Supplementary Information
Radchuk et al. Adaptive responses of animals to climate change: not universal, likely insufficient

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Figure S1. Data availability for 1413 species in the PRC dataset (‘Phenotypic Response to Climate’ data). For each species, a single horizontal black line indicates availability of data on different climatic factors, trait categories (phenological and morphological) and selection, as well as on the duration of the study (years: <10, 10-20, 20-30 and >30) and the study location: Northern Hemisphere Europe (NHE), Northern Hemisphere America (NHAm), Northern Hemisphere Asia (NHAs) or Southern Hemisphere (SH). Pictograms show the taxon to which a species belongs (Aves, Mammalia, Amphibia, Reptilia, Insecta and Arachnida) and the number next to the pictogram specifies the number of studies for that taxon.
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Figure S2. Locations of studies in the PRC dataset (‘Phenotypic Response to Climate’, including both studies with and without data on selection) are shown with empty circles, and locations of studies in the PRCS dataset (‘Phenotypic Responses to Climate with Selection data’, a subset with only studies for which selection data were available) are filled with orange colour. The size of the circles is proportional to the duration of the study (in years). Insets show for each dataset the relative coverage of a) different taxa; b) different climatic factors; and c) different trait categories.
Figure S3. Phenotypic responses of species to the amount of precipitation: a) effect of year on precipitation, b) effect of precipitation on trait values and c) weighted mean selection over time (WMSD) acting on traits over the study period. Each study case is identified by a) the country and publication identity (publication identities are given in Supplementary Table S3), b) the trait and publication identity, and c) the trait, fitness measure and publication identity. Only phenological traits were covered by the studies extracted from the publications that focused on the effects of precipitation. The mean effects across studies in the PRCS dataset (‘Phenotypic Responses to Climate with Selection data’, shown in black) and the PRC dataset (‘Phenotypic Response to Climate’, shown in blue) suggest: a) the absence of a directional change of precipitation with time, b) the absence of a relationship between precipitation and trait, and c) evidence for negative selection on phenological traits, with significant variation in WMSD measured using different fitness components (recruitment, reproduction and adult survival).
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Figure S4. Probability density of the duration (years) of the studies in the PRC dataset (‘Phenotypic Response to Climate’, shown in black) and in the PRCS dataset (‘Phenotypic Responses to Climate with Selection data’, shown in orange). The vertical lines show median study duration in each dataset. Probability densities were smoothed using Gaussian kernel density estimation based on the default bandwidth selection in the geom_density() function (ggplot2 package in R).
Figure S5. Linear models explaining the warming rates by a) number of years in the time series and b) first year in the time series, and c) Pearson correlation between the number of years in the time series and the first year in the time series. Warming rates are lower for longer time series, as shown by the significant slope in a) and they are higher for series that started the most recently, as shown by the significant slope in b).
Figure S6. Effect of temperature (blue), year (red), and abundance (green) on the phenological traits shown on the y axis. Effect sizes were obtained from the mixed-effects models including the abundance as an explanatory variable (eq. 1 in Supplementary Methods). Each study is identified by publication identity, trait and species. Studies are sorted by species and within it by publication identity. Effects of temperature are generally larger compared to the effects of year and abundance, and negative (i.e. advancement of phenology with increasing temperature).
Figure S7. Temporal trend in selection acting on phenological (black) and morphological (grey) traits. Each study is identified by publication identity, trait and fitness component. Bars show 95% confidence intervals and the symbol size is proportional to the study sample size. Across studies, we found no significant directional change in selection on either phenological (Slope = 0.0005±0.0019 (year*SD)$^{-1}$, LRT between the model with and without linear change in selection over years: $\chi^2 = 0.09$, df = 1, p = 0.764) or morphological traits (Slope = 0.0005±0.0008 (year*SD)$^{-1}$, LRT: $\chi^2 = 0.46$, df = 1, p = 0.497).
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Figure S8. Product of the weighted mean selection differential (WMSD) with the sign of the slopes obtained when assessing condition 2 and 3 (the overall sign of the climate-driven phenotypic change over time). The product, computed as WMSD*sign(condition 1* condition 2), is shown separately for phenological (black) and morphological (grey) traits. This product is positive if selection acts in the same direction as the observed climate-driven trait change over time, indicating adaptive trait change. If this product is negative, the trait change is maladaptive. Each study is identified by publication identity, trait, and fitness component. Studies are sorted by trait category (phenological, morphological), and within it by species, fitness category and publication identity. Repeated labels correspond to either different locations reported in the same publication, or to measurements on different sexes. Across studies, changes in phenological traits were mainly adaptive, whereas there was no consistent change in morphological traits.
Figure S9. Distribution of the proportion of studies at risk for 100,000 random values of $\omega^2$. Since we do not have $\omega^2$ values for each study, we draw those values from a published compilation of $\omega^2$ values\(^1\). Here we represent the proportion of studies for which the estimated observed lag is larger than the estimated critical lag (i.e. population growth $\lambda < 1$) when one value of $\omega^2$ is drawn per study. The distribution shows that the probability that none of study species is at risk is virtually zero (red arrow).
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Figure S10. Relations between year and temperature for each study (titles above panels indicate authors and study species) in the PRCS (‘Phenotypic Responses to Climate with Selection data’) dataset. \( pv \) is a p-value of the slope as estimated by LRT. Note that the range of the x- and y-axes can differ among studies.
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Figure S11. Relationships between phenological traits (z-scaled) and temperature for each study in the PRCS (‘Phenotypic Responses to Climate with Selection data’) dataset (titles above panels indicate authors and study species). pv is a p-value of the slope as estimated by LRT. Note that the range of the x- and y-axes can differ among studies.
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Figure S12. Relationships between morphological traits (z-scaled) and temperature for each study in the PRCS (‘Phenotypic Responses to Climate with Selection data’) dataset (titles above panels indicate authors and study species). pv is a p-value of the slope as estimated by LRT. Note that the range of the x- and y-axes can differ among studies.
Figure S13. Yearly selection differentials (and their CI, shown with bars) measured on phenological traits shown for each study (titles above panels indicate authors and study species). Red solid line shows the estimate of WMSD (weighted mean selection differential) and the shaded polygon indicates ± SE of WMSD. The overlap of the red shaded polygon with 0 indicates that selection is not significantly different from 0. Note that the range of x- and y-axes can differ among studies.
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Continuation Figure S13
Figure S14. Yearly selection differentials (and their CI, shown with bars) measured on morphological traits shown for each study (titles above panels indicate authors and study species). Red solid line shows the estimate of WMSD (weighted mean selection differential) and the shaded polygon indicates 95% CI of the estimate of WMSD. The overlap of the red shaded polygon with 0 indicates that selection is not significantly different from 0. Note that the range of x- and y-axes can differ among studies.
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Continuation Figure S14

Year
Selection differential

Teplitsky et al
Larus novaehollandiae scopulinus
−0.3 −0.2 −0.1 0.0 0.1 0.2 0.3
Teplitsky et al
Larus novaehollandiae scopulinus
1980 1990 2000
−0.3 −0.2 −0.1 0.0 0.1 0.2 0.3
Teplitsky et al
Larus novaehollandiae scopulinus
1985 1990 1995
−1.0 −0.5 0.0 0.5 1.0
Teplitsky et al
Larus novaehollandiae scopulinus
−0.3 −0.2 −0.1 0.0 0.1 0.2 0.3
Teplitsky et al
Larus novaehollandiae scopulinus
−0.3 −0.2 −0.1 0.0 0.1 0.2 0.3
Teplitsky et al
Larus novaehollandiae scopulinus
1980 1990 2000
−0.3 −0.2 −0.1 0.0 0.1 0.2 0.3
Teplitsky et al
Larus novaehollandiae scopulinus
1980 1990 2000
Figure S15. Funnel plots of the effect sizes obtained when testing each of the three conditions with the PRCS dataset. Shown are sample sizes (number of years) and effect sizes: a) an effect of year on temperature, b) an effect of temperature on phenological traits; c) an effect of temperature on morphological traits; d) selection on phenological traits; e) selection on morphological traits. Solid line is a null effect and dashed line depicts the mean effect size across all the studies for each model. z- and p-values above each panel show the results of Egger’s test assessing the asymmetry of the funnel plot (p < 0.05 indicates a significant asymmetry signaling a potential publication bias).
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Figure S16. Funnel plots of the effect sizes obtained when testing two conditions with the PRC dataset. Shown are sample sizes (number of years) and effect sizes: a) an effect of year on temperature, b) an effect of temperature on phenological traits; and c) an effect of temperature on morphological traits. Solid line is a null effect and dashed line depicts the mean effect size across all the studies for each model. \( z \)- and \( p \)-values above each panel show the results of Egger’s test assessing the asymmetry of the funnel plot (\( p < 0.05 \) indicates a significant asymmetry signaling a potential publication bias).
SUPPLEMENTARY TABLES

Table S1. Model estimates and their standard errors obtained from mixed-effects meta-analyses used to assess each of the three conditions required to infer adaptive responses across the studies. The models were fitted separately for each climatic factor in both PRCS (‘Phenotypic Responses to Climate with Selection data’) and PRC (‘Phenotypic Response to Climate’) datasets. For details on the levels of the fixed effects see Methods.

(Supplied as a Microsoft Excel document, because it is longer than 1 page)
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Table S2. Significance of the effects tested with mixed-effects meta-analyses used to assess each of the three conditions required to infer adaptive responses across the studies. The significance was estimated with asymptotic likelihood ratio chi-square test (LRT) comparing the model that includes the effect specified in the column ‘Effect’ to the model without this effect. Significant effects ($p < 0.05$) are highlighted in bold and marginally significant ($p < 0.10$) in italic. For each model we also show the variance of the random effects: study and publication identity.
(Supplied as Microsoft Excel document, because it is longer than 1 page)
Table S3. Full references for publication identities used in the PRC (‘Phenotypic Response to Climate’) dataset and referred to in Figs. 2-4 and Supplementary Figs. S3, S6, S7 and S8. For each publication we indicate taxa, trait(s) and climatic factor(s) for which the data were reported and whether selection data were reported (if ‘Yes’, then the study also belongs to the PRCS ‘Phenotypic Responses to Climate with Selection data’ dataset).
(Supplied as Microsoft Excel document, because it is longer than 1 page)
Table S4. Sensitivity analyses assessing how the estimates of mixed-effects meta-analytical models fitted to the PRCS (‘Phenotypic Responses to Climate with Selection data’) dataset were affected when excluding 1) the outlier-like study (Goodenough et al. 2011), 2) the only study on mammals (Plard et al. 2014), and 3) both of them. The columns are the same as in Table S1.

<table>
<thead>
<tr>
<th>Excluding</th>
<th>Response</th>
<th>Effect</th>
<th>Modality</th>
<th>Estimate</th>
<th>SE</th>
</tr>
</thead>
<tbody>
<tr>
<td>The study by Goodenough et al. (2011), outlier</td>
<td>Slope of phenological traits on temperature</td>
<td>Intercept</td>
<td></td>
<td>-0.239</td>
<td>0.067</td>
</tr>
<tr>
<td></td>
<td>Mean selection across phenological traits</td>
<td>Intercept</td>
<td></td>
<td>-0.114</td>
<td>0.022</td>
</tr>
<tr>
<td></td>
<td>separately (presumably induced by temperature)</td>
<td>Fitness component</td>
<td>Recruitment</td>
<td>-0.185</td>
<td>0.032</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>-0.091</td>
<td>0.028</td>
</tr>
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<td></td>
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<td>-0.020</td>
<td>0.042</td>
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<td></td>
<td></td>
<td>Generation length</td>
<td></td>
<td>-0.014</td>
<td>0.005</td>
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<tr>
<td>The only study on mammal (Plard et al. 2014)</td>
<td>Slope of phenological traits on temperature</td>
<td>Intercept</td>
<td></td>
<td>-0.276</td>
<td>0.070</td>
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<td>0.065</td>
</tr>
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<td>Fitness component</td>
<td>Recruitment</td>
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<td>0.076</td>
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<td>-0.149</td>
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<td>-0.064</td>
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<td></td>
<td>Generation length</td>
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<td>-0.019</td>
<td>0.011</td>
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<tr>
<td>Both the only study on mammal (Plard et al. 2014) and the outlier study (Goodenough et al. 2011)</td>
<td>Slope of phenological traits on temperature</td>
<td>Intercept</td>
<td></td>
<td>-0.256</td>
<td>0.068</td>
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<tr>
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<td>Mean selection across phenological traits</td>
<td>Intercept</td>
<td></td>
<td>-0.113</td>
<td>0.023</td>
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<tr>
<td></td>
<td>separately (presumably induced by temperature)</td>
<td>Fitness component</td>
<td>Recruitment</td>
<td>-0.181</td>
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<td>-0.090</td>
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<td>0.008</td>
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<td></td>
<td>Generation length</td>
<td></td>
<td>-0.014</td>
<td>0.005</td>
</tr>
</tbody>
</table>
Table S5. Sensitivity analyses assessing how the significance of the effects obtained with the mixed-effects meta-analytical models fitted to the PRCS (‘Phenotypic Responses to Climate with Selection data’) dataset was affected when excluding 1) the outlier-like study (Goodenough et al. 2011), 2) the only study on mammals (Plard et al. 2014), and 3) both of them. The columns are the same as in Table S2.

<table>
<thead>
<tr>
<th>Excluding</th>
<th>Response</th>
<th>Effect</th>
<th>LRT</th>
<th>df</th>
<th>p value</th>
<th>Random variance due to study ID</th>
<th>Random variance due to publication ID</th>
</tr>
</thead>
<tbody>
<tr>
<td>The study by Goodenough et al. (2011), outlier</td>
<td>Slope of phenological traits on temperature</td>
<td>Intercept</td>
<td>10.10</td>
<td>1</td>
<td>0.0015</td>
<td>4.46E-02</td>
<td>3.94E-02</td>
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<tr>
<td></td>
<td>Mean selection across phenological traits separately (presumably induced by temperature)</td>
<td>Intercept</td>
<td>14.47</td>
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<td>0.0001</td>
<td>9.68E-03</td>
<td>2.08E-03</td>
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<td></td>
<td>Fitness component</td>
<td>Generation length</td>
<td>0.39</td>
<td>1</td>
<td>0.5331</td>
<td>9.15E-03</td>
<td>7.15E-03</td>
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<tr>
<td>The only study on mammal (Plard et al. 2014)</td>
<td>Slope of phenological traits on temperature</td>
<td>Intercept</td>
<td>11.93</td>
<td>1</td>
<td>0.0006</td>
<td>4.33E-02</td>
<td>4.66E-02</td>
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<td>Mean selection across phenological traits separately (presumably induced by temperature)</td>
<td>Intercept</td>
<td>5.58</td>
<td>1</td>
<td>0.0182</td>
<td>9.78E-03</td>
<td>6.31E-02</td>
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<td>Fitness component</td>
<td>Generation length</td>
<td>0.38</td>
<td>1</td>
<td>0.5384</td>
<td>9.69E-03</td>
<td>7.69E-02</td>
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<tr>
<td>Both the only study on mammal (Plard et al. 2014) and the outlier study (Goodenough et al. 2011)</td>
<td>Slope of phenological traits on temperature</td>
<td>Intercept</td>
<td>10.79</td>
<td>1</td>
<td>0.0010</td>
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<td>3.97E-02</td>
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<td>Intercept</td>
<td>13.00</td>
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<td>9.92E-03</td>
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<td>Fitness component</td>
<td>Generation length</td>
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<td>0.5602</td>
<td>9.16E-03</td>
<td>7.40E-03</td>
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Table S6. Baseline parameter values (used if not specified otherwise) and parameter ranges used to assess the sensitivity of the difference between actual and critical lags. The sources for the parameter values are also given.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Baseline value</th>
<th>Range</th>
<th>Data source</th>
</tr>
</thead>
<tbody>
<tr>
<td>Heritability, (h^2)</td>
<td>0.15</td>
<td>0.04 – 0.33</td>
<td>PRCS dataset</td>
</tr>
<tr>
<td>The width of the fitness function, (\omega^2)</td>
<td>10</td>
<td>3 – 50</td>
<td>Estes and Arnold (2007)(^1), based on the dataset from Kingsolver et al. (2001)(^2)</td>
</tr>
<tr>
<td>Effective population size, (N_e)</td>
<td>100</td>
<td>1 – 10000</td>
<td>Frankham (1995)(^3)</td>
</tr>
<tr>
<td>Maximum number of offspring produced per individual, (B)</td>
<td>1.6</td>
<td>1.2 – 2</td>
<td>Gienapp et al. (2012)(^4)</td>
</tr>
<tr>
<td>Stochastic variation of the phenotypic optimum around the (linear) trend, (\sigma_0^2)</td>
<td>0</td>
<td>0</td>
<td>Because of the lack of data for assessing this parameter(^4) we assumed no environmental variability, with the caveat that our analyses are over-optimistic about the fate of populations</td>
</tr>
<tr>
<td>Linear selection differential, (\beta)</td>
<td>0.171</td>
<td>0.01 – 0.0351</td>
<td>Mean±2SE obtained for WMS in this study</td>
</tr>
</tbody>
</table>
Table S7. Heterogeneity estimates for the mixed-effect meta-analyses used in this study. Q is the total amount of heterogeneity and the column ‘p value’ indicates whether this amount of heterogeneity is significant, I² reflects the proportion of the total heterogeneity due to between-study variance and ranges from 0 to 1, and H² is the ratio showing the proportion of observed heterogeneity in relation to what would be expected under the null hypothesis. The heterogeneity estimates are shown for the models fitted to both datasets and for the models testing how sensitive the results are to excluding two studies.

<table>
<thead>
<tr>
<th>Data</th>
<th>Response</th>
<th>I²</th>
<th>H²</th>
<th>Q</th>
<th>p value</th>
</tr>
</thead>
<tbody>
<tr>
<td>PRCS</td>
<td>Slope of temperature on years</td>
<td>0.640</td>
<td>2.8</td>
<td>104.8</td>
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<td></td>
<td>Slope of phenological traits on temperature</td>
<td>0.915</td>
<td>11.8</td>
<td>365.2</td>
<td>&lt;0.0001</td>
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<tr>
<td></td>
<td>Slope of morphological traits on temperature</td>
<td>0.000</td>
<td>1.0</td>
<td>6.4</td>
<td>0.7024</td>
</tr>
<tr>
<td></td>
<td>Mean selection across phenological traits (presumably induced by temperature)</td>
<td>1.000</td>
<td>120425.2</td>
<td>413110.5</td>
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<tr>
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<td>Mean selection across morphological traits (presumably induced by temperature)</td>
<td>0.940</td>
<td>16.8</td>
<td>178.1</td>
<td>&lt;0.0001</td>
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<td>Slope of precipitation on years</td>
<td>0.002</td>
<td>1.0</td>
<td>6.0</td>
<td>0.7377</td>
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<td>Slope of phenological traits on precipitation</td>
<td>0.750</td>
<td>4.0</td>
<td>20.5</td>
<td>0.0085</td>
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<td>Mean selection across phenological traits (presumably induced by precipitation)</td>
<td>0.971</td>
<td>34.1</td>
<td>348.9</td>
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<td>PRC</td>
<td>Slope of temperature on years</td>
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<td>Slope of phenological traits on temperature</td>
<td>0.716</td>
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<td>Slope of morphological traits on temperature</td>
<td>0.301</td>
<td>1.4</td>
<td>193.2</td>
<td>0.0001</td>
</tr>
<tr>
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<td>Slope of precipitation on years</td>
<td>0.211</td>
<td>1.3</td>
<td>50.2</td>
<td>0.3857</td>
</tr>
<tr>
<td></td>
<td>Slope of phenological traits on precipitation</td>
<td>0.634</td>
<td>2.7</td>
<td>762.6</td>
<td>&lt;0.0001</td>
</tr>
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<td>Sensitivity</td>
<td>Slope of phenological traits on temperature after removing an outlier (Goodenough et al. 2011)</td>
<td>0.914</td>
<td>11.7</td>
<td>360.1</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>analysis,</td>
<td>Mean selection across phenological traits (presumably induced by temperature) after removing an outlier (Goodenough et al. 2011)</td>
<td>1.000</td>
<td>38169.4</td>
<td>412972.2</td>
<td>&lt;0.0001</td>
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<td>PRCS dataset</td>
<td>Slope of phenological traits on temperature after removing the only study on mammal (Plard et al. 2014)</td>
<td>0.916</td>
<td>11.9</td>
<td>356.3</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td></td>
<td>Mean selection across phenological traits (presumably induced by temperature) after removing the only study on mammal (Plard et al. 2014)</td>
<td>1.000</td>
<td>48625.2</td>
<td>408249.8</td>
<td>&lt;0.0001</td>
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<tr>
<td></td>
<td>Slope of phenological traits on temperature after removing both the study on mammal (Plard et al. 2014) and an outlier (Goodenough et al. 2011)</td>
<td>0.915</td>
<td>11.7</td>
<td>351.3</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td></td>
<td>Mean selection across phenological traits (presumably induced by temperature) after removing both the study on mammal (Plard et al. 2014) and an outlier (Goodenough et al. 2011)</td>
<td>1.000</td>
<td>15415.8</td>
<td>408111.7</td>
<td>&lt;0.0001</td>
</tr>
</tbody>
</table>
Table S8. Metadata for all studies in the PRC dataset and effect sizes obtained for each study per each of the three conditions. (Supplied as Microsoft Excel document, because it is longer than 1 page).
SUPPLEMENTARY METHODS

Literature search on Web of Knowledge

To identify the studies satisfying the criteria necessary to assess adaptation, as specified in Methods, we searched Web of Knowledge (on 23.05.2016) using the following keywords:

(“climate change” OR “temperat*” OR “global change” OR “precipit*”) AND (“plastic*” OR “adapt*” OR “selection” OR “reaction norm”) AND (“body size” OR “body mass” OR “body length” OR “emerg* date” OR “arriv* date” OR “breed* date”) AND (“bird*” OR “mammal*” OR “arachnid*” OR “insect*” OR “reptil*” OR “amphibia*” OR “spider*”).

Next, to increase the probability of finding the relevant papers we run the search by using instead of taxa names detailed genera names within each taxon, as following: (“rodent*” OR “primat*” OR “rabbit*” OR “hare” OR “mole” OR “shrew*” OR “viverrid*” OR “hyaena” OR “bear*” OR “seal*” OR “mustelid*” OR “skunk*” OR “Ailurid*” OR “walrus*” OR “pinniped*” OR “Canid*” OR “mammal*”) OR “bird*” OR “flamingo*” OR “pigeon*” OR “grouse*” OR “cuckoo*” OR “turaco*” OR “rail*” OR “wader*” OR “shorebird*” OR “penguin*” OR “stork*” OR “pelican*” OR “condor*” OR “owl*” OR “hornbill*” OR “hoopoe*” OR “kingfisher*” OR “woodpecker*” OR “falcon*” OR “parrot*” OR “songbird*” OR “turtl*” OR “tortoise*” OR “lizard*” OR “snake*” OR “crocodil*” OR “caiman*” OR “alligator*” OR “reptil*” OR “frog*” OR “salamander*” OR “toad*” OR “amphibia*” OR “insect*” OR “beetle*” OR “butterfl*” OR “moth*” OR “mosquito*” OR “midge*” OR “dragonfly*” OR “wasp*” OR “bee*” OR “ant*” NOT (“fish*” OR “water*” OR “aquatic*”). These genera names were combined with the same key words for climate change, adaptation and trait as before. Finally, we joined the unique records from each of these two searches in a single database.

Assessing temporal change in selection

We estimated the temporal (linear) change in the annual linear selection differentials similarly to the analysis conducted to obtain the weighted mean selection differential (WMSD) estimates. First, we estimated the temporal change in selection for each study by fitting a mixed-effects model that accounted for temporal autocorrelation and we weighted the residual variance by the variance of the annual linear selection differentials (i.e. the reported squared SE) to account for uncertainty in the estimates of annual selection differentials. The fitted model was:

\[ Sel_t = \alpha + \beta_{Sel} \times Year_t + \varepsilon_t + \varepsilon; \]  

(1)
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where $Sel$ is the estimate of the yearly linear selection differential, Year the quantitative year covariate, $t$ the time, $\varepsilon_t$ is a Gaussian random variable with mean zero and following a lag-1 autoregressive (AR1) model over years, and $\varepsilon$ is an independent Gaussian random variable with mean zero and variance proportional to the estimated variance of the yearly linear selection differential (which depends on $t$). The $\beta_{Sel}$ is the regression coefficient that corresponds to the slope of the annual linear selection differentials on the year for the study.

Second, to assess whether these slopes were significant across the studies, we fitted a mixed-effects meta-analysis by using these slopes as a response and study identity and publication identity as categorical variables defining random effects influencing the intercept.

Heterogeneity among studies for the effect of temperature

We tested whether total amount of heterogeneity ($Q$) was statistically significant and estimated Higgins $I^2$ and $H^2$. Higgins $I^2$ reflects the proportion of total heterogeneity due to between-study variation (i.e. random effects) and ranges from 0 to 1. A value of 0 means that heterogeneity is due to within-study variation exclusively, whereas a value of 1 indicates that heterogeneity is due to between-study variation. This metric is, therefore, comparable among different meta-analyses. $H^2$ is the ratio showing the proportion of observed heterogeneity in relation to what would be expected under the null hypothesis of homogeneity. For example, a value of 2 means that there is twice as much variation as would be expected if no between-study variation were present (i.e., $H^2 = 1$).

The meta-analytical models differed in the amount of heterogeneity among studies (Supplementary Table S7). The amount of heterogeneity was moderate (Higgins $I^2$ between 0.3 and 0.6) for the models describing the change in temperature over years and the change of morphological traits with temperature in the PRC dataset. The amount of heterogeneity was substantial (Higgins $I^2$ between 0.6 and 0.75) for the model assessing the change of temperature over years in the PRCS dataset and the model of association between temperature and phenological traits in the PRC dataset. We found considerable heterogeneity (Higgins $I^2 > 0.75$) for models assessing WMS on both phenological and morphological traits and the model of the relationship between temperature and phenological traits in the PRCS dataset. The amount of heterogeneity was low in the model describing the association of temperature and morphological traits in the PRCS dataset.
Sensitivity of phenological responses to variation in population size

Variation in phenological responses may be caused by methodological factors in addition to ecological factors, in particular temporal trends in abundance of the sampled species may bias the estimates of phenology. Indeed, if species abundance increases over time, the probability of recording earlier events increases (especially if phenology is measured as the first occurrence date), meaning that species abundance can affect mean of the distribution of a phenological trait. For the same reason, the variance around the mean phenological response may be sensitive to population size, with higher variance at lower population sizes. To assess the sensitivity of our results to potential changes in population sizes over time, we fitted the model in which population abundance was included both as a fixed-effect explanatory variable and as an explanatory variable for the residual variance. This model is an extension of the models (eq. 2 in Main text) used to assess condition 2, and was fit to each study for which abundance data were available and duration of the study was at least 11 years (28 out of 42 studies). The fitted model was:

\[ \text{Trait}_t = \alpha + \beta \times \text{Clim}_t + \gamma \times \text{Year}_t + \delta \times \text{Abund}_t + \varepsilon_t + \varepsilon; \]  

(2)

where \( \text{Trait} \) is the mean phenotypic trait (z-scaled across the years within each study), \( \text{Clim} \) the quantitative climate covariate, \( \text{Year} \) the quantitative year covariate, \( \text{Abund} \) the quantitative covariate for species abundance, \( t \) the time, \( \varepsilon_t \) is a Gaussian random variable with mean zero and following a lag-1 autoregressive (AR1) model over years, and \( \varepsilon \) is an independent Gaussian random variable with mean zero and variance proportional to the estimated variance of the mean phenotypic trait (which depends on \( t \)). The \( \beta \), \( \gamma \) and \( \delta \) are the regression coefficients that correspond to the slopes of respectively the trait on the climatic variable, the trait on year, and the trait on abundance for the study. To avoid overfitting, we refitted the same model without the AR1 structure and retained, for each study, the model structure leading to the lowest marginal AIC, analogously to how it was done for the models presented in the main text (Methods).
SUPPLEMENTARY RESULTS

Effects of precipitation

No systematic change across years and studies was observed for precipitation in either dataset (Supplementary Fig. S3a). This finding is contrary to the increase in precipitation recorded over the last decades in the Northern Hemisphere \(^8,9\). Such a discrepancy may be related to high local variation in precipitation\(^8\) combined with the small number of studies focusing on this climatic variable in our dataset. The dataset focusing on the effects of precipitation consisted of phenological traits only. We found no significant association between precipitation and phenological traits in both datasets (Supplementary Fig. S3b, Supplementary Table S2). In the dataset investigating effects of precipitation on traits, we found marginally significant negative weighted mean selection over time (WMSD = -0.102± 0.048 SD\(^{-1}\); LRT between the model assuming WMSD is non-zero and the one assuming it equals zero: \(\chi^2 = 3.2, df = 1, p = 0.073\)). We found significant variation in selection among fitness components with most negative selection found for recruitment (Supplementary Table S1). The amount of heterogeneity was low for the models testing the change in precipitation over years in both datasets (Table S7), but it was substantial (\(I^2 > 0.6\)) in the models describing the association of traits with precipitation in both datasets and the WMSD.

Variation in morphological responses depending on the type of traits

The effect of temperature on morphological traits did not differ among the types of morphological responses (size vs. mass) in either dataset (LRT between the model with and without the type of morphological measure as a predictor in the PRCS dataset: \(\chi^2 = 0.02, df = 2, p = 0.991\), and in the PRC dataset: \(\chi^2 = 4.6, df = 2, p = 0.101\), Supplementary Tables S1 & S2).

Test of publication bias

We have not found evidence of the small-study effect for the effect sizes used to assess all three conditions with the PRCS dataset (Supplementary Fig. S15). For the effect sizes obtained with the PRC dataset, no evidence of the small-study effect was found when testing condition 2 (Fig. S16b,c). However, we found funnel plot asymmetry when testing condition 1 (Fig. S16a, Egger’s test: \(z = 5.88, p < 0.001\)). Such evidence of plot asymmetry is unlikely to result from a publication bias in this particular case. Instead, as we show in Fig. S5, studies spanning shorter period of time are associated with faster rate of climate change because 1)
they correspond to more recent studies, and 2) the pace of climate change has been increasing. Interestingly, the fact that shorter time series revealed higher rates of warming is in line with the recent study\textsuperscript{10} reporting the same findings.

\textbf{Variation in phenological responses depending on the type of traits}

We have tested whether, as shown recently\textsuperscript{11}, phenological responses differ among the types of traits. For this we have categorized all the phenological traits into three general categories: arrival (migration), breeding/rearing (nesting, egg laying, birth, hatching) and development (time in a certain developmental stage, antler casting date). This type of phenological measure was used as a fixed predictor in the mixed-effects models testing condition 2 (effect of climate on phenological trait, eq. 2, Methods in the main text). Phenological responses did not differ significantly among the types of phenological measure in either PRCS (Supplementary Table S2, LRT between the model with and without the trait type as a predictor: $\chi^2 = 0.56$, df = 2, p = 0.755) or PRC dataset ($\chi^2 = 0.42$, df = 2, p = 0.809).

\textbf{SUPPLEMENTARY DISCUSSION}

\textbf{Possible mechanisms underlying the observed adaptive phenological responses}

Our results suggest that selection seems to predominantly act via reproduction of adults and survival of young, as inferred from the strongest negative selection via recruitment, followed by selection via reproduction (Fig. 4, main text). In birds, such selection pressure has been shown to be triggered by environmental conditions and food availability during the breeding period and shortly afterwards, and it depends strongly on the synchrony of breeding with the availability of resources\textsuperscript{12–14}. 
**Supplementary Information**

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**SUPPLEMENTARY REFERENCES**


