial resolution and coverage for this analysis). Analyses were carried out at 1km grid resolution and only colonisations occurring at species' distribution leading edges were included (defined as 10 km grid squares which were unoccupied in 1995-99 but colonised by

2005-09; N = 11 species, total colonisations = 12234 colonisations at 1km grid resolution, 14-1722 per species); colonisations occurring in 10 km grid squares where the species was already present were considered to be distribution infilling and were not included in these analyses.

Colonisation distances were extracted in R. The function ndist2 in the package splancs was implemented to calculate the straight line distance from each new colony (grid square centre point) in 2005-09 to the nearest existing colony (grid square centre point) present in 1995-99. Records were included regardless of whether one individual or multiple individuals of species were recorded. There are, however, likely to be effects of spatial and temporal variation in recording effort, thus we explored different definitions of 'existing' and 'new' colonies (see Fig. S1). Existing colonies can be considered to be (i) any 1 km grid square where the species was recorded in 1995-99, or they can be considered to be (ii) only the 1 km grid squares where the species was recorded in both 1995-99 and 2005-09. New colonies can be considered to be (i) any new 1 km grid square where a species was first recorded in 2005-09, or (ii) only 1 km grid squares where the species was known to be absent in 1995-99 (i.e. the grid square was visited but the species was not recorded), and colonised in 2005-09.

We elected to present results using the most rigorous definitions, thus existing colonies were those recorded in both 1995-99 and 2005-09, and new colonies were those which were visited in 1995-99 but the species was not recorded present until 2005-09. Colonisation distance distributions for each species were binned at 2 km intervals and fitted with an inverse power function, which is a better fit than the negative exponential distribution for fat-tailed distributions[33]. Since colonisation kernels describe a curve rather than a single value, the median distance (i.e. the distance at which the cumulative proportion of frequencies of colonisation distances was 0.5) was used as a summary value of the fitted distributions (Fig 2,

Table S5). A multi-model inference framework was applied following the same methods as outlined above for analysing distribution changes, to determine relationships between median colonisation distance and habitat availability, dispersal ability and change in abundance (Table S6).

In order to determine how our results varied according to the different definitions of existing and new colonies, we extracted colonisation distance distributions using all alternative combinations and applied all alternative median colonisation distances to our analyses. In each case, habitat availability was found to be the most important explanatory variable, with some less important positive associations shown for dispersal ability and change in abundance (Table S7). This suggests that recording effort has a quantitative impact on our results, but that this effect is not sufficient to change our qualitative conclusions, which maintain that habitat availability is the most important variable for determining colonisation distance once the expansion is taking place.

Phylogenetic analyses

In order to assess the importance of species' phylogenetic relationships in our analyses, we used AICc values and Akaike weights to compare global models incorporating phylogenetic structure against global models without phylogenetic structure. A phylogenetic tree for European butterflies was obtained from the literature[33] and branch lengths were calculated based on Grafen's methods using the function compute.brln in the package ape in R[28]. The phylogenetic tree was then trimmed to include only the study species. We built generalized least squares (GLS) models containing all three explanatory variables and their interactions (GLS models produce the same results as linear models but are directly comparable with models including phylogeny), and used AICc values and Akaike weights to compare these GLS models against phylogenetic generalized least squares (PGLS) models incorporating phylogeny as the within-group correlation structure. We found that models incorporating phylogeny had consistently higher AICc scores and lower Akaike weights than models without phylogeny (Table S3), and therefore were a poorer fit to the data.

Phylogenetic analyses make the assumption that a phylogenetic signal is present in the data[34], therefore if no signal is detected it may not be appropriate to carry out phylogenetic analyses[35]. We tested whether a phylogenetic signal was present in our dataset in order to determine whether the poorer fit of the PGLS models was due to a lack of phylogenetic signal. We used the pgls function in the R package caper to estimate the value of λ (a branch length scaling parameter) using maximum likelihood. Where $\lambda = 0$ there is no evidence of a phylogenetic signal, and where $\lambda = 1$ there is strong support for a Brownian model of evolution[34,36]. We found that in all cases there was no evidence for a phylogenetic signal in our data (Table S3). Detection of a phylogenetic signal is reliant on sample size as well as the accuracy of the phylogenetic tree and the data[37] therefore a lack of signal may be due to the relatively small sample size of our dataset[38] or uncertainties in Lepidoptera phylogeny. Nevertheless we found no evidence that phylogenetic analyses would be appropriate or that inclusion of phylogenetic correlations would produce models with a better fit to our data. Thus we present data for non-phylogenetically-controlled analyses in the main text.

Supplementary figures

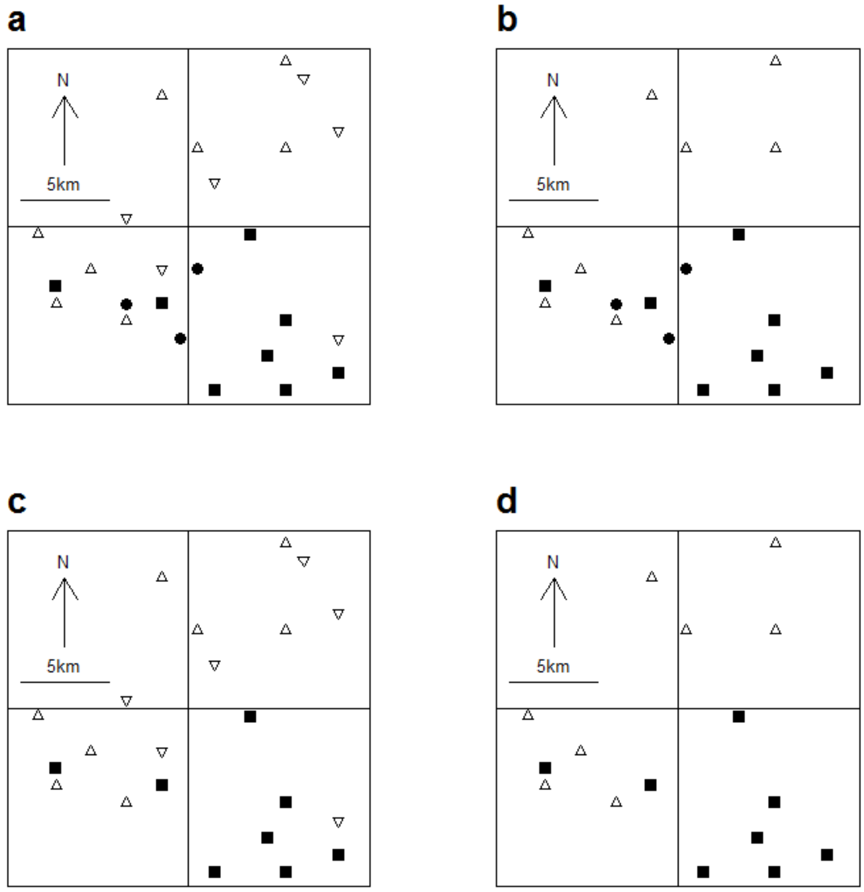

Figure S1. Schematic of different definitions of ‘existing’ and ‘new’ colonies, illustrating an example of a 20 km x 20 km square area containing butterfly records at a 1km grid square resolution. Existing colonies are 1 km grid squares with a species record in 1995-99 (solid symbols), however these consist of those colonies which were recorded only in 1995-99 (solid circles), or colonies which were recorded in both 1995-99 and 2005-09 (solid squares). New colonies are 1 km grid squares with a new species record in 2005-09 (open symbols), and these consist of grid squares which were visited in 1995-99 and the species was not recorded (upward open triangles), and grid squares which were not visited in 1995-99 so previous absence of the species is not confirmed (downward open triangles). Thus the available combinations of definitions are: **a** any existing colony (solid symbols) and any new colony (open symbols), **b** any existing colony (solid symbols) and previously visited new colonies (upward open triangles) **c** continuously occupied existing colonies (solid squares) and any new colonies (open symbols), and **d** continuously occupied existing colonies (solid squares) and previously visited new colonies (upward open triangles). The results of using different definitions are shown in Table S7.

Supplementary tables

Table S1. Species' change in distribution area, change in abundance, dispersal ability and habitat availability in the first and second study period.

		First study period (1970-82 to 1995-99)				Second study period (1995-99 to 2005-09)			
Species	Dispersal ability*	Change in distribution area (% yr^{-1})‡	Change in abundance at continuously occupied sites (% yr^{-1})§	Change in abundance across all sites (% yr^{-1}) §	Habitat availability†	Change in distribution area (% yr^{-1})‡	Change in abundance at continuously occupied sites (% yr^{-1}) §	Change in abundance across all sites (% yr^{-1}) §	Habitat availability†
Aglais io	39	0.55	1.06	3.30	0.039	1.71	-6.09	-2.99	0.015
Anthocharis cardamines	32	0.65	3.80	1.52	0.080	-0.02	-4.28	-0.96	0.021
Aphantopus hyperantus	16	0.75	1.57	6.82	0.005	0.77	-2.37	2.49	0.007
Argynnis paphia	31	-1.54	0.38	0.86	0.006	1.06	6.84	3.45	0.008
Aricia agestis	12	1.06	1.27	0.82	0.007	0.61	-9.23	-5.20	0.003
Boloria euphrosyne	18	-3.09	5.56	-3.28	0.005	-	-	-	-
Boloria selene	19	-1.68	4.28	-2.59	0.012	-1.33	29.38	-1.91	0.014
Callophrys rubi	14	-1.53	-23.65	-0.53	0.006	0.39	-21.17	-3.35	0.014
Celastrina argiolus	34	-	-	-	-	-0.87	-19.15	-3.58	0.017
Cupido minimus	1	-2.10	-12.62	0.41	0.001	-	-	-	-
Erynnis tages	10	-2.67	2.02	-1.04	0.003	-0.72	-53.32	-2.28	0.001
Gonepteryx rhamni	36	-0.15	-7.23	0.26	0.035	-0.10	-2.22	-0.01	0.029
Hesperia comma	15	-0.71	10.09	13.70	0.001	3.55	-11.75	-2.07	0.001
Hipparchia semele	22	-2.41	-0.57	-2.21	0.004	-2.06	4.45	-4.09	0.002
Lasiommata megera	30	-2.24	-17.58	-4.07	0.008	-2.18	-17.59	-4.32	0.008
Limenitis camilla	27	-	-	-	-	1.37	-4.53	-1.16	0.006
Lycaena phlaeas	26	-0.88	-3.41	0.49	0.011	-0.65	-11.54	-2.86	0.010
Melanargia galathea	24	0.61	5.50	3.81	0.008	0.03	-2.22	-2.54	0.004
Melitaea athalia	5	-1.05	4.88	-3.71	0.002	-	-	-	-
Pararge aegeria	23	1.43	3.98	2.89	0.037	2.13	5.78	4.05	0.022
Pieris rapae	40	-0.31	-2.31	0.63	0.032	-0.53	-7.14	-3.19	0.016
Plebejus argus	2	-	-	-	-	-0.65	-10.11	-3.55	0.002
Polygonia c-	33	1.62	-4.21	4.48	0.029	0.68	6.51	3.23	0.019

album									
Polyommatus bellargus	8	-1.42	7.44	0.53	0.003	0.27	11.93	3.31	0.002
Polyommatus coridon	11	-2.04	19.30	2.41	0.004	-0.05	-5.30	-3.78	0.001
Pyronia tithonus	21	0.66	-3.50	-0.58	0.031	-0.35	-7.93	-2.85	0.020
Ochlodes sylvanus	20	-0.49	-2.65	1.61	0.028	-0.87	-19.15	-4.77	0.014
Thymelicus sylvestris	19	0.30	-6.15	0.70	0.012	-0.32	-20.37	-10.13	0.012

* Dispersal ability is a ranked index from expert opinion[17]

‡ Change in distribution area is the percentage change in the number of 10km grid squares occupied per year (from BNM data[14], see supplementary methods)

§ Change in abundance was calculated using BMS data[15] at continuously occupied transect sites (where the focal species was present every year during the study period) and across all transect sites (see supplementary methods)

†Habitat availability from LCM 2000[19] and LCM2007[18] (see supplementary methods and Table S2)

Missing values indicate insufficient species' data for the species to be included in analyses for that study period.

Table S2. Habitat availability data for each species, giving species' scientific names and the land cover category(s) which they are considered to use as breeding habitat.

a 1970-82 to 1995-99

Species	Land cover category*		Proportion in landscape†	Weight‡	Available§	Total habitat availability¶
Aglais io	1.1	Broadleaved woodland	0.0687	0.2849	0.0195	0.0393
	17.1	Suburban	0.0508	0.2810	0.0142	
	17.2	Urban	0.0216	0.2531	0.0054	
Anthocharis cardamines	1.1	Broadleaved woodland	0.0708	0.2173	0.0153	0.0798
	5.1	Improved grassland	0.2345	0.1914	0.0448	
	6.1	Neutral grass	0.0510	0.1655	0.0084	
	17.1	Suburban	0.0523	0.2125	0.0111	
Aphantopus hyperantus	5.2	Setaside grass	0.0083	0.1644	0.0013	0.0050
	6.1	Neutral grass	0.0486	0.0746	0.0036	
Argynnis paphia	1.1	Broadleaved woodland	0.1144	0.0514	0.0058	0.0058
Aricia agestis	5.2	Setaside grass	0.0235	0.0835	0.0019	0.0067
	6.1	Neutral grass	0.0178	0.0313	0.0005	
	7.1	Calcareous grass	0.0567	0.0689	0.0039	
	8.1	Acid grass	0.0064	0.0176	0.0001	
	19.1	Supra-littoral sediment	0.0015	0.1273	0.0002	
Boloria euphrosyne	1.1	Broadleaved woodland	0.0918	0.0204	0.0018	0.0052
	9.1	Bracken	0.0091	0.0260	0.0002	
	10.2	Open dwarf shrub heath	0.1276	0.0247	0.0031	
Boloria selene	1.1	Broadleaved woodland	0.0641	0.0198	0.0012	0.0123
	5.2	Setaside grass	0.0013	0.0058	0.0000	
	9.1	Bracken	0.0151	0.0662	0.0010	
	10.2	Open dwarf shrub heath	0.1222	0.0820	0.0100	
Callophrys rubi	5.2	Setaside grass	0.0092	0.0334	0.0003	0.0056
	7.1	Calcareous grass	0.0552	0.0315	0.0017	
	10.2	Open dwarf shrub heath	0.0545	0.0526	0.0028	
	12.1	Bogs	0.0121	0.0597	0.0007	
Cupido minimus	7.1	Calcareous grass	0.0632	0.0208	0.0013	0.0014
	19.1	Supra-littoral sediment	0.0018	0.0601	0.0001	

Erynnis tages	7.1	Calcareous grass	0.0673	0.0411	0.0027	0.0028
	19.1	Supra-littoral sediment	0.0014	0.0607	0.0001	
Gonepteryx rhamni	1.1	Broadleaved woodland	0.0812	0.1805	0.0146	0.0349
	5.2	Setaside grass	0.0129	0.1697	0.0021	
	6.1	Neutral grass	0.0326	0.0719	0.0023	
	17.1	Suburban	0.0725	0.1651	0.0119	
	17.2	Urban	0.0330	0.1141	0.0037	
Hesperia comma	7.1	Calcareous grass	0.0665	0.0210	0.0013	0.0013
Hipparchia semele	7.1	Calcareous grass	0.0460	0.0175	0.0008	0.0039
	10.2	Open dwarf shrub heath	0.0523	0.0511	0.0026	
	18.1	Supra-littoral rock	0.0003	0.3636	0.0001	
	19.1	Supra-littoral sediment	0.0024	0.1532	0.0003	
Lasiommata megera	5.2	Setaside grass	0.0101	0.0446	0.0004	0.0081
	7.1	Calcareous grass	0.0603	0.0807	0.0048	
	8.1	Acid grass	0.0356	0.0751	0.0026	
	19.1	Supra-littoral sediment	0.0010	0.1746	0.0001	
Lycaena phlaeas	5.2	Setaside grass	0.0088	0.1356	0.0012	0.0111
	7.1	Calcareous grass	0.0554	0.1299	0.0072	
	10.2	Open dwarf shrub heath	0.0313	0.0790	0.0024	
	19.1	Supra-littoral sediment	0.0010	0.3013	0.0003	
Melanargia galathea	5.2	Setaside grass	0.0186	0.1200	0.0022	0.0084
	6.1	Neutral grass	0.0213	0.0415	0.0008	
	7.1	Calcareous grass	0.0587	0.0899	0.0052	
Melitaea athalia	1.1	Broadleaved woodland	0.1216	0.0110	0.0013	0.0020
	10.2	Open dwarf shrub heath	0.0177	0.0412	0.0007	
Pararge aegeria	1.1	Broadleaved woodland	0.0745	0.2999	0.0223	0.0370
	17.1	Suburban	0.0647	0.2266	0.0146	
Pieris rapae	5.2	Setaside grass	0.0076	0.3126	0.0023	0.0324
	6.1	Neutral grass	0.0554	0.2488	0.0137	
	17.1	Suburban	0.0470	0.3457	0.0162	
Polygonia c-album	1.1	Broadleaved woodland	0.0798	0.1727	0.0137	0.0288
	17.1	Suburban	0.0669	0.1630	0.0109	
	17.2	Urban	0.0292	0.1410	0.0041	
Polyommatus bellargus	7.1	Calcareous grass	0.0685	0.0526	0.0036	0.0036
Polyommatus	7.1	Calcareous grass	0.0713	0.0503	0.0035	0.0035

coridon						
Pyronia tithonus	5.2	Setaside grass	0.0113	0.3064	0.0034	0.0307
	6.1	Neutral grass	0.0357	0.1613	0.0057	
	7.1	Calcareous grass	0.0623	0.2452	0.0152	
	17.2	Urban	0.0344	0.1814	0.0062	
Ochlodes sylvanus	1.1	Broadleaved woodland	0.0779	0.1621	0.0126	0.0275
	5.2	Setaside grass	0.0109	0.1725	0.0018	
	6.1	Neutral grass	0.0413	0.1213	0.0050	
	7.1	Calcareous grass	0.0597	0.1344	0.0080	
Thymelicus sylvestris	5.2	Setaside grass	0.0113	0.1963	0.0022	0.0120
	6.1	Neutral grass	0.0395	0.1448	0.0057	
	8.1	Acid grass	0.0387	0.1058	0.0040	

b 1995-99 to 2005-09

Species	Land cover category		Proportion in landscape	Weight	Available	Total habitat availability
Aglias io	1	Broadleaved woodland	0.0349	0.2868	0.0100	0.0146
	22	Urban	0.0040	0.2331	0.0009	
	23	Suburban	0.0127	0.2888	0.0036	
Anthocharis cardamines	1	Broadleaved woodland	0.0418	0.1986	0.0083	0.0211
	5	Rough grassland	0.0493	0.1572	0.0077	
	6	Neutral grassland	0.0034	0.2158	0.0007	
	23	Suburban	0.0226	0.1927	0.0043	
Aphantopus hyperantus	5	Rough grassland	0.0458	0.1437	0.0065	0.0072
	6	Neutral grassland	0.0041	0.1484	0.0006	
Argynnis paphia	1	Broadleaved woodland	0.0816	0.0969	0.0079	0.0079
Aricia agestis	5	Rough grassland	0.0285	0.0693	0.0019	0.0025
	6	Neutral grassland	0.0089	0.0440	0.0003	
	7	Calcareous grassland	0.0000	0.2272	0.0001	
	8	Acid grassland	0.0022	0.0239	0.0001	
	18	Supra-littoral sediment	0.0018	0.0597	0.0001	
Boloria selene	1	Broadleaved woodland	0.0412	0.0358	0.0014	0.0139
	5	Rough grassland	0.0576	0.0504	0.0029	
	11	Heather grassland	0.0964	0.0990	0.0095	

Callophrys rubi	5	Rough grassland	0.0508	0.0459	0.0023	0.0140
	7	Calcareous grassland	0.0017	0.1151	0.0002	
	10	Heather	0.0398	0.0833	0.0033	
	11	Heather grassland	0.0629	0.0761	0.0047	
	12	Bog	0.0348	0.0984	0.0034	
Celastrina argiolus	1	Broadleaved woodland	0.0534	0.1026	0.0054	0.0170
	5	Rough grassland	0.0438	0.0724	0.0031	
	23	Suburban	0.0425	0.1978	0.0084	
Erynnis tages	7	Calcareous grassland	0.0005	0.2146	0.0001	0.0010
	10	Heather	0.0194	0.0246	0.0004	
	11	Heather grassland	0.0140	0.0179	0.0002	
	18	Supra-littoral sediment	0.0019	0.0957	0.0001	
Gonepteryx rhamni	1	Broadleaved woodland	0.0513	0.1965	0.0100	0.0285
	5	Rough grassland	0.0388	0.136	0.0052	
	6	Neutral grassland	0.0067	0.1613	0.0010	
	22	Urban	0.0189	0.1058	0.0020	
	23	Suburban	0.0556	0.1815	0.0100	
Hesperia comma	7	Calcareous grassland	0.0075	0.0906	0.0006	0.0006
Hipparchia semele	7	Calcareous grassland	0.0001	0.0377	0.0001	0.0024
	10	Heather	0.0160	0.0494	0.0007	
	11	Heather grassland	0.0365	0.0349	0.0012	
	17	Supra-littoral rock	0.0001	0.0606	0.0001	
	18	Supra-littoral sediment	0.0032	0.0830	0.0002	
	21	Saltmarsh	0.0026	0.0208	0.0001	
Lasiommata megera	5	Rough grassland	0.0520	0.0752	0.0039	0.0080
	7	Calcareous grassland	0.0009	0.1434	0.0001	
	8	Acid grassland	0.0522	0.0731	0.0038	
	18	Supra-littoral sediment	0.0013	0.1279	0.0001	
Limenitis camilla	1	Broadleaved woodland	0.0843	0.0677	0.0057	0.0057
Lycaena phlaeas	5	Rough grassland	0.0486	0.1182	0.0057	0.0095
	7	Calcareous grassland	0.0012	0.1321	0.0001	
	11	Heather grassland	0.0424	0.0816	0.0034	
	18	Supra-littoral sediment	0.0008	0.1591	0.0001	
Melanargia galathea	5	Rough grassland	0.0361	0.0953	0.0034	0.0040
	6	Neutral grassland	0.0070	0.085	0.0005	
	7	Calcareous grassland	0.0001	0.2317	0.0001	

Pararge aegeria	1	Broadleaved woodland	0.0401	0.3293	0.0132	0.0215
	23	Suburban	0.0303	0.2762	0.0083	
Pieris rapae	5	Rough grassland	0.0540	0.1837	0.0099	0.0161
	6	Neutral grassland	0.0028	0.2674	0.0007	
	23	Suburban	0.0174	0.3109	0.0054	
Plebejus argus	10	Heather	0.0038	0.1832	0.0007	0.0016
	11	Heather grassland	0.0049	0.1858	0.0009	
Polygonia c-album	1	Broadleaved woodland	0.0504	0.2019	0.0101	0.0190
	22	Urban	0.0111	0.1470	0.0016	
	23	Suburban	0.0346	0.2091	0.0072	
Polyommatus bellargus	7	Calcareous grassland	0.0086	0.2050	0.0017	0.0017
Polyommatus coridon	7	Calcareous grassland	0.0082	0.1573	0.0013	0.0013
Pyronia tithonus	5	Rough grassland	0.0523	0.1938	0.0101	0.0202
	6	Neutral grassland	0.0056	0.2131	0.0011	
	7	Calcareous grassland	0.0022	0.1985	0.0004	
	23	Suburban	0.0467	0.1821	0.0085	
Ochlodes sylvanus	1	Broadleaved woodland	0.0515	0.1384	0.0071	0.0138
	5	Rough grassland	0.0479	0.1216	0.0058	
	6	Neutral grassland	0.0062	0.1222	0.0007	
	7	Calcareous grassland	0.0005	0.1292	0.0001	
Thymelicus sylvestris	5	Rough grassland	0.0482	0.1286	0.0062	0.0120
	6	Neutral grassland	0.0064	0.1434	0.0009	
	8	Acid grassland	0.0520	0.0938	0.0048	

a the earlier study period (1970-82 to 1995-99, LCM2000[19])

b the later study period (1995-99 to 2005-09, LCM2007[18])

* land cover category numbers given refer to the class number associated with each land cover category in the respective datasets

† the proportional area that the specific land cover type covers at the species' distribution leading edges

‡ calculated by dividing the number of 100m BNM records which contained both the species record and their preferred land cover type, by the number of 100m BNM records (of any species) that contained the land cover type

§ proportion of land cover type at the distribution leading edge multiplied by the weight

¶ the sum of 'available' for each species

Note that these land cover types are relatively coarse and hence habitat availability is a relative metric and does not represent the absolute proportion of landscape that is actually suitable habitat.

Table S3. Comparison of global models with and without phylogenetic structure using AICc and Akaike weights, and maximum likelihood estimation of the parameter λ.

	Global model without phylogenetic correlations*		Global model including phylogenetic correlations†		Maximum likelihood estimates for λ ‡
Response variable	AICc	Weight	AICc	Weight	λ estimate (95% CI)
1970-82 to 1995-99					
Distribution change (abundance at continuously occupied sites)	87.59	0.9999	107.62	<0.0001	0 (NA, 0.482)
Distribution change (abundance at all sites)	73.78	0.9999	95.06	<0.0001	0 (NA, 0.502)
1995-99 to 2005-09					
Distribution change (abundance at continuously occupied sites)	97.09	0.9893	106.13	0.0107	0 (NA, 0.338)
Distribution change (abundance at all sites)	91.21	0.9978	103.44	0.0022	0 (NA, 0.351)
Median colonisation distance	103.56	0.7231	105.47	0.2769	0 (NA, 0.598)

* Generalized least squares global model with all three explanatory variables (change in abundance, habitat availability and dispersal ability) and their interactions but no phylogenetic structure.

† Phylogenetic generalized least squares global model with all three explanatory variables and their interactions, and species' phylogenetic relationships incorporated as the within-group correlation structure.

‡ Maximum likelihood estimates for λ. A global model was built including phylogenetic correlations with a Brownian model of evolution assumed and maximum likelihood was used to estimate the value of λ (a branch length scaling parameter). Where $\lambda = 0$ there is no evidence of phylogenetic signal, and where $\lambda = 1$ there is strong support that the trait matches a Brownian model of evolution.

Table S4. Alternative general linear models assessed using an information-theoretic approach.

a Change in distribution area (1970-82 to 1995-99, species' change in abundance from continuously-occupied transect sites only)

Intercept	Abundance	Habitat	Dispersal	Abundance x Habitat	Abundance x dispersal	Habitat x dispersal	df	logLik	AICc	ΔAICc	Weight	Adj R^2
-0.67		1.69					3	-36.9	81.0	0.00	0.480	0.35
-0.67		2.20	-0.66				4	-36.5	82.9	1.91	0.185	0.35
-0.67	0.35	1.74					4	-36.6	83.2	2.22	0.158	0.34
-0.67	0.31	2.21	-0.62				5	-36.2	85.5	4.53	0.050	0.33
-0.71		2.20	-0.65			0.25	5	-36.4	86.0	4.99	0.040	0.32
-0.67	0.33	1.74		-0.06			5	-36.6	86.4	5.37	0.033	0.31
-0.64	0.50	2.11	-0.46		0.75		6	-35.9	88.5	7.54	0.011	0.31
-0.68	0.18	2.30	-0.70	-0.49			6	-36.1	88.9	7.90	0.009	0.30
-0.71	0.31	2.21	-0.61			0.25	6	-36.1	89.0	7.96	0.009	0.30
-0.67			1.05				3	-40.9	89.0	8.02	0.009	0.11
-0.67							2	-42.9	90.3	9.34	0.004	0.00
-0.66	0.17	2.38	-0.59	-2.79	2.47		7	-34.9	90.4	9.42	0.004	0.33
-0.67	0.29		1.09				4	-40.8	91.6	10.55	0.002	0.08
-0.66	0.49	2.12	-0.46		0.72	0.11	7	-35.9	92.4	11.45	0.002	0.28
-0.75	0.14	2.31	-0.72	-0.62		0.36	7	-36.0	92.7	11.67	0.001	0.27
-0.67	0.12						3	-42.9	92.9	11.89	0.001	-0.04
-0.61	0.65		1.25		1.43		5	-40.1	93.4	12.38	0.001	0.09
-0.71	0.14	2.39	-0.61	-2.85	2.44	0.24	8	-34.9	94.8	13.75	0.000	0.30

b Change in distribution area (1995-99 to 2005-09, species' change in abundance from continuously-occupied transect sites)

Intercept	Abundance	Habitat	Dispersal	Abundance x Habitat	Abundance x dispersal	Habitat x dispersal	df	logLik	AICc	ΔAICc	Weight	Adj R^2
0.23	1.43						3	-39.0	85.1	0.00	0.411	0.15
0.29	1.52	-0.36					4	-38.7	87.5	2.35	0.127	0.13
0.26	1.49		-0.30				4	-38.8	87.6	2.42	0.123	0.12
0.31							2	-41.5	87.6	2.42	0.123	0.00
0.24	1.56	-0.35		1.28			5	-38.0	89.2	4.08	0.053	0.13
0.33			-0.12				3	-41.5	90.1	4.96	0.034	-0.04
0.33		-0.10					3	-41.5	90.1	4.98	0.034	-0.04
0.22	1.65		-0.33		1.09		5	-38.5	90.2	5.03	0.033	0.10
0.29	1.53	-0.25	-0.17				5	-38.7	90.6	5.43	0.027	0.09
0.24	1.57	-0.25	-0.16	1.28			6	-38.0	92.6	7.51	0.010	0.09
0.33		-0.04	-0.10				4	-41.5	93.0	7.82	0.008	-0.09
0.25	1.68	-0.23	-0.21		1.07		6	-38.4	93.5	8.41	0.006	0.06
0.24	1.54	-0.17	-0.24			0.30	6	-38.7	94.0	8.87	0.005	0.04
0.32		-0.01	-0.12			0.09	5	-41.5	96.1	10.97	0.002	-0.14
0.25	1.50	-0.26	-0.14	1.59	-0.57		7	-38.0	96.5	11.37	0.001	0.05
0.25	1.56	-0.27	-0.14	1.30		-0.10	7	-38.0	96.6	11.43	0.001	0.05
0.22	1.68	-0.19	-0.24		1.04	0.15	7	-38.4	97.5	12.32	0.001	0.01
0.26	1.49	-0.29	-0.11	1.62	-0.58	-0.11	8	-38.0	100.9	15.77	0.000	0.00

c Change in distribution area (1970-82 to 1995-99, species' abundances from all transect sites)

Intercept	Abundance	Habitat	Dispersal	Abundance x Habitat	Abundance x dispersal	Habitat x dispersal	df	logLik	AICc	ΔAICc	Weight	Adj R^2
-0.65	2.23	1.50		1.78			5	-27.7	68.6	0.00	0.241	0.66
-0.65	2.21	2.20	-0.86	1.56			6	-26.0	68.7	0.14	0.224	0.69
-0.70	1.77	2.28	-0.76		1.86		6	-26.4	69.4	0.80	0.161	0.68
-0.67	1.49	2.56	-1.03				5	-28.3	69.7	1.14	0.136	0.65
-0.67	1.39	1.76					4	-30.3	70.6	2.04	0.087	0.60
-0.57	2.28	2.18	-0.86	1.68		-0.40	7	-25.8	72.2	3.63	0.039	0.68
-0.57	1.87	2.24	-0.72		2.30	-0.69	7	-25.8	72.2	3.63	0.039	0.68
-0.67	2.11	2.19	-0.79	1.08	0.81		7	-25.8	72.3	3.71	0.038	0.68
-0.66	1.49	2.56	-1.03			-0.04	6	-28.3	73.2	4.65	0.024	0.63
-0.56	2.16	2.16	-0.75	0.96	1.32	-0.62	8	-25.4	75.8	7.21	0.007	0.67
-0.67		1.69					3	-36.9	81.0	12.42	0.000	0.35
-0.71	1.76		1.06		3.10		5	-34.6	82.4	13.79	0.000	0.41
-0.67		2.20	-0.66				4	-36.5	82.9	14.33	0.000	0.35
-0.67	1.25		0.97				4	-37.5	85.0	16.43	0.000	0.29
-0.71		2.20	-0.65			0.25	5	-36.4	86.0	17.41	0.000	0.32
-0.67	1.31						3	-39.7	86.5	17.93	0.000	0.19
-0.67			1.05				3	-40.9	89.0	20.44	0.000	0.11
-0.67							2	-42.9	90.3	21.76	0.000	0.00

d Change in distribution area (1995-99 to 2005-09, species' abundances from all transect sites)

Intercept	Abundance	Habitat	Dispersal	Abundance x Habitat	Abundance x dispersal	Habitat x dispersal	df	logLik	AICc	ΔAICc	Weight	Adj R^2
0.09	1.26						3	-37.6	82.4	0.00	0.518	0.35
0.10	1.30	-0.28					4	-37.4	84.8	2.46	0.151	0.36
0.09	1.29		-0.18				4	-37.5	85.1	2.71	0.134	0.33
0.15	1.54	-0.29		-1.11			5	-37.1	87.3	4.92	0.044	0.33
0.10							2	-41.4	87.3	4.95	0.044	0.00
0.11	1.30	-0.29	0.02				5	-37.4	88.0	5.62	0.031	0.33
0.10	1.27		-0.17		-0.31		5	-37.5	88.2	5.81	0.028	0.31
0.10			0.06				3	-41.4	89.9	7.53	0.012	-0.04
0.10		-0.05					3	-41.4	89.9	7.54	0.012	-0.04
0.15	1.54	-0.33	0.07	-1.13			6	-37.1	90.8	8.42	0.008	0.30
0.11	1.29	-0.28	0.02		-0.24		6	-37.4	91.5	9.09	0.005	0.30
0.09	1.30	-0.26	0.00			0.10	6	-37.4	91.5	9.12	0.005	0.30
0.11		-0.15	0.17				4	-41.4	92.7	10.34	0.003	-0.09
0.15	1.65	-0.38	0.09	-1.55	0.65		7	-37.0	94.6	12.17	0.001	0.27
0.11	1.53	-0.25	0.02	-1.18		0.26	7	-37.0	94.7	12.29	0.001	0.26
0.09	1.28	-0.23	-0.01		-0.27	0.16	7	-37.4	95.4	13.00	0.001	0.27
-0.01		0.06	0.03			0.72	5	-41.2	95.6	13.20	0.001	-0.14
0.12	1.64	-0.32	0.06	-1.56	0.61	0.19	8	-37.0	98.9	16.55	0.000	0.23

a distribution change in the first study period (1970-82 to 1995-99, using species' change in abundance at continuously-occupied transect sites)

b distribution change in the second study period (1995-99 to 2005-09, using species' change in abundance at continuously-occupied sites only)

c distribution change in the first study period (using species' change in abundance across all transect sites)

d distribution change in the second study period (using species' change in abundance across all transect sites)

Variable estimates are given, along with the log likelihood, AICc value, difference in AICc between the top model and all other models (ΔAICc), Akaike weights and the adjusted R-squared value for each model. Models are ordered starting with the best fit.

Table S5. Summary data for colonisation distance distributions for each species for the second study period (1995-99 to 2005-09).

Species	Sample size†	Inverse power function‡		
		Fitted equation	R^2	Median distance (km)
Aglais io	1285	$I = 2.52 (\pm 0.48) D^{1.39 (\pm 0.13)}$	0.71	10.06
Anthocharis cardamines	384	$I = 2.00 (\pm 0.38) D^{1.56 (\pm 0.11)}$	0.86	5.61
Aphantopus hyperantus	1018	$I = 3.38 (\pm 0.48) D^{2.13 (\pm 0.13)}$	0.85	6.78
Argynnis paphia	444	$I = 3.19 (\pm 0.40) D^{1.72 (\pm 0.10)}$	0.81	9.57
Aricia agestis	569	$I = 1.68 (\pm 0.62) D^{1.30 (\pm 0.22)}$	0.65	6.24
Boloria selene	258	$I = 1.93 (\pm 0.66) D^{1.49 (\pm 0.23)}$	0.68	5.75
Callophrys rubi	408	$I = 2.20 (\pm 0.65) D^{1.57 (\pm 0.21)}$	0.69	6.33
Celastrina argiolus	597	$I = 3.42 (\pm 0.46) D^{1.96 (\pm 0.12)}$	0.82	8.18
Erynnis tages	153	$I = 2.17 (\pm 0.47) D^{1.63 (\pm 0.15)}$	0.82	4.70
Gonepteryx rhamni	556	$I = 2.78 (\pm 0.29) D^{1.91 (\pm 0.07)}$	0.90	6.19
Hesperia comma	48	$I = 1.70 (\pm 0.60) D^{1.49 (\pm 0.22)}$	0.73	4.97
Hipparchia semele	190	$I = 1.33 (\pm 0.19) D^{0.90 (\pm 0.05)}$	0.86	9.55
Lasiommata megera	514	$I = 1.99 (\pm 0.75) D^{1.64 (\pm 0.27)}$	0.67	5.15
Limenitis camilla	241	$I = 2.39 (\pm 0.37) D^{1.70 (\pm 0.11)}$	0.87	6.13
Lycaena phlaeas	764	$I = 3.01 (\pm 0.47) D^{2.25 (\pm 0.14)}$	0.88	5.18
Melanargia galathea	246	$I = 2.13 (\pm 0.23) D^{1.35 (\pm 0.05)}$	0.89	8.03
Pararge aegeria	1722	$I = 4.37 (\pm 0.48) D^{2.05 (\pm 0.11)}$	0.79	12.69
Pieris rapae	538	$I = 2.39 (\pm 0.21) D^{1.61 (\pm 0.05)}$	0.93	6.76
Plebejus argus	14	$I = 0.82 (\pm 0.40) D^{0.77 (\pm 0.16)}$	0.63	7.12
Polygonia c-album	750	$I = 3.28 (\pm 0.33) D^{1.74 (\pm 0.08)}$	0.86	9.74
Polyommatus bellargus	52	$I = 1.23 (\pm 0.43) D^{1.21 (\pm 0.16)}$	0.78	4.91
Polyommatus coridon	71	$I = 1.04 (\pm 0.31) D^{0.97 (\pm 0.11)}$	0.80	5.94
Pyronia tithonus	258	$I = 1.38 (\pm 0.24) D^{1.36 (\pm 0.07)}$	0.92	4.61
Ochlodes sylvanus	614	$I = 2.36 (\pm 0.94) D^{1.99 (\pm 0.34)}$	0.67	4.62
Thymelicus sylvestris	540	$I = 1.76 (\pm 0.27) D^{1.46 (\pm 0.08)}$	0.90	5.37

† sample size is number of new 1 km colonies included in analysis

‡ the fitted inverse power function equation with the R-squared value indicating the fit of the function to the raw data and the median colonisation distance from the fitted equation

Total sample size = 12234 colonisations at the 1 km resolution.

Table S6. Alternative general linear models assessed using an information-theoretic approach for species' median colonisation distance in the later study period (1995-99 to 2005-09).

Intercept	Abundance	Habitat	Dispersal	Abundance x Habitat	Abundance x dispersal	Habitat x dispersal	df	logLik	AICc	ΔAICc	Weight	Adj R^2
7.77		3.80					3	-20.0	49.5	0.00	0.476	0.55
7.77	1.46	3.62					4	-18.7	52.1	2.61	0.129	0.60
7.77		2.77	1.73				4	-18.8	52.3	2.83	0.116	0.59
7.77			3.38				3	-21.5	52.4	2.93	0.110	0.41
7.67	1.35	3.93		3.66			5	-15.2	52.5	2.99	0.107	0.76
7.77							2	-25.0	55.5	6.02	0.023	0.00
7.77	1.24		3.12				4	-20.8	56.3	6.82	0.016	0.42
7.77	1.25	2.77	1.47				5	-17.7	57.3	7.85	0.009	0.62
7.77	1.90						3	-24.1	57.7	8.18	0.008	0.05
7.53		3.23	1.41			1.74	5	-18.6	59.2	9.72	0.004	0.55
7.63	2.07		2.77		2.90		5	-20.1	62.2	12.75	0.001	0.41
7.68	1.28	3.58	0.56	3.31			6	-15.0	63.0	13.55	0.001	0.73
7.70	1.67	2.57	1.41		1.48		6	-17.4	67.7	18.27	0.000	0.58
7.73	1.21	2.86	1.42			0.32	6	-17.7	68.3	18.83	0.000	0.56
7.73	0.82	4.02	0.39	4.15	-1.66		7	-14.7	80.6	31.15	0.000	0.70
7.64	1.25	3.65	0.51	3.30		0.27	7	-15.0	81.4	31.87	0.000	0.67
7.57	1.61	2.77	1.27		1.65	0.86	7	-17.3	86.0	36.49	0.000	0.51
7.78	0.83	3.96	0.43	4.21	-1.77	-0.32	8	-14.6	117.3	67.80	0.000	0.62

Variable estimated are given, along with the log likelihood, AICc value, difference in AICc between the top model and all other models (ΔAICc), Akaike weights and the adjusted r-squared value for each model. Models are ordered starting with the best fit.

Table S7. Average model parameter estimates, standard errors and relative variable importance for median colonisation distance using different definitions of existing and new colonies.

Best-fit model variables	Estimate	Unconditional S.E.	Relative variable importance*
(a) Using any existing and any new			
Habitat availability	3.441	0.857	1
Change in abundance	1.372	0.668	0.62
Habitat x abundance	4.414	1.272	0.62
(b) Any existing and previously visited new			
Habitat availability	3.319	1.023	0.79
Change in abundance	1.445	0.783	0.43
Habitat x abundance	5.074	1.492	0.43
Dispersal ability	2.975	1.291	0.21
(c) Continuously occupied existing and any new			
Habitat availability	3.776	1.143	1
Dispersal ability	2.039	1.018	0.4

a any existing and any new colonies (SI Fig 1a)

b any existing and previously visited new colonies (SI Fig 1b)

c continuously occupied existing colonies and any new colonies (SI Fig. 1c)

* Relative importance of variables of 1 indicates that the variable was present in all top models, or was the only variable when model averaging was not necessary because the difference in AICc between the first and second highest ranking models was > 2.

Supplementary References

29 Sekar, S. A meta-analysis of the traits affecting dispersal ability in butterflies: can wingspan be used as a proxy? J. Anim. Ecol. **81**, 174-184 (2012).

30 Dennis, R. L. H. & Shreeve, T. G. Butterflies on British and Irish offshore islands. (Gem Publishing Company, 1996).

31 Hill, J. K. et al. Impacts of landscape structure on butterfly range expansion. Ecology Letters **4**, 313-321 (2001).

32 Chapman, D. S., Dytham, C. & Oxford, G. S. Modelling population redistribution in a leaf beetle: an evaluation of alternative dispersal functions. J. Anim. Ecol. **76**, 36-44 (2007).

33 Cizek, O. & Konvicka, M. What is a patch in a dynamic metapopulation? Mobility of an endangered woodland butterfly, Euphydryas maturna. Ecography **28**, 791-800 (2005).

34 Hernández, C. E. et al. Using phylogenetic information and the comparative method to evaluate hypotheses in macroecology. Methods in Ecology and Evolution **4**, 401-415 (2013).

35 Ashton, K. G. Comparing phylogenetic signal in intraspecific and interspecific body size datasets. Journal of Evolutionary Biology **17**, 1157-1161 (2004).

36 Pagel, M. Inferring the historical patterns of biological evolution. Nature **401**, 877-884 (1999).

37 Blomberg, S. P., Garland, T. & Ives, A. R. Testing for phylogenetic signal in comparative data: behavioural traits are more labile. Evolution **57**, 717-745 (2003).

38 Freckleton, R. P., Harvey, P. H. & Pagel, M. Phylogenetic analysis and comparative data: A test and review of evidence. The American Naturalist **160**, 712-726 (2002).