Electronic Supplementary Material

Evolvability meets biogeography: multi-species analyses reveal greatest evolutionary potential at intermediate levels of environmental favourability

Martínez-Padilla, J., Estrada, A., Early, R. and Garcia-Gonzalez, F.

A – Graphic representation of the methodological approach.

In the *Figure A1* below, we describe graphically a schematic representation of the methodological rationale followed in our paper.

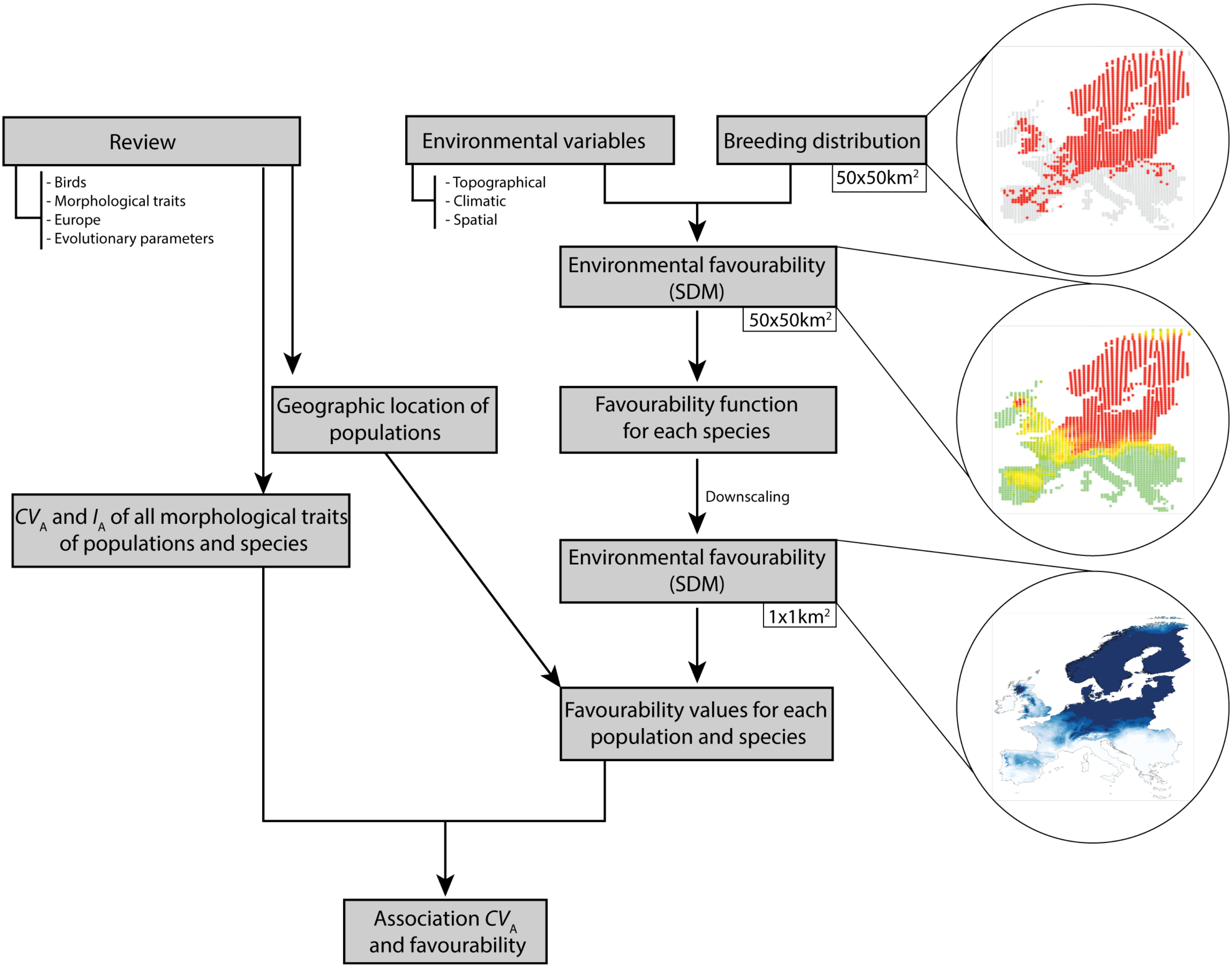


Figure A1. Schematic representation of the methodological approach followed

B – Morphological variables considered

In the *Table B1* below, we show the number of estimations of morphological variables per population and species considered in this study. These traits have been also grouped in body size and body mass, which are the two categories considered in the analyses. This grouping variable is called “trait” in Table 1 of the manuscript.

Morphological trait	**Specific trait**	**Number of estimations**	**Number of populations**	**Number of species**
Body size	Bill depth	7	3	3
	Bill length	10	3	3
	Bill width	6	2	2
	Feather growth	1	1	1
	First primary length	2	1	1
	Skull length	4	1	1
	Tail length	6	2	2
	Tarsus length	46	18	9
	Wing length	17	6	6
	Wing projection	4	1	1
	Head length	12	1	1
Body mass	Weight	20	12	6
	TOTAL	**135**		

Table B1. Sample size for each type of morphological trait.

C – Animal model for pied flycatcher population from southern Europe

To estimate genetic and environmental variance components for adult tarsus length, wing length and body mass for both males and females separately at the time of breeding of pied flycatcher we fitted a univariate animal model using restricted maximum likelihood (REML) in ASReml-R v3.0[1]. We used a long-term and individual-based monitoring of a population located in central Spain followed for over 31 years[2]. The estimation of the additive genetic variance made use of pedigree information for 2860 adults and 5480 captures overall (1522 females, 2917 captures; 1338 males, 2563 captures). Siblings from the same brood for which paternal and/or maternal identity was unknown were assigned a common 'dummy' parental identity to preserve sibship information[3]. Mean maternal and paternal sibship sizes in the pedigree were 6.41 and 4.96, respectively.

The univariate animal model for each trait included age class as a fixed effect with two levels to account for a difference in morphological traits between 1- and > 1-year-old individuals. In addition to the random additive genetic animal effect (a_i), which uses the phenotypic resemblance among related individuals to provide an estimate of the additive genetic variance, we included a permanent environment (pe_i), which accounts for the non-independence of repeated measures made on the same individual in different years due to constant differences in the environmental conditions they experience throughout their lives[4]. Finally, a year effect (y_i) quantifies the covariance among individuals living in the same year and experiencing similar environmental conditions. The variance explained by the additive genetic (a_i), permanent environment (pe_i), year (y_i) and residual (e_i) terms (V_A, V_{PE}, V_Y and V_R, respectively) were estimated using REML.

Estimations of CV_A, I_A, V_A and mean for each phenotypic trait are given in the complete data set compiled accompanying this paper. The exclusion, however, of these parameters for the southern population of pied flycatchers, did not change the outcome of the models (see *Table C1* for comparison with the results given in the main text that included this southern population of pied flycatchers).

	Resolution	**50x50km^2**				**1x1km^2**		
CV_A		*estimate (±SE)*	*t value*	*p*		*estimate (±SE)*	*t value*	*p*
	Intercept	0.0061 (0.0178)	0.346	0.736		0.0073 (0.0180)	0.404	0.695
	Favourability	0.1131 (0.0575)	1.966	0.067		0.1107 (0.0565)	1.960	**0.007**
	Favourability^2	-0.0849 (0.0420)	-2.021	**0.053**		-0.0843 (0.0407)	-2.068	**0.050**
	Trait:size	-0.0050 (0.0039)	-1.305	0.194		-0.0050 (0.0038)	-1.297	0.196

	Method: full-sib	0.0017 (0.0072)	0.243	0.808		-0.0016 (0.0072)	0.224	0.823
	Method: parent-offspring	0.0020 (0.0034)	0.588	0.557		0.0020 (0.0034)	0.590	0.556
I_A		*estimate (±SE)*	*t value*	*p*		*estimate (±SE)*	*t value*	*p*
	Intercept	-0.0004 (0.0006)	-0.451	0.663		-0.0003 (0.0009)	-0.357	0.729
	Favourability	0.0067 (0.0028)	2.343	**0.036**		0.0063 (0.0028)	2.231	**0.047**
	Favourability^2	-0.0052 (0.0020)	-2.584	**0.017**		-0.0048 (0.0019)	-2.481	**0.023**
	Trait:size	-0.0003 (0.0001)	-1.982	**0.049**		-0.0003 (0.0001)	-1.979	**0.050**
	Method: full-sib	-0.000008 (0.000334)	-0.003	0.997		-0.000001 (0.000147)	-0.005	0.996
	Method: parent-offspring	0.0001 (0.0001)	0.691	0.691		0.0001 (0.0001)	0.684	0.495

Table C1. Results of the association between environmental favourability and evolvability (untransformed CV_A and I_A) excluding the values obtained for one population of pied flycatcher whose values of evolvability were not published and instead obtained through an animal model approach (see above).

D — Published studies used to obtain evolvabilities for each species, population and trait.

In the *Table D1* below, we show the references used in this study to obtain all CV_A an I_A values as detailed in the main text. In addition, we include the species to which each reference refers to, the area and country where the study was carried out, and also the number of estimations of evolutionary parameters for the two categories considered in this study, body mass and size. Note that there is also one population that has been added to the ones shown below, a southern population of pied flycatcher (See above, ESM C).

Reference	**Species**	**Area (country)**	**Body mass**	**Size**
Akesson, M., Bensch, S., & Hasselquist, D. (2007). Genetic and phenotypic associations in morphological traits: a long term study of great reed warblers *Acrocephalus arundinaceus*. *Journal of Avian Biology*, **38:** 58–72.	*Acrocephalus arundinaceus*	Lake Kvismaren (Sweden)		8
Akesson, M., Bensch, S., Hasselquist, D., Tarka, M., & Hansson, B. (2008). Estimating heritabilities and genetic correlations: comparing the “animal model” with parent-offspring regression using data from a natural population. *PloS one*, **3:** e1739.	*Acrocephalus arundinaceus*	Lake Kvismaren (Sweden)		21
Cadee, N. (2000). Genetic and environmental effects on morphology and fluctuating asymmetry in nestling barn swallows. *Journal of Evolutionary Biology* **13**: 359-370.	*Hirundo rustica*	Bronderslev (Denmark)		1
Charmantier, A., L. E. B. Kruuk and M. M. Lambrechts (2004). Parasitism reduces the potential for evolution in a wild bird population. *Evolution* **58**: 203-206.	*Parus caeruleus*	Pirio, Corsica (France)		3
Charmantier, A., L. E. B. Kruuk, J. Blondel and M. M. Lambrechts (2004). Testing for microevolution in body size in three blue tit populations. *Journal of Evolutionary Biology* **17**: 732-743.	*Parus caeruleus*	La Rouviere, Corsica Muro, Corsica Pirio, Corsica (France)	1 1 1	1 1 1
Christe, P., A. P. Moller, N. Saino and F. De Lope (2000). Genetic and environmental components of phenotypic variation in immune response and body size of a colonial bird, *Delichon urbica* (the house martin). *Heredity* **85**: 75-83.	*Delichon urbica*	Badajoz (Spain)	1	2
De Neve, L., J. J. Soler, T. Perez-Contreras and M. Soler (2004). Genetic, environmental and maternal effects on magpie nestling-fitness traits under different nutritional conditions: a new experimental approach." *Evolutionary Ecology Research* **6**: 415-431.	*Pica pica*	Hoya de Guadix (Spain)		2
Garant, D., L. E. B. Kruuk, T. A. Wilkin, R. H. McCleery and B. C. Sheldon (2005). Evolution driven by differential dispersal within a wild bird population. *Nature* **433**: 60-65.	*Parus major*	Wytham Woods (UK)	2	
Gienapp, P. and J. Merila (2010). Genetic and environmental effects on a condition-dependent trait: feather growth in Siberian jays. *Journal of Evolutionary Biology* **23**: 715-723.	*Perisoreus infaustus*	Ostrobothnia (Finland)		1
Husby, A., Hille, S. M., & Visser, M. E. (2011). Testing mechanisms of Bergmann’s rule: phenotypic decline but no genetic change in body size in three passerine bird populations. *The American naturalist*, **178:** 202–13.	*Parus major*	Hoge Veluwe Oosterhout Vlieland (Netherlands)	1 1 1	1 1 1
Jensen, H., B. E. Saether, T. H. Ringsby, J. Tufto, S. C. Griffith and H. Ellegren (2003). Sexual variation in heritability and genetic correlations of morphological traits in house sparrow (*Passer domesticus*)." *Journal of Evolutionary Biology* **16**: 1296-1307.	*Passer domesticus*	Helgeland (Norway)	2	8

Jensen, H., I. Steinsland, T. H. Ringsby and B. E. Saether (2008). Evolutionary dynamics of a sexual ornament in the house sparrow (*passer domesticus*): The role of indirect selection within and between sexes. *Evolution* **62**: 1275-1293.	*Passer domesticus*	Helgeland (Norway)	2	8
Kim, S. Y., J. A. Fargallo, P. Vergara and J. Martinez-Padilla (2013). Multivariate heredity of melanin-based coloration, body mass and immunity. *Heredity* **111**: 139-146.	*Falco tinnunculus*	Campo Azálvaro (Spain)	4	
Larsson, K., Rattiste, K., & Lilleleht, V. (1997). Heritability of head size in the common gull *Larus canus* in relation to environmental conditions during offspring growth. *Heredity*, **79**: 201–207.	*Larus canus*	Matsalu National Park (Estonia)		12
Lifjeld, J. T., & Slagsvold, T. (1989). How frequent is cuckoldry in pied flycatchers *Ficedula hypoleuca*?: Problems with the use of heritability estimates of tarsus length. *Oikos*, **54:** 205.	*Ficedula hypoleuca*	Oslo Trondheim (Norway)		6 6
McCleery, R. H., Pettifor, R. a, Armbruster, P., Meyer, K., Sheldon, B. C., & Perrins, C. M. (2004). Components of variance underlying fitness in a natural population of the great tit *Parus major. The American Naturalist*, **164:** E62–72.	*Parus major*	Wytham Woods (UK)		4
Merila, J. (1997). Expression of genetic variation in body size of the collared flycatcher under different environmental conditions. *Evolution* **51**: 526-536.	*Ficedula albicollis*	Gotland (Sweeden)		4
Merilä, J., & Sheldon, B. (2000). Lifetime reproductive success and heritability in nature. *The American Naturalist*, **155:** 301–310.	*Ficedula albicollis*	Gotland (Sweeden)		14
Nilsson, J., Akesson, M., & Nilsson, J. F. (2009). Heritability of resting metabolic rate in a wild population of blue tits. *Journal of Evolutionary Biology*, **22:** 1867–74.	*Parus caeruleus*	Revingehed (Sweeden)	1	1
Tarka, M., Akesson, M., Hasselquist, D. & Hansson, B. (2014). Intralocus sexual conflict over wing Length in a wild migratory bird. *The American Naturalist* **183**: 62-73.	*Acrocephalus arundinaceus*	Lake Kvismaren (Sweeden)		4
Own unpublished data (see ESM - *C*)	*Ficedula hypoleuca*	La Hiruela (Spain)	2	4

Table D1. Location, sample size of different phenotypic traits and species considered in this study.

E – Climatic variables considered in SDMs

In the *Table E1* below, we describe all climatic variables considered in our analyses. Highlighted in bold are those variables with VIF's < 10 that were finally included into the SDMs, as stated in Methods. The column named "Order" denotes the order by which variables were excluded. "Annual temperature (range)" was excluded instead of "Rainfall january-march (mean)". Both variables were correlated (Pearson correlation, rho=-0.652), but the latter has more biological relevance than the former, since the mean rainfall between January and March undoubtedly has stronger influence on the distribution of breeding birds. VIF values in bold are those obtained with the final set of selected variables. VIF values of excluded variables are those that the variable had before being removed from the set of variables.

Explanatory variables	Code	R^2	Tolerance	VIF	Order
Rainfall april-july (mean)	**Prjula**	**0.7855289**	**0.2144711**	**4.662634**	
Rainfall january-march (mean)	**Pmjanm**	**0.8857917**	**0.1142083**	**8.755928**	
Annual rainfall (Coefficient variation)	**Pcv**	**0.4255152**	**0.5744848**	**1.740690**	
Rainfall april-july (range)	**Pmajul**	**0.8398477**	**0.1601523**	**6.244056**	
Rainfall january-march (range)	**Prmjan**	**0.7554668**	**0.2445332**	**4.089424**	
Temperature april-july (mean)	**Tmajul**	**0.7346930**	**0.2653070**	**3.769219**	
Temperature july-april (range)	**Trjula**	**0.5585255**	**0.4414745**	**2.265136**	
Annual rainfall (Total)	Ptotal	1.000000	0.00000	inf	1
Temperature january-march (range)	Trmjan	1.000000	0.00000	inf	2
Annual Temperature (mean)	Tmy	0.999	0.001	1491.520	3
Temperature january-march (mean)	Tmjanm	0.984	0.016	61.723	4
Annual rainfall (mean)	Pmy	0.980	0.020	49.648	5
Annual temperature (range)	Try	0.8440499	0.15595013	6.412306	6

Table E1. Variation inflation factors and R^2 of all environmental variables considered in the Species distribution models.

F – Species-specific models

In the models specified below (*Tables F1-F12*), we show the environmental variables considered in the models and their coefficients (“*Estimate*”). All are models with binomial distribution. Climatic variable codes as in ESM - *E*, X: longitude, Y: latitude, alt: altitude. Significant codes are as follow: ***: $p<0.001$; **: $p<0.01$; * $p<0.05$; .: $p<0.1$.

These models correspond to "y" in equation 3 in ESM - *H* (estimates and variables). Probability values can be obtained using the equations (2) and (3) described below (ESM *H — Favourability and probability*). Favourability values can be obtained using equation (1) in order to obtain the favourability value for each species and square.

Table F1 - Acrocephalus arundinaceus

	Estimate	***Std. Error***	***z value***	***Pr(>lzl)***	***Sig***
(Intercept)	5.29E+00	2.63E+01	0.201	0.840552	
Tmajul	1.21E-01	3.16E-02	3.835	0.000126	***
Prjula	1.20E-02	4.22E-03	2.83	0.004654	**
Tmajul2	-3.43E-04	9.37E-05	-3.662	0.000251	***
XY2	1.60E-03	2.44E-04	6.564	5.24E-11	***
alt2	2.04E-06	4.49E-07	4.546	5.46E-06	***
X_lon	1.59E+00	3.92E-01	4.044	5.25E-05	***
XY	-1.06E-01	1.94E-02	-5.487	4.10E-08	***
alt	-3.82E-03	8.29E-04	-4.605	4.12E-06	***
Y_lat3	-1.05E-03	2.48E-04	-4.221	2.43E-05	***
Y_lat2	1.02E-01	3.43E-02	2.973	0.002947	**
X2Y	-9.61E-04	1.73E-04	-5.554	2.79E-08	***
X_lon2	4.06E-02	7.46E-03	5.445	5.18E-08	***
Trjula	1.33E-01	5.72E-02	2.322	0.020244	*
Y_lat	-2.95E+00	1.60E+00	-1.847	0.064692	.

Table F2 - Delichon urbica

	Estimate	***Std. Error***	***z value***	***Pr(>lzl)***	***Sig***
(Intercept)	-7.98E+00	4.07E+00	-1.963	0.049628	*
Prjula	6.36E-02	1.49E-02	4.269	1.96E-05	***
Y_lat3	-2.84E-04	4.94E-05	-5.742	9.37E-09	***
Prjula2	4.46E-04	2.07E-04	2.152	0.031381	*
Y_lat2	2E-02	3.93E-03	5.074	3.89E-07	***
XY2	1.37E-04	3.73E-05	3.678	0.000236	***
X_lon3	-2.26E-04	4.85E-05	-4.658	3.19E-06	***
Trjula	-2.80E-02	9.98E-03	-2.808	0.004991	**
Pcv	4.48E-02	1.55E-02	2.893	0.00381	**

Table F2 - Delichon urbica

XY	-2.86E-03	1.63E-03	-1.752	0.079733	.

Table F3 - Falco tinnunculus

	Estimate	***Std. Error***	***z value***	***Pr(>|z|)***	***Sig***
(Intercept)	-1.30E+02	4.11E+01	-3.162	0.001569	**
Y_lat3	9.82E-04	2.60E-04	3.782	0.000155	***
Prjula	1.08E-01	1.38E-02	7.804	6.02E-15	***
X_lon	-1.58E-01	2.51E-02	-6.263	3.78E-10	***
Trjula	6.85E-02	1.15E-02	5.973	2.34E-09	***
Pmjanm	2.50E-02	7.57E-03	3.299	0.00097	***
Y_lat2	-1.53E-01	4.24E-02	-3.62	0.000295	***
Tmajul2	-4.15E-04	9.36E-05	-4.429	9.47E-06	***
Tmajul	1.25E-01	2.45E-02	5.096	3.46E-07	***
Y_lat	7.56E+00	2.27E+00	3.331	0.000864	***
Pcv	3.23E-02	2.06E-02	1.566	0.117249	
Prmjan	-2.21E-02	1.45E-02	-1.521	0.128263	

Table F4 - Ficedula albicolis

	Estimate	***Std. Error***	***z value***	***Pr(>|z|)***	***Sig***
(Intercept)	-1.76E+02	3.77E+01	-4.654	3.26E-06	***
Pmajul	6.19E-02	3.23E-02	1.913	0.055705	.
Pmjanm	-6.58E-02	1.52E-02	-4.329	1.50E-05	***
Tmajul	-1.17E-01	2.23E-02	-5.228	1.72E-07	***
XY	-3.53E-01	1.07E-01	-3.312	0.000927	***
X2Y	2.37E-03	7.82E-04	3.026	0.002475	**
Y_lat3	-9.17E-04	1.78E-04	-5.15	2.60E-07	***
Y_lat	6.02E+00	1.20E+00	5.006	5.57E-07	***
X_lon2	-1.45E-01	3.77E-02	-3.849	0.000119	***
alt	-5.59E-03	1.30E-03	-4.298	1.72E-05	***
Prmjan	-7.47E-02	1.86E-02	-4.006	6.17E-05	***
X_lon	1.07E+01	2.63E+00	4.072	4.67E-05	***
Prjula	-3.65E-02	1.14E-02	-3.212	0.00132	**

Table F4 - Ficedula albicolis

Pcv	5.11E-02	1.28E-02	3.984	6.78E-05	***
XY2	3.14E-03	1.16E-03	2.706	0.006815	**
Pmajul2	-2.85E-04	1.84E-04	-1.544	0.122483	

Table F5 - Ficedula hypoleuca

	Estimate	***Std. Error***	***z value***	***Pr(>lzl)***	***Sig***
(Intercept)	1.39E+02	4.22E+01	3.285	0.00102	**
Y_lat	-1.03E+01	2.33E+00	-4.432	9.35E-06	***
Prjula	4.72E-02	8.59E-03	5.491	4.00E-08	***
X_lon2	4.23E-02	8.09E-03	5.237	1.64E-07	***
Trjula	2.17E-01	6.24E-02	3.486	0.000491	***
Y_lat3	-1.57E-03	2.88E-04	-5.428	5.70E-08	***
Trjula2	-9.07E-04	2.55E-04	-3.56	0.000371	***
Pcv	1.22E-01	3.62E-02	3.376	0.000736	***
X2Y	-1.26E-03	1.79E-04	-7.042	1.89E-12	***
alt2	-1.79E-06	5.57E-07	-3.208	0.001335	**
Tmajul2	-2.25E-04	1.20E-04	-1.873	0.061026	.
Tmajul	6.09E-02	4.20E-02	1.45	0.147132	
X_lon3	4.74E-04	1.25E-04	3.786	0.000153	***
X_lon	-2.84E+00	2.67E-01	-10.617	<2E-16	***
Pmjanm2	4.32E-04	9.56E-05	4.514	6.38E-06	***
XY	6.10E-02	5.66E-03	10.779	<2E-16	***
Pcv2	-2.13E-03	6.01E-04	-3.542	0.000398	***
Prjula2	-3.83E-04	1.19E-04	-3.229	0.001241	**
Y_lat2	2.23E-01	4.47E-02	4.98	6.36E-07	***
alt	3.03E-03	1.28E-03	2.378	0.017424	*
Pmjanm	-3.19E-02	1.63E-02	-1.955	0.050605	.

Table F6 - Hirundo rustica

	Estimate	***Std. Error***	***z value***	***Pr(>lzl)***	***Sig***
(Intercept)	-4.63E+00	6.13E+00	-0.755	0.4503	
Y_lat3	-2.78E-04	3.45E-05	-8.068	7.17E-16	***
Y_lat2	2.07E-02	3.10E-03	6.664	2.66E-11	***
X2Y	6.25E-05	2.23E-05	2.803	0.00506	**
alt	-5.21E-03	1.61E-03	-3.237	0.00121	**
alt2	1.70E-06	1.19E-06	1.437	0.15085	
Pcv	2.97E-02	1.29E-02	2.298	0.02159	*

Table F6 - Hirundo rustica

X_lon	-4.79E-02	2.59E-02	-1.852	0.06403	.
Tmajul	-4.01E-02	1.95E-02	-2.053	0.04007	*

Table F7 - Larus canus

	Estimate	***Std. Error***	***z value***	***Pr(>lzl)***	***Sig***
(Intercept)	-1.27E+01	5.65E+00	-2.248	0.024551	*
Y_lat	3.75E-01	3.95E-02	9.494	2.00E-16	***
Pcv	8.22E-02	1.69E-02	4.858	1.19E-06	***
X2Y	-2.48E-04	5.46E-05	-4.549	5.38E-06	***
Trjula2	1.86E-03	5.45E-04	3.405	0.000662	***
alt	-2.88E-03	6.45E-04	-4.474	7.69E-06	***
Trjula	-2.84E-01	1.02E-01	-2.793	0.005219	**
Prjula	9.25E-02	1.86E-02	4.979	6.40E-07	***
Prjula2	-1.05E-03	3.56E-04	-2.962	0.003055	**
X_lon3	3.00E-04	9.50E-05	3.158	0.001587	**
Pmjanm	2.24E-02	7.30E-03	3.066	0.002168	**

Table F8 - Parus caeruleus

	Estimate	***Std. Error***	***z value***	***Pr(>lzl)***	***Sig***
(Intercept)	1.11E+02	3.25E+01	3.415	0.000638	***
Y_lat3	-1.67E-03	2.48E-04	-6.731	1.69E-11	***
Y_lat2	2.08E-01	3.74E-02	5.557	2.74E-08	***
XY2	1.18E-03	2.22E-04	5.309	1.10E-07	***
X_lon3	-6.32E-04	1.25E-04	-5.071	3.96E-07	***
X_lon	1.38E+00	4.38E-01	3.142	0.001677	**
X_lon2	5.10E-02	6.89E-03	7.395	1.42E-13	***
X2Y	-7.55E-04	1.25E-04	-6.048	1.46E-09	***
XY	-8.41E-02	1.98E-02	-4.257	2.08E-05	***
Y_lat	-8.25E+00	1.90E+00	-4.351	1.35E-05	***
Trjula	-3.95E-02	1.07E-02	-3.703	0.000213	***
Pcv	-3.32E-02	1.43E-02	-2.321	0.02028	*

Table F9 - Parus major

	Estimate	*Std. Error*	*z value*	*Pr(>lzl)*	*Sig*
(Intercept)	-1.17E+01	2.19E+00	-5.366	8.03E-08	***
Pmajul	5.49E-02	1.24E-02	4.415	1.01E-05	***
Tmajul	1.49E-01	1.92E-02	7.766	8.13E-15	***
Prjula	6.44E-02	1.02E-02	6.302	2.94E-10	***
Tmajul2	-3.96E-04	7.72E-05	-5.126	2.96E-07	***
Prjula2	7.37E-04	1.69E-04	4.376	1.21E-05	***
Prmjan2	-1.32E-03	3.11E-04	-4.251	2.13E-05	***
Pcv2	1.75E-03	5.46E-04	3.206	0.00135	**
Pcv	-1.46E-01	5.17E-02	-2.831	0.00464	**
Trjula	2.44E-02	8.75E-03	2.794	0.00521	**
Prmjan	-4.26E-02	1.58E-02	-2.703	0.00688	**

Table F10 - Passer domesticus

	Estimate	*Std. Error*	*z value*	*Pr(>lzl)*	*Sig*
(Intercept)	-3.26E+02	7.72E+01	-4.228	2.36E-05	***
XY	1.32E-01	1.30E-02	10.185	<2E-16	***
X_lon2	2.64E-01	2.62E-02	10.07	<2E-16	***
Y_lat	2.15E+01	4.22E+00	5.08	3.77E-07	***
Y_lat3	2.12E-03	4.55E-04	4.66	3.16E-06	***
Prmjan	-3.29E-02	2.27E-02	-1.451	0.14676	
Tmajul	-2.12E-01	3.27E-02	-6.467	1.00E-10	***
alt	-1.16E-02	1.88E-03	-6.163	7.14E-10	***
X2Y	-5.20E-03	4.84E-04	-10.764	<2E-16	***
Pmjanm2	4.63E-04	2.77E-04	1.669	0.09521	.
X_lon	-7.20E+00	7.22E-01	-9.97	<2E-16	***
X_lon3	1.33E-03	2.88E-04	4.627	3.71E-06	***
Y_lat2	-3.88E-01	7.67E-02	-5.059	4.22E-07	***
Pcv	7.80E-02	2.60E-02	3.004	0.00266	**
Pmjanm	-6.93E-02	4.36E-02	-1.591	0.1117	

Table F11 - Perisoreus infaustus

	Estimate	*Std. Error*	*z value*	*Pr(>lzl)*	*Sig*
(Intercept)	-5.78E+03	2.08E+03	-2.781	0.005425	**
Y_lat	2.64E+02	9.72E+01	2.714	0.006641	**
Y_lat2	-4.03E+00	1.52E+00	-2.658	0.007871	**

Table F11 - Perisoreus infaustus

Prjula	2.46E-01	1.22E-01	2.019	0.043485	*
Prmjan	2.58E-01	4.53E-02	5.7	1.20E-08	***
Tmajul2	-3.46E-03	6.29E-04	-5.509	3.62E-08	***
Tmajul	5.89E-01	1.34E-01	4.385	1.16E-05	***
Pcv2	4.42E-03	1.20E-03	3.685	0.000228	***
Prjula2	-3.72E-03	1.67E-03	-2.223	0.026203	*
alt	1.45E-02	4.64E-03	3.124	0.001783	**
Y_lat3	2.05E-02	7.90E-03	2.6	0.009316	**

Table F12 - Pica pica

	Estimate	Std. Error	z value	Pr(>lzl)	Sig
(Intercept)	-3.6291476	4.1930977	-0.866	0.386762	
Pcv2	0.0015791	0.0004694	3.364	0.000768	***
Pmjanm	-0.0473308	0.0090164	-5.249	1.53E-07	***
Pmajul	0.1958809	0.0342961	5.711	1.12E-08	***
Tmajul	0.0403618	0.0096907	4.165	3.11E-05	***
Prmjan	-0.1276797	0.0203944	-6.261	3.84E-10	***
Trjula	0.0572102	0.0123179	4.644	3.41E-06	***
Pcv	-0.1763667	0.0459966	-3.834	0.000126	***
Prmjan2	-0.0011901	0.0003478	-3.422	0.000622	***
X_lon	-1.2325031	0.4035163	-3.054	0.002255	**
XY	0.0396101	0.015914	2.489	0.01281	*
Pmajul2	-0.0006717	0.0001704	-3.943	8.06E-05	***
Y_lat	-0.1427016	0.0449197	-3.177	0.001489	**
XY2	-0.0002813	0.0001483	-1.897	0.057856	.

G — Validation of Species Distribution Models

We assessed the classification power of the species-specific distribution models with the validation dataset (see *Table G1* below) by estimating the sensitivity (proportion of presences correctly classified), specificity (proportion of absences correctly classified), the Correct Classification Rate (CCR, proportion of cases correctly classified), and the true skill statistics (TSS: sensitivity+specificity-1) using the neutral favourability value of F = 0.5 as classification threshold, and evaluated the discrimination capacity using the Area Under the Curve (AUC) of the Receiver Operating Characteristic[5], which is independent of any favourability threshold[6]. For each species, we run 5 model set thresholds of 0.1, 0.2 and 0.3. These thresholds represent the proportion of presence/absence data randomly chosen to validate the model. Specifically, 0.1, 0.2 and 0.3 consider 90%, 80% and 70% of the data to build the model and the remaining 10%, 20% and 30% to validate it. Find below the average values for each species and threshold, for each parameter. Note that we have included threshold 0 for comparative purposes. Although prevalence is not a parameter for evaluation, we have included it to show that thresholds of presence/absence data did not influence prevalence.

Species(*)	**Threshold**	**Prevalence**	**AUC**	**Sensitivity**	**Specificity**	**CCR**	**TSS**
Acr_aru	0.1	0.5222	0.8963	0.8526	0.7266	0.7924	0.5793
Acr_aru	0.2	0.5231	0.8958	0.8570	0.7248	0.7940	0.5819
Acr_aru	0.3	0.5244	0.8948	0.8561	0.7302	0.7963	0.5863
Acr_aru	0	0.5214	0.8954	0.8492	0.7245	0.7895	0.5737
Del_urb	0.1	0.9691	0.9085	0.7797	0.8582	0.7821	0.6379
Del_urb	0.2	0.9689	0.9072	0.7834	0.8605	0.7858	0.6439
Del_urb	0.3	0.9668	0.8964	0.7827	0.8416	0.7847	0.6243
Del_urb	0	0.9690	0.9017	0.7805	0.8310	0.7821	0.6115
Fal_tin	0.1	0.9611	0.8580	0.7952	0.7652	0.7941	0.5605
Fal_tin	0.2	0.9608	0.8251	0.8033	0.6790	0.7985	0.4823
Fal_tin	0.3	0.9641	0.8561	0.7997	0.7504	0.7979	0.5501
Fal_tin	0	0.9616	0.8545	0.7888	0.7273	0.7865	0.5161
Fic_alb	0.1	0.1361	0.9391	0.9165	0.8204	0.8335	0.7369
Fic_alb	0.2	0.1352	0.9404	0.9184	0.8239	0.8367	0.7423
Fic_alb	0.3	0.1339	0.9407	0.9208	0.8235	0.8366	0.7443
Fic_alb	0	0.1358	0.9400	0.9196	0.8236	0.8367	0.7433
Fic_hyp	0.1	0.5454	0.9645	0.8617	0.9172	0.8869	0.7789
Fic_hyp	0.2	0.5425	0.9643	0.8650	0.9104	0.8858	0.7754
Fic_hyp	0.3	0.5466	0.9663	0.8664	0.9213	0.8913	0.7878
Fic_hyp	0	0.5454	0.9642	0.8639	0.9107	0.8852	0.7746
Hir_rus	0.1	0.9666	0.9012	0.8103	0.8663	0.8121	0.6765
Hir_rus	0.2	0.9672	0.8920	0.8049	0.8329	0.8058	0.6378
Hir_rus	0.3	0.9696	0.8987	0.8107	0.8907	0.8131	0.7014
Hir_rus	0	0.9672	0.8979	0.8144	0.8667	0.8162	0.6811
Lar_can	0.1	0.3641	0.9777	0.9078	0.9190	0.9149	0.8268
Lar_can	0.2	0.3621	0.9778	0.9090	0.9226	0.9177	0.8316

Lar_can	0.3	0.3674	0.9764	0.9033	0.9162	0.9114	0.8194
Lar_can	0	0.3633	0.9776	0.9075	0.9198	0.9153	0.8272
Par_car	0.1	0.8990	0.9520	0.8561	0.9020	0.8607	0.7581
Par_car	0.2	0.9011	0.9533	0.8572	0.9094	0.8623	0.7666
Par_car	0.3	0.8966	0.9513	0.8554	0.9036	0.8604	0.7590
Par_car	0	0.8987	0.9511	0.8547	0.9009	0.8594	0.7556
Par_maj	0.1	0.9687	0.9125	0.7947	0.8422	0.7962	0.6369
Par_maj	0.2	0.9688	0.9008	0.7805	0.8496	0.7826	0.6301
Par_maj	0.3	0.9688	0.9166	0.8006	0.8558	0.8024	0.6564
Par_maj	0	0.9690	0.8984	0.7666	0.8451	0.7690	0.6116
Pas_dom	0.1	0.9208	0.9760	0.9177	0.9362	0.9192	0.8539
Pas_dom	0.2	0.9191	0.9750	0.9146	0.9365	0.9164	0.8511
Pas_dom	0.3	0.9210	0.9782	0.9168	0.9301	0.9179	0.8469
Pas_dom	0	0.9210	0.9742	0.9161	0.9392	0.9179	0.8553
Per_inf	0.1	0.1313	0.9973	0.9889	0.9693	0.9719	0.9582
Per_inf	0.2	0.1272	0.9972	0.9914	0.9688	0.9717	0.9602
Per_inf	0.3	0.1281	0.9977	0.9913	0.9712	0.9738	0.9625
Per_inf	0	0.1297	0.9972	0.9899	0.9699	0.9725	0.9598
Pic_pic	0.1	0.9489	0.9161	0.8638	0.8369	0.8624	0.7006
Pic_pic	0.2	0.9476	0.9141	0.8487	0.8329	0.8479	0.6816
Pic_pic	0.3	0.9482	0.9154	0.8622	0.8289	0.8605	0.6911
Pic_pic	0	0.9493	0.9114	0.8487	0.8190	0.8472	0.6676

Table G1. Classification power of the species-specific distribution models by different parameters. (*) Acr_aru: *Acrocephalus arundinaceus*; Del_urb: *Delichon urbica*; Fal_tin: *Falco tinnunculus*; Fic_alb: *Ficedula albicolis*; Fic_hyp: *Ficedula hypoleuca*; Hir_rus: *Hirundo rustica*; Lar_can: *Larus canus*; Par_car: *Parus caeruleus*; Par_maj: *Parus major*; Pas_dom: *Passer domesticus*; Per_ inf: *Perisoreus infaustus*; Pic_pic: *Pica pica*.

H — Favourability and probability

In the favourability function the effect of the event's prevalence (in this case the proportion of the study region in which a species occurs) is mathematically eliminated in the logit of the logistic regression equation. Favourabilities (F) may be directly derived from logistic regression probabilities (P) as follows:

$$F = \frac{\frac{P}{(1-P)}}{\frac{n_1}{n_0} + \frac{P}{(1-P)}} (1) \qquad P = \frac{e^y}{1+e^y} (2) \qquad y = \alpha + \beta_1 \chi_1 + \beta_2 \chi_2 + \ldots + \beta_n \chi_n (3)$$

In equation (1), n_1 and n_0 represent the number of presences and absences, respectively, and P is the logistic probability value. In (2) e is the basis of the natural logarithm and y is the logit regression equation for P. In (3) α is a constant (the intercept) and β_1, β_2, …, β_n are the coefficients for the n predictor variables x_1, x_2, …, x_n. F is a logistic function with values between 0 and 1.

I — Models of log-transformed CV_A and I_A

Here we show the outcome (*Table I1*) of the models described in the manuscript, but considering log-transformed CV_A and I_A. Results are qualitatively the same than those described in the main text of the manuscript. Bold values highlight variables with $p<0.05$.

	Resolution	**50x50km^2**				**1x1km^2**		
CV_A		Estimate ± SE	*t* value	*p*		Estimate ± SE	*t* value	*p*
	Intercept	0.0082 ± 0.0141	0.585	0.565		0.0078 ± 0.0144	0.543	0.593
	Favourability	0.1073 ± 0.0517	2.073	**0.048**		0.1073 ± 0.0510	2.105	**0.047**
	Favourability^2	-0.0815 ± 0.0390	-2.090	**0.044**		-0.0815 ± 0.0379	-2.148	**0.040**
	Trait:size	-0.0059 ± 0.0034	-1.757	**0.081**		-0.0058 ± 0.0034	-1.713	0.089
	Method:full sibling	0.0015 ± 0.0066	0.236	0.081		0.0017 ± 0.0066	-0.256	0.798
	Method: parent-offspring	0.0018 ± 0.0030	0.611	0.542		0.0020 ± 0.0030	0.686	0.494
I_A		Estimate ± SE	*t* value	*p*		Estimate ± SE	*t* value	*p*
	Intercept	-0.0004 ± 0.0007	-0.585	0.563		-0.0003 ± 0.0007	-0.520	0.608
	Favourability	0.0067 ± 0.0025	2.661	**0.012**		0.0064± 0.0025	2.546	**0.017**
	Favourability^2	-0.0052 ± 0.0018	-2.761	**0.008**		-0.0094 ± 0.0018	-2.654	**0.012**
	Trait:size	-0.0003 ± 0.0001	-2.427	**0.016**		-0.00037 ± 0.00015	-2.408	**0.017**
	Method:full sibling	-0.0002 ± 0.0003	-0.001	0.999		-0.000007± 0.000319	0.022	0.982
	Method: parent-offspring	0.0001 ± 0.0001	0.771	0.441		0.0001 ± 0.0001	0.801	0.424

Table I1. Results of the linear mixed models considering log-transformed CV_A and I_A as dependent variables at resolution of 50x50 and 1x1Km^2.

J — Phylogenetic considerations

Below we show the phylogenetic tree obtained for all the species considered in this study (*Figure J1*). To model potental signal of trait evolution on species phylogeny, we down- loaded 10 000 trees from www.bird.tree.org[7] for the species considered in our study. We chose the backbone tree to obtain a 50% majority rule consensus tree. All statistical analyses were performed using R (ver. 3.1.2), with the *APE*[8] and *phytools*[9] packages. We estimated the magnitude of the phylogenetic signal using K statistics of the residuals of our models performed for CV_A and I_A. Means and standard deviations were calculated for each species and incorporated in our models. When K<1, closely related species are less similar than expected because of strong directional selection or disruptive sexual selection[10]. Instead, when K>1, close relatives are more similar than expected under a neutral model of evolution[11]. Our analyses confirm that the phylogenetic signal was very low for CV_A (K=0.688, P=0.644) and I_A (K=0.167, P=0.408). This result suggests that the patterns that we found are highly unlikely to be conditioned by phylogeny.

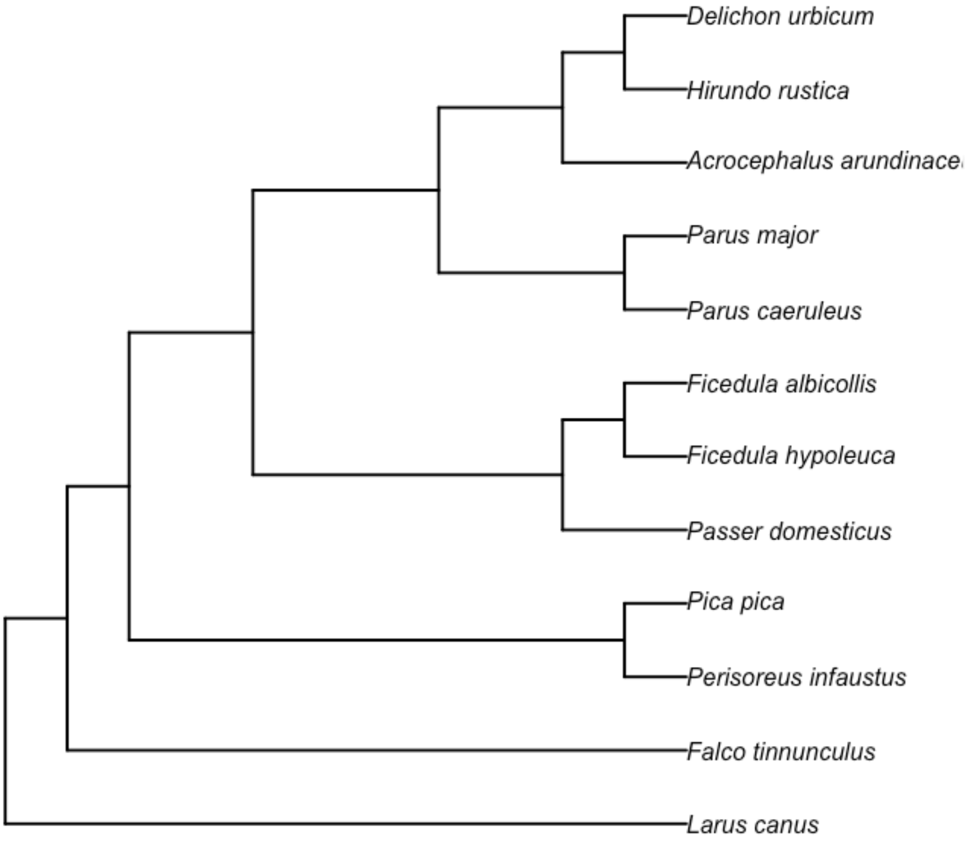
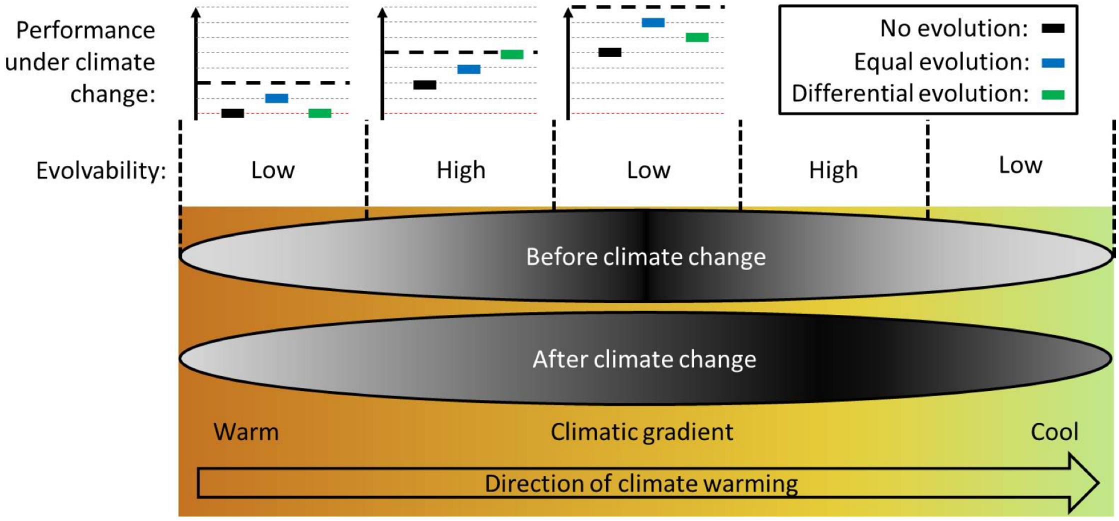


Figure J1. Phylogenetic tree obtained for the species considered in this study.

K— Evolutionary predictions under hypothetical climate change

Hypothetical relative population performances given climate warming and different evolvability. Gray shaded ovals illustrate current and future climatic favourability across the species geographic range, where dark shading indicates higher favourability. The coloured box illustrates the current climate gradient. As climate warms, favourability increases in the currently cooler areas, so the right hand portion of the range becomes more favourable, and the left hand portion becomes less favourable. The graphs illustrate relative changes in population performance (e.g. population growth rate) when climate becomes less favourable, coloured bars indicate performance given: (i) no evolution, (ii) evolutionary potential is equal among all populations, (iii) evolutionary potential is differential, i.e. highest in areas with currently intermediate climatic favourability (as obtained in our results). The red line on the graphs indicates population extinction, the thick dashed black line on each graph indicates current population performance. Performance values are based on the assumption that before climate warming, each population's fitness responds similarly to climatic conditions (i.e. populations are not adapted to local climatic conditions). This means that when climate warming occurs but no evolution, a population's fitness becomes the same as that in the population previously occupying the same climatic favourability (i.e. in the graph immediately to the left). The real magnitude of the change in performance will depend on the quantitative values of climatic favourability and evolvability.



References

1. Butler D. Asreml fits the linear mixed model. R package version 3.0. (2009).
2. Potti J, Canal D. Heritability and genetic correlation between the sexes in a songbird sexual ornament. Heredity 106, 945-954 (2010).
3. Kim SY, Fargallo JA, Vergara P, Martinez-Padilla J. Multivariate heredity of melanin-based coloration, body mass and immunity. Heredity 111, 139-146 (2013).
4. Kruuk LEB. Estimating genetic parameters in natural populations using the 'animal model'. Phil Trans R Soc B 359, 873-890 (2004).
5. Fielding AH, Bell JF. A review of methods for the assessment of prediction errors in conservation presence/absence models. Environ Conserv 24, 38-49 (1997).
6. Hosmer DW, Lameshow S. Applied logistic regression, 2nd edn. John Wiley and Sons, Inc. (2005).
7. Jetz W, Thomas GH, Joy JB, Hartmann K, Mooers AO. The global diversity of birds in space and time. Nature 491, (2012).
8. Paradis E, Claude J, Strimmer K. APE: analyses of phy- logenetics and evolution in R language. Bioinformatics 20, (2004).
9. Revell LJ. phytools: An R package for phylogenetic comparative biology (and other things). Methods in Ecology and Evolution 3, (2012).
10. Gavrilets S. Rapid evolution of reproductive barriers driven by sexual conflict. Nature 403, 886-889 (2000).
11. Bloomberg SP, Garland T, Ives AR. Testing for phylogenetic signal in comparative data: behavioral traits are more labile. Evolution 57, 717-745 (2003).