1   **Phenotypic plasticity is aligned with phenological adaptation on both micro- and**

2   **macroevolutionary timescales**

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Abstract

In seasonally-variable environments, phenotypic plasticity in phenology may be critical for

adaptation to fluctuating environmental (temperature) conditions. Using an 18-generation

longitudinal dataset from natural insect (damselfly) populations, we show that phenology has

strongly advanced. Individual fitness data suggest this is likely an adaptive response towards a

thermally-dependent fitness optimum. A laboratory experiment revealed that developmental

plasticity qualitatively matches environmental-dependence of selection, partially explaining

observed phenological advance. Expanding our analysis to the macroevolutionary level, we use a

database of over 1-million occurrence records and spatiotemporally-matched temperature data

from 49 Swedish Odonate species to infer macroevolutionary dynamics of phenology.

Phenological plasticity was more closely aligned with adaptation for species that have recently

colonized northern latitudes, with more phenological mismatch at lower latitudes. Our results

show that phenological plasticity plays a key role in microevolutionary dynamics within a single

species, and such plasticity may have facilitated post-Pleistocene range expansion in this insect

clade.

Introduction

In many organism, life is characterized by dramatic life-history transitions between discrete stages that correspond to the unique demands of resource acquisition versus reproduction. For organisms with complex lifecycles, these life history transitions span disparate ecological niches, such as aquatic versus terrestrial environments, that demand irreversible metamorphosis to achieve such extreme ontogenetic niche shifts (Wilbur 1980; Werner & Gilliam 1984). The timing of such life history transitions, or phenology, is particularly crucial for organisms with complex life cycles that undergo their metamorphosis in seasonally variable environments. This is because success during a given life stage must depend not only on biotic factors such as predation, competition and seasonally-changing resources, but also on aspects of the abiotic environment, such as temperature, that vary across both time (generations) and space (between populations) (Hassal *et al.* 2007; Angilletta 2009; Plard *et al.* 2014; Visser *et al.* 2015; Bonamour *et al.* 2020). Thus, phenology is expected to be under net-stabilizing selection (Villemereuil *et al.* 2020) with an optimum that is shaped by various counteracting selection pressures that are in turn influenced by multiple biotic and abiotic environmental variables, including temperature, precipitation, competition and resource availability.

The location of phenological optima may fluctuate randomly in response to environmental stochasticity across years in seasonally variable environments (Hadfield 2016). Concomitantly, such fitness optima may show directional change and track advancing temperatures and resource abundances associated with anthropogenic climate change (Brashaw & Holzapfel 2001; Bradshaw & Holzapfel 2006; Parmesan 2006; Anderson *et al.* 2012; Thackeray & al. 2016). In both scenarios, phenological plasticity (phenotypic plasticity in the timing of life history transitions) is expected to be a target of natural selection (Chevin *et al.*

2010; Chevin & Lande 2015). Individuals that adaptively alter their developmental trajectory in

response to available environmental cues regarding the conditions occurring during or after the

life history transition (Whiteman 1994), will undergo metamorphosis to closely match the

phenological optimum and will therefore have a selective advantage (Chevin *et al.* 2010).

Phenotypic plasticity in phenology is therefore an expected key evolutionary adaptation to

seasonally variable environments (Levins 1968). This classical hypothesis has obtained

qualitative support in a number of studies across a range of taxa that all suggest a key role for

plasticity in explaining between- and within population differences in phenological traits

(Charmantier *et al.* 2008 ; Boutin & Lane 2014; Crozier & Hutchings 2014; Franks *et al.* 2014 ;

Nashoba & Kono 2020; Stamp & Hadfield 2020). Only a few of these studies includeorganisms

with complex life cycles (Phillimore *et al.* 2010; Stoks *et al.* 2014; Urban *et al.* 2014; Buckley &

Kingsolver 2019).

Recent work has recast the concepts of plasticity, fitness, and environmental variation in

terms of estimable quantitative genetic parameters that together describe plasticity's potential

contribution to adaptive evolution.   In this framework (Figure 1) plasticity, termed *b*, and the

environmental dependence of selection, termed *B*, jointly determine the extent that phenotypic

plasticity contributes to local adaptation (Chevin *et al.* 2010). The strength of plasticity *b*

describes the relationship between expressed population mean phenology and the average

environment experienced by a population. This parameter (*b*) represents the population-mean

reaction norm. The environmental dependence of selection, *B,* describes the relationship between

the optimum phenology and the mean environment, and so represents the degree to which natural

selection changes as a function of environmental variation. Importantly, estimation and

comparison of these parameters can provide insight into plasticity's role in adaptation (ability to

track the optimum) to spatio-temporal environmental variation (Hadfield 2016). New statistical

and analytical approaches have allowed researchers to leverage observational individual

occurrence records to estimate these parameters indirectly, via space-for-time substitution

(Phillimore *et al.* 2010). A growing body of studies have employed these or similar time-series

based approaches (Phillimore *et al.* 2010; Crozier *et al.* 2011; Phillimore *et al.* 2012; Phillimore

et al. 2016; del Mar Delgado *et al.* 2020; D. & Wilson 2021). This work (see also Villemereuil *et*

al. 2020) indicates that plasticity can explain a substantial fraction of spatio-temporal variation in

phenology across natural populations in the wild.

It is, however, still unclear whether and to what extent plastic variation in phenology

matches our expectations for plasticity's role in evolution. In particular, two critical open

questions on phenological plasticity's role in evolution remain unanswered: 1) does phenotypic

plasticity correspond to environmental-dependence of phenological optima at the

microevolutionary scale, thus amplifying or accelerating adaptation? and 2) is the role of

plasticity in adaptation greater for lineages inhabiting variable and/or recently colonized

environments? Answering the first question requires long-term data on individual fitness in the

wild. Answering the second requires comparative analysis of multiple species or lineages that

vary in ecology yet which share a similar and conserved complex life cycle.

Here we combine three independent, large-scale datasets from the insect order Odonata

(damselflies and dragonflies). Odonates are semi-aquatic insects with a phylogenetically

conserved complex life cycle characterized by metamorphosis from aquatic nymph (henceforth,

'larvae') to aerial reproductive adult (Stoks & Córdoba-Aguilar 2012). Our aim was to address

the above two related questions on phenological plasticity's role in adaptation at short and deep

timescales.

Methods – Data Collection

Long term study of Ischnura elegans

We analyzed data on individual phenology and fitness in a set of populations (approximately 16)

of the damselfly *Ischnura elegans* in province of Skåne, southern Sweden, for 18 years (2000-

2017). Each year, these populations were surveyed in a standardized approach during the

reproductive season of *I. elegans*. All captured individuals were sexed and their copulation status

(mated or not) was recorded. In this study, we used data on one major male fitness component:

male mating success (a binomially distributed variable) to estimate the strength of selection on

phenology through mating success.

Laboratory experiment on thermal plasticity in development time

We reared larvae of individual *I. elegans* from the egg stage, through hatching and

metamorphosis to adults, under two different larval temperature environments: 20 °C and 24 °C.

Maternal egg clutches (full sib clutches) were obtained from females caught *in copula* in the

field in the general population survey described above. Individual eggs and larvae from a total of

101 full-sib clutches were reared in a split-clutch GxE design across both environments.

Occurrence records of Swedish Odonata

We obtained public, spatiotemporally referenced observational records of adult Swedish

odonates identified to species level from the Swedish Species Observation System (Artportalen:

https://www.artportalen.se/). We used data from a ten year period from 2006-2015, the range of

years for which we had accurate temperature data and for which substantial observational

records were available in this public database. We obtained spatiotemporally matched estimates

of spring mean surface temperature from the publicly accessible NOAA Global Forecast System

Analysis (GFS ANL) database (https://www.ncdc.noaa.gov/data-access/model-data/model-

datasets/global-forcast-system-gfs). We obtained the mean surface temperature from

corresponding lat-long grid cell in the GFS ANL database for two time windows: the first 120

days of the year and the month of April. The first time window corresponds to a substantial

period of pre-metamorphosis larval development and covers the last instar for all the species in

our database, and so represents a long-term average temperature environment experienced during

a key stage of development. The second time window represents a shorter time slice from late

spring, just prior to the flight period of many early season species. Finally, we note that the scale

and purpose of our analysis precludes use of a "sliding window" approach; Our interest is to

compare developmental-temperature reaction norm variation across species (and so any such

comparison requires use of similar or the same environmental cues), rather than to identify a

specific time slice of spring temperature variation that is most important for a single species.

Methods – Statistical Analysis

Long term field study of Ischnura elegans

To infer selection on phenology, we modify the Lande-Arnold (Lande & Arnold 1983) equation

to include temperature dependence in the form of directional selection on phenology:

$$w = a + \beta z * (1 + \varphi t) + \frac{1}{2}\gamma z^2 + \varepsilon \qquad\qquad 1$$

175 where $\varphi = \frac{\phi}{\beta}$, ϕ is an interaction term as estimable in a regression model. Setting the first

176 derivative of equation 1 with respect to z to zero and solving yields the stationary point:

$$\theta_z = \frac{\beta}{-\gamma} + \frac{\phi}{-\gamma}t \qquad\qquad 2$$

where θ_z is the optimum phenology (if selection is stabilizing, otherwise it is a fitness

minimum). The slope of the relationship between temperature and θ_z is $\frac{\phi}{-\gamma}$, and represents a

direct estimate of the temperature dependence of selection (B).

Laboratory temperature experiment: raising damselfly families

We used a mixed effects model to estimate the relationship between thermal developmental

environment of larvae (two temperature treatments) and emergence time from our laboratory

experiment. Our model featured emergence day as the response variable, temperature treatment

as a fixed effect, and random intercepts for tank and maternal full-sib family

Occurrence records of Swedish Odonata and phylogenetic comparative analyses

We used a bivariate mixed modelling approach (Phillimore *et al.* 2010; Phillimore *et al.* 2012) to

infer interspecific variation in thermal reaction norms in phenology from our observational

records of Swedish Odonata combined with paired estimates of temperature in the first 120 days

of the year. We fit the bivariate model

$$\zeta_i = \mu_i + \beta_{1,i} * y + \beta_{2,i} * x + a_{lat} + a_{time(lat)} + \varepsilon \qquad\qquad 3$$

where ζ_i is the response vector of individual values of two variables: i = observed phenology or

spring temperature. β is a fixed effect regression coefficient between continuous latitude (y) or

year (x) and variable i. Two nested random effects are included in this model: a_{lat} is a random

effect describing (co)variation across binned latitude, and $a_{time(lat)}$ is a random effect describing

co(variation) across binned annual seasons within latitudinal grids. For each a and the residual ε

we estimated the full 2x2 unstructured covariance matrix $\begin{bmatrix} \sigma^2_{phenology} & \sigma_{phenology,temp} \\ \sigma_{phenology,temp} & \sigma^2_{temperature} \end{bmatrix}$,

for a total of three 2x2 random effect covariance matrices. We focus on analysis of latitudinal

spatial variation because Sweden spans a far greater latitudinal than longitudinal range, and

corresponding species distributions within Sweden reflect substantial latitudinal span but little

longitudinal span.

From this model we can interpret the ratio of the fixed effect parameter estimates,

particularly $\frac{\beta_{lat,\ phenology}}{\beta_{lat,\ temperature}}$ as approximating the environmental dependence of the optimum, B

(Hadfield 2016). From the random effects, we can interpret $b \sim \sigma_{phenology,\ temperature}/$

$\sigma^2_{temperature}$ where σ and σ^2 are estimated across time points within binned latitude ($a_{time(lat)}$).

This bivariate model was fit separately for each species in our dataset. We then used the

corresponding estimates of B and b in phylogenetic mixed models (Hadfield & Nakagawa 2010)

to explore the relationship between species mean latitude, species mean phenology, and the

strength and form of inferred phenological plasticity. Our models accommodated uncertainty in

our estimates of B and b.

Results

We found evidence of significant phenological advance during the 18 year study period of *I.*

elegans in the field ($F_{1, 47526} = 1231.38$, P <0.0001, Figure 2B). Although there was significant

among-year heterogeneity, on average the emergence date has advanced by .58 days (SE =

0.017) per year, corresponding to a predicted total advance of 10.44 days across the entire 18-

year period.

Using data on male mating success (N = 21,384 individuals for which we also had

annual temperature data, consisting of 5,487 mated males and 15,897 non-mated males), we find

evidence of statistically significant but annually variable (Figure 3B) sexual selection on

phenology. Overall, we found evidence of significant stabilizing selection on phenology

(estimates of parameters in equation 1, in units of raw days: γ = -0.00016, SE = 0.000072, χ_1^2 =

4.51, P = 0.0336; β = 0.001308, SE = 0.000972, χ_1^2 = 1.18, P = 0.2; binomial glmm: γ χ_1^2 =

6.99, P = 0.0177; β χ_1^2 = 2.16, P = 0.16), along with a significant temperature-dependence of

selection on phenology (ϕ = -0.00156, SE = 0.000593, χ_1^2 = 6.90, P = 0.0086; binomial glmm:

χ_1^2 = 5.02, P = 0.0251). Fitting a simplified model with directional selection only and random

variation among years to variance-standardized data indicates standardized directional selection

gradients varied substantially among seasons (ΔAIC = 265, overall estimate β = 0.027, SE =

0.021; see figure S1). The resulting estimate of the relationship between θ_z and spring mean

temperature indicates a temporal advance in the optimum phenology with increasing temperature

(Figure 3C). Our point estimate of B, the slope of the relationship between temperature and θ_z ,

given by the ratio of the parameter estimate $\frac{\phi}{-\gamma}$, indicates an advance of 10.24 days

(Bootstrapped 95% CI: -66.7995 – -0.59705) in the phenological optimum for each degree

Celsius of spring warming (Figure 3C). We also found evidence of negative B using an

independent dataset of 1695 observations from the Artportalen database when we inferred B

indirectly from interspecific data on phenology, although this indirect estimate was significantly

shallower than direct estimate we obtained from this long-term population study (Supplemental

material, Figure S2).

We obtained individual and family emergence time records from 521 individuals from

101 full-sib genetic families across two temperature treatments in our laboratory experiment.

We found significant acceleration of development in response to our experimental manipulation

of temperature ($F_{1,\,367} = 65.61$, P <0.0001, Figure 3A), with an estimated reaction norm of -17.38

(SE = 2.15) days per 1 °C warming of the developmental environment. This laboratory estimate

therefore corresponds in sign, and to some extent in magnitude, with our estimate of the

environmental dependence of θ_z estimated from the field data in the natural populations of *I.*

elegans (Figure 3C). We found statistically significant broad-sense heritability in the timing

emergence ($H^2 = 0.24$, $\chi_1^2 = 17.54$, P < 0.0001; SE: 0.078, 95% CI: 0.079-0.39; $V_a = 993$ SE:

245, $V_p = 4156$ SE = 326; $CV_A = 5.3\%$). Our finding of a negative thermal reaction norm in

larval development time that aligns with the environmental dependence of selection on

phenology was supported by an independent, indirect inference of *b* using observational data

(although the magnitude of these estimates differs substantially; Figure S2).

We analyzed paired temperature and phenology data from 1,027,952 records from 49

species of Swedish Odonates (see Table S1). We explored two temperature windows as

predictors of phenological variation: the mean temperature of the first 120 days of the year, and

the mean April temperature. We found substantial support for the 120 day window, as these

models consistently fit better than the April mean models for nearly all species (Figure S3). We

then kept the 120 day average models for downstream analysis.

Reaction norm estimates varied across species, although most estimates where within the

range of ± five days per °C of spring temperature variation (Figure 4A, Table S1). Notably, there

were a mix of both positive and negative reaction norm estimates and many species that showed

positive reaction norm slopes (Fig. 4). These analyses show that temperature during the last

instar larval stage can either advance or delay emergence, depending on species, and some

species were relatively insensitive to spring temperature (Fig. 4A). On average, the estimated

thermal reaction norms explained 1.4% of the all variation in phenology (Table S1). In

comparison to our estimates of b, estimates of B exhibited substantial sampling variance (Table

S1).

We found evidence of a significant phylogenetic signal in the phenological reaction norm

(Phylogenetic h^2 = 0.96 ΔDIC = 239, posterior distribution in Figure 4B), revealing that closely

related species have similar magnitude of thermal plasticity in phenology (Figure 4). Estimated

reaction norms were correlated with mean phenology across species, with early season species

exhibiting more negative reaction norms and late season species exhibiting positive reaction

norms (posterior mean coefficient: 0.03192, 95% CI: 0.01915 – 0.04435, pMCMC < 0.001,

Figure 5A). We also found a significant negative relationship between reaction norm slope and

latitude in a phylogenetic mixed model with latitude as a predictor of estimated reaction norm

(posterior mean coefficient: 0.40298, 95% CI: 0.03198 – 0.78868, pMCMC = 0.036, Figure

5B).

The alignment between the estimated phenological reaction norms, b, and the estimated

environmental dependence of selection, B, scaled by the magnitude of B (i.e., |B-b|/|B|), varied

significantly with species mean latitude (posterior mean coefficient: -0.054454, 95% CI: -

0.115952 – -0.004226, pMCMC = 0.048; with outlier dropped, posterior mean coefficient: -

0.055290, 95% CI: -0.105413 – 0.004944, pMCMC = 0.046; Figure 5C). When |B-b|/|B| is less

than unity plasticity can be considered adaptive; when above unity plasticity can be described as

maladaptive (Phillimore *et al.* 2016). Species at northern latitudes had thermal reaction norms

that were more closely aligned with their estimated environmental dependence of phenological

optima, resulting in adaptive plasticity at northern latitudes (Figure 5C). Finally, plasticity b

explained a greater amount of detrended variation in phenology (calculated as

$p*([\sigma_{phenology,temp}/\sqrt{\sigma^2_{phenology}}\sqrt{\sigma^2_{temp}}]^2)$ were the term in parentheses is at the level of

time(lat) and p is the proportion of the total variance in phenology that is explained by the

time(lat) level) in Northern than in Southern species (posterior mean coefficient: -0.6489, 95%

CI: - 1.1821 $-$ - 0.1102, pMCMC = 0.018, Figure 5D).

Discussion

Here we combine three independent datasets, together representing well over 1 million

individual insect records, to test two related questions on the role of phenotypic plasticity in the

evolution of phenology. First, we demonstrate pronounced recent phenological advance in a

single damselfly species, *Ischnura elegans*, using a long term study of individuals in the wild.

We find that thermal plasticity in developmental time in the laboratory is substantial,

corresponding in sign and to some degree in magnitude with the relationship between

temperature and the optimum phenology of the same species estimated in the field. This suggests

an important role for thermal plasticity in adaptation to seasonal environmental variability, and

also suggests plasticity could contribute to advancing phenology that corresponds to recent

anthropogenically-caused climate change in Sweden (SMHI 2015). At the macroevolutionary

scale, we used a large interspecific database of individual emergence records of 49 species of

odonates spanning the extensive latitudinal gradient of Sweden. Combining these occurrence

records with spatiotemporally-matched estimates of spring mean temperature, we found that

species-specific mean phenological reaction norms are more positive and more closely aligned

with indirect inferences of the environmental dependence of the optimum for northern than for

southern species. We also find that plasticity contributes more to variation in phenology at

Northern latitudes. Our combined intra- and interspecific results indicate that temperature-

dependent plasticity in phenology underlies both microevolutionary adaptation to contemporary

climate change as well as the macroevolutionary expansion into harsh high-latitude climatic

conditions that took place when species colonized these areas after the last Ice Age in

Fennoscandia, about 10,000 years before present.

We found a phenological advance in a single species (*Ischnura elegans*) of 0.58

days/year, almost six days per decade or 10.44 days over the entire 18-year study period (Fig. 1).

This is a dramatic phenological advance during the first two decades of the century in Sweden.

In fact, this is almost twice as large advancement of phenology as was documented previously

for *I. elegans* in a study of British Odonata for the period 1960-2004 (0.58 vs. 0.33; Hassall *et al.*

2007). Thus, although our findings of phenological advance are consistent with previous study in

Britain, the new results presented here suggest temperature-dependent phenological advance in

odonates may be more extreme than previously appreciated.

We find some correspondence between point estimates of the environmental dependence

of selection in *Ischnura elegans* and the population mean reaction norm, using three independent

datasets and approaches. Our direct estimate of *B* using data on individual fitness from the long-

term study on *I. elegans* and our indirect estimates using a public database of individual

occurrence records both suggest that the optimum emergence time advances substantially for

every centigrade degree of spring warming in *I. elegans*. Our direct estimate of the phenological

reaction norm matches with our direct estimate of the environmental dependence of selection,

and the correspondence is also found using a bivariate mixed model approach to indirectly

estimate these parameters (see Supplemental Material). Although absolute values of *B* and *b*

differ substantially across these two approaches (direct vs indirect), the qualitative conclusion –

that phenotypic plasticity can explain the close match between local optima set by environmental

variation – is similar across these different approaches and datasets. One the one hand, this

correspondence in qualitative interpretation (alignment of *B* and *b*) is encouraging and suggests

that our space-for-time substitution approach to estimating environmental dependence of optimal

phenologies may be robust to inevitable violation of the assumptions (e.g., local adaptation and

limited dispersal) that underlie the theory behind the method (Hadfield 2016). On the other

hand, we found a significant disparity in the magnitude of both *B* and *b* using these different

approaches; our estimates of *B* and *b* were significantly steeper in our direct assessment (Figure

S2). A likely explanation for this is that our direct estimate of these parameters was focused on a

more limited section of the geographic range, compared to our indirect estimate using data from

I. elegans across the latitudinal breadth of Sweden. In another comparison between these types

of approaches, Phillimore et al. (Phillimore *et al.* 2016) found relatively close correspondence

between different estimates of *B* in great tits (see also van Benthem *et al.* 2017 for a comparison

of other related approaches). The results presented here echo past suggestions (Phillimore *et al.*

2016) that further validation of indirect estimates of *B* is warranted.

Our laboratory breeding experiment revealed a strong effect of temperature at larval stage

on development and emergence time, with an advance of 17 days per degree Celsius. The fact

that this estimate of the mean reaction norm was steeper than our estimate of the environmental-

dependence of selection might suggest 'hyper plasticity' (Stamp & Hadfield 2020) wherein

plastic responses have the potential to exceed fluctuations in the optimum (see Radersma et al.

2020). Nevertheless, our laboratory experiment indicates that the strength of temperature-

dependent plasticity is qualitatively similar to our estimate of the environmental dependence of

selection and is broadly aligned with the direction of temporal phenological advance in response

to rising temperatures in natural populations (Fig. 3C). Indeed, the estimated population reaction

norm in *I. elegans* suggests that an adaptive fit between the thermal optimum and mean

phenology could be explained entirely by phenotypic plasticity. This indicates that *I. elegans*

may already be well-adapted to cope with changing climates and increasing temperature

compared to many other animal taxa, such as birds (Radchuk *et al.* 2019). Previous studies on

gene expression of heat- and cold shock proteins in *I. elegans* adults originating from different

parts of the geographic range indicate that adaptive thermal plasticity plays an important role in

the northward range expansion of this species (Lancaster *et al.* 2015; Lancaster *et al.* 2016), in

addition to genetic adaptation (Dudaniec *et al.* 2018).

Our laboratory experiment also revealed that development time was modestly heritable,

with a point estimate of $H^2 = 0.24$. This is considerably lower than a previous estimate of the

heritability of development time in this species (0.52), estimated in a single thermal environment

(Abbott & Svensson 2010). The modest level of heritability of development that we document

here would require a persistent variance-standardized directional selection gradient of

approximately $\beta = -.13$ to result in the observed annual phenological advance of 0.58 days/year

(approximately .03 within-year standard deviations). This would be relatively strong selection

compared to available evidence from field studies on phenotypic selection (Kingsolver *et al.*

2001). Although our results and analyses do indeed suggest that selection can be strong, we also

find little evidence of persistent directional selection of the magnitude required to produce such a

dramatic response. In fact, across all years, net selection on phenology is actually slightly

positive rather than negative as would be expected if earlier phenology was consistently favored

(Fig. S1). Therefore, it is unlikely that genetic evolution alone can entirely explain the strong

phenological advance of more than 10 days across the entire 18-year period, given the substantial

among-year variation (Figure 2) of *I. elegans* in southern Sweden. Instead, our analyses suggest

that phenotypic plasticity may have an important role in driving both inter-annual variation in

phenology and the progressively earlier flight seasons that we have documented here. These data

suggest that *I. elegans* can track changing phenological optima through plasticity, which will in

effect reduce or counteract directional selection for earlier phenology, a conclusion that was also

reached in a recent study of 21 bird and mammal species with long-term data (Villemereuil *et al.*

2020). More generally, various forms of phenotypic plasticity have been proposed to "buffer"

organisms against external stress from temperature extremes (Huey *et al.* 2003).

We found significant, phylogenetically-structured among-species variation in inferred

reaction norms in an analysis that explicitly accounted for uncertainty in these species-specific

estimates. Our point estimate indicates a phylogenetic heritability of near unity, indicating that

closely related species share similar phenological responses to temperature variation. The

significant phylogenetic signal in the reaction norm estimates is consistent with the idea that

species differences in ecology and physiology play important roles in generating reaction norm

variation across this clade, most likely because closely related species show a high degree of

niche conservatism (Wiens & Graham 2005; Svensson 2012; Wellenreuther *et al.* 2012). Our

findings add to a growing body of evidence from other taxa (Davis *et al.* 2010; Davies *et al.*

2013; Rafferty & Nabity 2017), indicating strong phylogenetic signal in phenological response to

climatic change.

Theory suggests that the fitness benefit of phenological plasticity depends upon the

existence of environmental cues that accurately predict the conditions that determine fitness in

the next life stage (Chevin & Lande 2015). Here we have focused on spring mean temperature

as a potential environmental cue (or correlate thereof). This is justified by substantial empirical

evidence linking temperature and corresponding thermal tolerance to various aspects of adult

fitness in insects in general (Punzalan *et al.* 2008; Garcia-Roa *et al.* 2020), and our study species

I. elegans in particular (Lancaster *et al.* 2015; Lancaster *et al.* 2016; Dudaniec *et al.* 2018;

Svensson *et al.* 2020b). Moreover, our laboratory experiment confirms that larval developmental

temperature is a predictor of emergence time into the transition to the adult aerial life-stage.

Across all our interspecific dataset, all but one species in our comparative analysis over-winter as

either aquatic larvae or eggs, and so are exposed to spring temperatures at a similar

developmental stage. The only exception to this rule is the winter damselfly *Sympecma fusca*,

which overwinters as an adult in vegetation refugia. Consistent with this, *S. fusca* exhibited one

of the most extreme negative estimate of *B* (Table S1)*,* as well as a negative estimate of *b* (Fig.

4A). This fits with previous research showing that temperature-phenology reaction norms tend to

be strongest in insects that over winter as adults (Forrest 2016). Across all the species included

in this study, other environmental cues are also likely to be important for determining

developmental rate; including aspects of the biotic environment, such as density of con- or

heterospecific competitors, resource availability, and photoperiod. These unknown additional

cues could explain much of the residual variance in phenology. Nevertheless, our focus on

temperature is relevant in light of anthropogenic climate change (Parmesan 2006) and the

general consensus that temperature is a strong determinant of fitness in ectotherms (Angiletta

2009).

The degree of alignment between the phenological reaction norms and environmental

dependence of selection, and the contribution of plasticity to variation in phenology, changed

across the latitudinal range of these 49 species in Sweden (Fig. 5). This indicates that adaptive

phenological plasticity has played an important role in the northern range expansion of this

clade. Insect colonization of the Scandinavian peninsula occurred relatively recently following

retreat of the Fenno-Scandian ice sheet, which covered the region from the last glacial maximum

until its recession at the end of the Pleistocene approximately 10,000 years ago (Hewitt 1999,

2000). Thus, odonate species that currently occur in northern Sweden have established

themselves in this region more recently than the ones in southern Sweden. Our findings of

stronger evidence of adaptive plasticity in northern species in our phylogenetic comparative

analysis (Fig. 5) is consistent with theoretical predictions (Lande 2009; Chevin & Lande 2011)

that plasticity might be particularly important in adaption to novel and variable environments,

such as near range limits (Lancaster *et al.* 2015; Lancaster *et al.* 2016). Conversely, we found

that southern species currently show some degree of non-adaptive or even maladaptive plasticity

in relation to temperature as they show values of scaled |B-b| greater than unity (Fig. 5C). A

caveat here is that our estimates of *B* (both direct and indirect) exhibit substantial sampling

variance (Table S1; Results, Figure 3C), due in large part to ratio effects that amplify effects of

latitudinal regression coefficients / selection coefficients that compose the indirect/direct

estimate of *B*, respectively. Even our direct estimate of *B* from *I. elegans*, inferred using a large

dataset of individual component fitness measures, exhibited high sampling variance, which

highlights the challenges of estimating and interpreting these parameters even in the presence of

a large dataset.

Despite these challenges, our analyses are broadly consistent with recent research and

indicate that phenotypic plasticity can be adaptive (Noble *et al.* 2019; Stamp & Hadfield 2020;

Svensson *et al.* 2020a; Johansson *et al.* 2021), although we note that the much observed

plasticity in our study is not necessarily adaptive. Interestingly, there was some degree of mis-

alignment between *b* and *B* in the southern species *I. elegans* (Fig. 3C), which is broadly

consistent with the greater mis-alignment in southern, compared to northern species at the

macroevolutionary level (Fig. 5C). More generally, plasticity can be adaptive and selected

against in unpredictable environments (Leung *et al.* 2020) and recent meta-analyses have

documented that the degree of plasticity sometimes exceeds genetic differentiation, revealing

non-adaptive or maladaptive plasticity (Radersma *et al.* 2020; Stamp & Hadfield 2020).

By combining multiple and independent datasets, we have revealed a potential role for

phenotypic plasticity in explaining intra- and interspecific variation in phenology. Our combined

intraspecific and phylogenetic-comparative analyses enabled us to evaluate the role of

phenological plasticity in post-Pleistocene micro- and macroevolution of the temperature-

dependence of insect phenology. Our work indicates that temperature-dependent phenological

plasticity can at least partly track changing optima due to recent climate change, and that such

adaptive phenological plasticity may also have facilitated historical range expansion into variable

and extreme northern environments.

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Figure 1. The environmental dependence of selection and the mean reaction norm jointly determine the role that phenotypic plasticity plays in adaptation. The x-axis represents an environmental variable important for individual fitness; the y-axis represents phenology, the timing of a key life history transition. The slope of the regression of the optimal phenology on environmental variation, B, represents the degree to which selection on phenology depends on the environment, shown in black. The degree to which expressed population mean phenology depends on environmental variation is represented by the population mean reaction norm, b, shown in blue. The degree to which B and b align determines the potential contribution of phenotypic plasticity to adaptation to environmental variation. Importantly, plasticity b is

494   adaptive when it moves a population closer to the optimum than it would otherwise be following

495   an environmental shift.

Figure 2. Reproductive advance in *I. elegans* in Southern Sweden. *Ischnura elegans*, a

common European damselfly, exhibits an aerial reproductive adult stage (**A**) that follows a

prolonged aquatic larval growth stage. Long term study of a set of populations in southern

Sweden over 18 years indicates a significant advance in the timing of the aerial adult phase (**B**).

Conclusions were unaffected by exclusion of data from the year 2000. Blue shading in B shows

95% confidence limit of the prediction.

Figure 3. Temperature dependent selection and plasticity are aligned in *I. elegans*. In a

laboratory experiment, increased larval developmental temperature was associated with

accelerated time to metamorphosis as adults. **A**. Y axis shows days from hatching to emergence.

In a long term study of *I. elegans* in the wild, selection on phenology (measured as male mating

success) varied across years but overall, selection was net-stabilizing, **B**, with optima that vary

slightly across years (lines show model fits from the fixed effects across years; each color

represents a unique year). The estimated optimum was negative temperature dependent, **C**.

Panel C shows the linear relationship between θ_z and spring mean temperature (equation 2 in

text); black line shows original ML estimates, grey lines show 400 samples from a multivariate

normal distribution centered at the ML estimates with covariance equal to the covariance matrix

of fixed effected from the fitted model (i.e. a parametric bootstrap). Dashed blue line shows the

estimated reaction norm from the plasticity experiment (see panel A).

Figure 4. Inferred temperature reaction norms for phenology across Swedish Odonates. A,
Estimated reaction norms for temperature dependent phenology show variation among 49
damselfly and dragonflyspecies, although most are relatively shallow and the phylogenetic
signal is high and statistically significant. Species images (photos by S. De Lisle, top down):
Calopteryx splendens (ID 32), *Lestes dryas* (ID 44), *Aeshna cyanea* (ID 1), *Brachytron praetense*
(ID 9). Full species names for each ID number are provided in Table S1. Panel **B** shows the
posterior distribution and point estimate (red line) for the phylogenetic heritability of the
phenological reaction norm.

Figure 5. Macroevolutionary dynamics of phenological plasticity. Early-emerging odonate

species have more negative thermal reaction norms than late-emerging species. Species that

emerge late in the season instead tend to exhibit positive reaction norms to winter/spring

temperature, **A**. There is evidence that negative reaction norms, reflecting accelerated

development in response to warm temperatures, evolve in southern latitudes **B**. Across species,

the alignment between inferred reaction norm slope, b, and the inferred environmental

dependence of the optimum phenology B, becomes greater (smaller absolute difference scaled by

the magnitude of B) for species with Northern geographic ranges **C**. Green line in C equals

unity; values of $|B-b|/|B| < 1$ indicate adaptive plasticity and values > 1 maladaptive plasticity.

Inferred plasticity explains a greater proportion of the detrended variation in phenology in

Northern species, Panel **D**. Together these data suggest that reaction norms have diversified at

the macroevolutionary scale and that this diversity may have played a an important role during

Odonate range expansion into northern latitudes. In all panels, red lines show posterior mean

model fits, blue lines show the posterior distribution. All models accounted for phylogenetic

relationships and uncertainty in the species-specific estimates of the *B* and *b*. In panel **C** an

extreme single outlier (*Aeshna grandis*) is not shown in the figure, but inclusion/exclusion of this

species had no effect on general conclusions (see text).

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Supplemental Material

Detailed Methods- Data Collection

Long term study of Ischnura elegans

We analyzed data on individual phenology and fitness in a set of populations (approximately 16)

of the damselfly *Ischnura elegans* in province of Skåne, southern Sweden, for 18 years (2000-

2017). This set of populations spans an area of approximately 40x40 km. Each year, these

populations were surveyed in a standardized approach during the reproductive season of *I.*

elegans, beginning in late May when they start to emerge from the aquatic larval stage and

continuing throughout the major part of the flying season until the end of July. Field work took

place daily, except during days of low temperature (< 14 °C), heavy wind and rain, when adult

damselflies are not active. Each population was visited at intervals between one and two weeks,

within the lifespan limits for adult *I. elegans* and corresponding to approximately 5 sampling

visits per site per year (Willink & Svensson 2017). Sampling was conducted for approximately

60 minutes at each site during a sampling session. See Willink and Svensson (2017) for more

details about general field and laboratory work procedures.

I. elegans adults were captured in the field. Copulating pairs were kept separate from

single-caught individuals in individual plastic containers. In the laboratory, all individuals were

sexed and their copulation status (mated or not) was recorded. In this study, we used data on one

major male fitness component: male mating success (a binomially distributed variable) to

estimate the strength of selection on phenology through mating success. Our focus on male

component fitness was due to two reasons: first, statistical power, in that we obtained far more

estimates of male mating success across seasons, and the nonlinear, random-regression

approaches (see below) to estimating variation in selection are data hungry. Second, our previous

work has shown that this fitness measure is correlated with female fitness (fecundity) in these

populations, corresponding to male and female phenotypic selection estimates that are

significantly and positively correlated with each other across these populations (Gosden &

Svensson 2008). This finding indicates that a broad patterns of selection acting through male

component fitness are indeed reflective of patterns of selection acting through female fecundity

in this system. We also note that female multiple mating is rare due to mate guarding in copula.

Hence, male mating success is a reasonable proxy of mean population fitness as a whole. Our

surveys yielded data on phenology (date of capture) from 47,615 individuals (28,978 males,

18,637 females) during this 18 year period (2000-2017). As the majority of individuals of *I.*

elegans in these populations in southern Sweden are univoltine and emerge as adults after one

year in the larval stage, these 18 years correspond to approximately the same number of

generations.

Laboratory experiment on thermal plasticity in development time

We reared larvae of individual *I. elegans* from the egg stage, through hatching and

metamorphosis to adults, under two different larval temperature environments: 20 °C and 24 °C.

These temperatures were chosen for two reasons. First, they mimic typical and elevated summer

conditions in Sweden, respectively, under a projected climatic shift of 4°C (De Block *et al.* 2013;

Dinh *et al.* 2013). Second, past work in odonates has indicated that temperature differences on

this scale can manifest significant affects on larval development (Dinh *et al.* 2013). Our choice

of only two temperature treatments also precludes estimation of more complex, nonlinear

reaction norms. Although this is a limitation of our design, we note that because statistical

theory (Phillimore *et al.* 2010; Chevin *et al.* 2015) behind reaction norm inference at other levels

of analysis in our study is limited to the case of linearity, we are most interested in the linear

approximation of the reaction norm. Maternal egg clutches (full sib clutches) were obtained in

2017 from females caught *in copula* in the field in the general population survey described

above. Females caught *in copula* were set up for oviposition in individual plastic cups at room

temperature, and provided with a wet filter paper for egg laying surface. Two days later, the

female was removed, the eggs were scanned and counted from the digital images. See Svensson

and Abbott (2005) and Svensson et al. (2005) for further methodological details about laboratory

procedures. Individual eggs and larvae from a total of 101 full-sib clutches were reared in a split-

clutch GxE design across both environments. We started with 20 full siblings per environmental

treatment for a total of approximately 4000 larvae across this rearing experiment. Upon hatching,

individual larvae were transferred to plastic cups where they were housed individually in

temperature-controlled water baths. Larvae were fed *Artemia* daily and kept at a constant

midsummer light cycle (16:8). Towards the end of larval development and when the larvae

reached the last instar, each cup received a wooden stick as an emergence aid and cups were

covered with mesh to prevent escape of emerging adults. This experiment continued until all

individuals had either died as larvae or emerged as adults. Of the 4000 larvae, 523 (13%)

successfully emerged as adults, with recorded emergence time for 521 individuals. Although

mortality in this experiment may appear nominally high, it is consistent with the high larval

mortality observed in other odonates (Anholt 1994; Stoks & Córdoba-Aguilar 2012), and we

note that over 500 adults recruited from 101 females corresponds to an absolute fitness (discrete

time per capita growth rate) ≈ 5, an exceptionally high number.   Larval development time was

calculated as date of emergence as an adult minus the date of hatching, consistent with our

previous procedures (Abbott & Svensson 2005).

Occurrence records of Swedish Odonata

We obtained public, spatiotemporally referenced observational records of adult Swedish

odonates identified to species level from the Swedish Species Observation System (Artportalen:

https://www.artportalen.se/). These data represent a combination of validated citizen science

records, as well as records reported by professional scientists and naturalists throughout Sweden,

and these data are also subsequently exported to the Global Biodiversity Information Facility

(GBIF: https://www.gbif.org/). We used data from a ten year period from 2006-2015, the range

of years for which we had accurate temperature data (see below) and for which substantial

observational records were available in this public database. We excluded observations of

larvae, as well as for rare taxa for which records were unavailable in some years in this range, as

well as taxa that were not included in our phylogeny (see below). Our final dataset consists of

1,027,952 records from 49 species, which is the majority of odonate species (75 %) that have so

far been recorded in Sweden (currently a total of 65; 43 dragonflies (Anisoptera) and 22

damselflies (Zygoptera)).

We obtained spatiotemporally matched estimates of spring mean surface temperature

from the publicly accessible NOAA Global Forecast System Analysis (GFS ANL) database

(https://www.ncdc.noaa.gov/data-access/model-data/model-datasets/global-forcast-system-gfs).

The NOAA GFS ANL provides global weather data estimated four times per day gridded at .5°

resolution (corresponding to approximately 25km in Sweden), using a system of satellites and

globally-distributed weather stations. Comparison of these surface temperature estimates to

direct temperature records from a weather station in Malmö, Sweden, obtained from the Swedish

Meteorological and Hydrological Institute (https://www.smhi.se/en), indicates the GFS ANL

data are an accurate representation of surface temperature ($r > 0.99$ between temperature

records). For each record in our dataset of Swedish odonates, we obtained the mean surface

temperature (GFS ANL database variable: tmp2m) from corresponding lat-long grid cell in the

GFS ANL database for two time windows: the first 120 days of the year and the month of April.

The first time window corresponds to a substantial period of pre-metamorphosis larval

development and covers the last instar for all the species in our database, and so represents a

long-term average temperature environment experienced during a key stage of development.

The second time window represents a shorter time slice from late spring, just prior to the flight

period of many early season species. We focused on mean temperature, because daily

fluctuations in air temperature are unlikely to correlate strongly with water temperature, although

average temperatures are a strong predictor of average water temperatures (Livingstone & Lotter

1998). We note that surface air temperatures are strong a strong predictor of water temperatures

in freshwater bodies, particularly in the upper 1m of the water column (Livingstone & Lotter

1998) where odonate larvae are most abundant. Finally, we note that the scale and purpose of our

analysis precludes use of a "sliding window" approach; Our interest is to compare

developmental-temperature reaction norm variation across species (and so any such comparison

requires use of similar or the same environmental cues), rather than to identify a specific time

slice of spring temperature variation that is most important for a single species.

We obtained phylogenic information for all 49 species in our dataset, using a recently

published large dated molecular phylogeny of the odonates (Waller & Svensson 2017). This

tree is available publicly from the Odonate Phenotypic Database

(http://www.odonatephenotypicdatabase.org/shiny/odonates/).

Detailed Methods- Data Analysis

Long term field study of Ischnura elegans

We used a linear mixed effects model to assess phenological advance in the timing of the adult

aerial period in *I. elegans* during our 18 year study period. This model featured the date (in

ordinal day of the year; January 1 = day 1) of an observation of an individual as the response

variable and year as a fixed effect. Our model also included a random intercept for population to

account for spatial variation in phenology among the study populations; our model did not

explore spatial autocorrelation, which we expect to be low as populations differ primarily in

microenvironment that is uncorrelated with geography.

To infer selection on phenology, we seek a statistical description of individual fitness as a

function of phenology, where the functional relationship between phenology and fitness varies

with spring temperature cues. We modify the Lande-Arnold (Lande & Arnold 1983) equation to

include temperature dependence in the form of directional selection on phenology:

$$w = a + \beta z * (1 + \varphi t) + \frac{1}{2}\gamma z^2 + \varepsilon \qquad\qquad 1$$

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1011   where $\varphi = \frac{\phi}{\beta}$, ϕ is an interaction term as estimable in a regression model, w is individual

1012   fitness, β is the linear selection gradient on phenology z, t is the temperature cue and γ is the

1013   nonlinear selection gradient on phenology. Setting the first derivative of equation 1 with respect

1014   to z to zero and solving yields the stationary point:

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$$\theta_z = \frac{\beta}{-\gamma} + \frac{\phi}{-\gamma}t \qquad\qquad 2$$

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where θ_z is the optimum phenology (if selection is stabilizing, otherwise it is a fitness

minimum). We note that this quadratic description of environmental-dependence of selection

also approximates environmental dependence of a Gaussian fitness function (Chevin *et al.*

2015). The first part of the right hand side of equation 2 is an intercept equal to the fixed location

of the optimum obtained from the standard Lande-Arnold equation (Phillips & Arnold 1989).

The second term on the right hand side describes a temperature-dependent slope. Thus, the

simple modification of the Lande-Arnold equation in 1 yields a statistical description of a linear

relationship between temperature cue and optimal phenology, where the slope of the relationship

between temperature and θ_z is $\frac{\phi}{-\gamma}$, and represents a direct estimate of the temperature dependence

of selection (*B*).

We fit equation 1 to our *I. elegans* field dataset using a linear mixed effects model with

male copulation success as a response, i. e. a measure of sexual selection. For comparison, we

also fit a simplified model, with directional selection only (i.e., no temperature-dependence or

nonlinear terms). Although environmental effects on non-linear terms have not received

theoretical or empirical attention (Chevin *et al.* 2015; Villemereuil *et al.* 2020), we nonetheless

found no evidence for such effects and so focus on temperature effects on linear gradients. We

focus on males only in this analysis, as copulation success is likely a more critical determinant of

male fitness than it is for females; and also note that selection via male and female fitness

components are strongly correlated across space and time in the wild (Gosden & Svensson

2008). We used absolute copulation success as a response, as this resulted in more consistent

model convergence and eases interpretation; however, qualitatively equivalent conclusions were

obtained using relativized (by subpopulation, season or globally) copulation success. We

estimated β, γ, and φ from the fixed effect parameters (doubling the nonlinear regression

coefficient; Stinchcombe *et al.* 2008), and included random (co)variation in β and γ among years

to accommodate variation in selection independent of temperature and possible relationships

between temperature and height of the fitness function emerging from equation 1. We fit an

unstructured covariance matrix as we found no evidence for temporal autocorrelation in selection

(ΔAIC = 135 for first order autoregressive covariance structure). We fit a gaussian-distributed

model for consistency with theory and to provide estimates of the parameters in equation 1

(Chevin *et al.* 2015), although we also provide p-values from an equivalent mixed model

assuming binomial error. Temperature was obtained as the mean of the first 120 days from the

NOAA GFS ANL database for the corresponding grid cell of our study populations, with the

exception of records from 2000-2005 for which we instead calculated this value from the

Swedish Meteorological and Hydrological Institute data since the GFS data was unavailable for

this period. We found close correspondence for the two years in which we had data from both of

these sources (120 day mean, 2006: 1.061°C SMHI, 0.75°C NOAA; 2007: 5.89°C SMHI,

5.02°C NOAA).

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Laboratory temperature experiment: raising damselfly families

We used a mixed effects model to estimate the relationship between thermal developmental

environment of larvae (two temperature treatments) and emergence time from our laboratory

experiment. Our model featured emergence day as the response variable, temperature treatment

as a fixed effect, and random intercepts for tank and maternal full-sib family. We calculated

phenotypic variances, additive genetic variances and heritability (h^2), the latter as twice the

family variance over the total variance of the random effects (the sum of tank, family, and

residual variance components). We assessed statistical significance of h^2 using a likelihood ratio

test of the family variance component. We also calculated standard error and 95% confidence

intervals by empirically constructing the sampling distribution of h^2 by taking 1 million draws

from a multivariate normal distribution centered on our original REML estimates of the variance

components with covariance equal to the Hessian matrix of the fitted model (Houle & Meyer

2015). We note that our estimate of heritability is conditioned on the fixed effect of temperature

treatment (Lynch & Walsh 1998).

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Occurrence records of Swedish Odonata and phylogenetic comparative analyses

We used a bivariate mixed modelling approach (Phillimore *et al.* 2010; Phillimore *et al.* 2012) to

infer interspecific variation in thermal reaction norms in phenology from our observational

records of Swedish Odonata combined with paired estimates of temperature in the first 120 days

of the year. The premise behind this approach is to use detrended covariation in temperature and

phenology, within geographic grid cells, as an estimate of population mean reaction norms.

From the same model, covariation in mean phenology and temperature across latitudinal

geographic grid cells provides an estimate of the environmental dependence of selection

(Hadfield 2016). We thus fit the bivariate model

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$$\zeta_i = \mu_i + \beta_{1,i} * y + \beta_{2,i} * x + a_{lat} + a_{time(lat)} + \varepsilon \qquad\qquad 3$$

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where ζ_i is the response vector of individual values of two variables: i = observed phenology or

spring temperature. β is a fixed effect regression coefficient between continuous latitude (y) or

year (x) and variable i. Two nested random effects are included in this model: a_{lat} is a random

effect describing (co)variation across binned latitude, and $a_{time(lat)}$ is a random effect describing

co(variation) across binned annual seasons within latitudinal grids. For each a and the residual ε

we estimated the full 2x2 unstructured covariance matrix $\begin{bmatrix} \sigma^2_{phenology} & \sigma_{phenology,temp} \\ \sigma_{phenology,temp} & \sigma^2_{temperature} \end{bmatrix}$,

for a total of three 2x2 random effect covariance matrices. Thus, in this model space (latitude)

and time (year) are included as both continuous fixed effects, as well as binned levels in nested

random effects.

We focus on analysis of latitudinal spatial variation because Sweden spans a far greater

latitudinal than longitudinal range, and corresponding species distributions within Sweden reflect

substantial latitudinal span but little longitudinal span. Our dataset of odonate observations

spanned latitudes from $55° - 69°$, corresponding to the full latitudinal range of Sweden. We

note, however, that longitudinal variation, when present, will be captured in variation in

estimated spring mean temperatures for observations recorded from differing longitudes within

the same latitudinal resolution, and thus is a source of residual within-bin variation

accommodated in our model. For estimation of our mixed model random effects, we binned

latitude by half degree increments, with the exception of extreme northern latitudes (over 62°)

due to limited data from these sparsely populated Swedish regions. Our dataset contained 14

latitudinal bins with each species containing observations represented in at least 4 adjacent bins.

From this model we can interpret the ratio of the fixed effect parameter estimates,

particularly $\frac{\beta_{lat,\ phenology}}{\beta_{lat,\ temperature}}$ as approximating the environmental dependence of the optimum, B

(Hadfield 2016). From the random effects, we can interpret $b \sim \sigma_{phenology,\ temperature}/$

$\sigma^2_{temperature}$ where σ and σ^2 are the elements of the random effect covariance matrix estimated

across time points within binned latitude ($a_{time(lat)}$). Thus, b is the de-trended regression of

phenology across temperature within latitudinal bins (Phillimore *et al.* 2010; Phillimore *et al.*

2012). This bivariate model was fit separately for each species in our dataset.

We then used the corresponding estimates of B and b in phylogenetic mixed models

(Hadfield & Nakagawa 2010) to explore the relationship between species mean latitude, species

mean phenology, and the strength and form of inferred phenological plasticity. We focus on

species mean latitude because we were interested in how plasticity has evolved with Northern

range expansion. These models included species as a random effect, with covariance among

levels equal to the phylogenetic-variance-covariance matrix from our species level phylogeny,

standardized to a depth of 1 (i.e., using the correlation matrix). These models also included a

residual term. We accommodated uncertainty in our estimates of B and b in these phylogenetic

mixed models by modelling the posterior variance of the species-specific estimates as a non-

fitted random effect. We also estimated phylogenetic signal ("phylogenetic heritability") in the

inferred reaction norms b as the phylogenetic variance over the sum of the phylogenetic and

residual variance (Pagel 1999; Hadfield & Nakagawa 2010) from a mixed model with b as the

response, an intercept, and species as a random effect (in addition to the posterior variance in b,

as above).

All bivariate and phylogenetic mixed models were fit by Bayesian MCMC using

MCMCglmm in R and assuming weak priors. All other models were fit in SAS using the

glimmix procedure. SAS and R scripts to reproduce our analyses and figures, as well as all raw

data, are provided at: https://github.com/spdelisle/OdonatePhenology. All datasets have also

been deposited as .csv files on Dryad

https://datadryad.org/stash/share/FKHv4E_XmOX2f4yEi63pTibgzqmNFuXXhJLi_lnV3J0.

Table S1. Summary statistics for 49 species of Swedish Odonata. B is the indirect estimate of the environmental dependence of the optimum, b is the indirect estimate of the temperature-phenology reaction norm. R2 is the variance in phenology explained by plasticity. Parameter values are posterior modes; standard errors are the square root of the posterior variance See text for further details.

Species	Species ID #	Mean Phenology	Mean Latitude	Mean Temperature	B	SE_B	b	SE_b	R2	SE_R2	|B-b|/|B|	SE_|B-b|/|B|
Aeshna cyanea	1	233.0	57.6	1.442	-12.406	4.095	2.5608	0.6320	0.0518	0.026012	1.206422	0.0844
Aeshna grandis	2	215.6	58.3	0.646	-0.003	0.345	4.6119	0.8505	0.0985	0.025757	1615.617342	412.9258
Aeshna juncea	3	225.0	59.6	-0.289	4.442	0.574	2.8877	0.7127	0.0538	0.027019	0.349861	0.1680
Aeshna mixta	4	241.2	56.5	1.975	-16.852	1.153	1.3509	0.7323	0.0081	0.009180	1.080163	0.0441
Aeshna serrata	5	206.5	58.7	0.171	48.812	8.887	1.0600	1.7186	0.0012	0.006108	0.978285	0.0362
Aeshna subarctica	6	228.9	57.7	1.192	290.459	7623.444	2.0766	1.3736	0.0053	0.008642	0.992851	0.0076
Aeshna viridis	7	216.7	58.5	0.263	32.910	2.436	3.6705	1.1661	0.0135	0.011257	0.888469	0.0351
Anax imperator	8	193.3	56.2	2.529	4.809	1.908	0.0994	0.9901	0.0001	0.012450	0.979327	11.3041
Brachytron pratense	9	155.9	57.0	1.523	13.764	6.111	-1.0166	0.4538	0.0364	0.028240	1.073857	0.0723
Cordulegaster boltonii	10	193.3	58.6	-0.027	-9.118	0.897	-0.7787	0.7096	0.0035	0.008274	0.914595	0.0767
Cordulia aenea	11	161.8	57.9	0.783	-19.209	1.434	-0.4265	0.6294	0.0012	0.005941	0.977796	0.0331
Epitheca bimaculata	12	169.6	57.7	0.411	-28.628	1055.377	-0.5089	1.0138	0.0080	0.028895	0.982223	0.0676
Gomphus vulgatissimus	13	162.8	57.7	0.973	35.321	2.908	-1.4637	0.9210	0.0022	0.003554	1.041438	0.0268
Leucorrhinia albifrons	14	179.8	58.2	0.870	-3.666	0.534	0.3605	0.9089	0.0011	0.013577	1.098343	0.2528
Leucorrhinia caudalis	15	173.8	58.6	0.247	-27.909	7.367	-2.4957	0.7459	0.0566	0.039911	0.910575	0.0328
Leucorrhinia dubia	16	177.8	59.4	-0.260	8.546	1.022	-0.1009	0.7446	0.0001	0.005767	0.988188	0.0888
Leucorrhinia pectoralis	17	169.5	58.1	0.830	26.900	3.789	-1.0400	0.6179	0.0103	0.011496	1.038663	0.0244
Leucorrhinia rubicunda	18	156.8	58.7	0.177	0.753	0.490	-1.1531	0.6833	0.0138	0.019647	2.530831	184.0942
Libellula depressa	19	166.2	57.0	1.854	2.794	1.590	-0.3093	0.6055	0.0013	0.010124	1.110712	22.2029
Libellula fulva	20	175.6	57.6	1.097	3.919	1.652	-0.9911	1.0366	0.0080	0.015304	1.252859	0.9418
Libellula quadrimaculata	21	171.1	57.9	1.005	-1.558	0.431	-0.0468	0.4086	0.0002	0.008075	0.969989	0.6462
Onychogomphus forcipatus	22	192.1	58.1	0.496	-236.086	64.794	0.4264	1.1429	0.0002	0.001650	1.001806	0.0051
Orthetrum coerulescens	23	194.5	57.9	0.925	-5.314	1.082	2.0682	0.7418	0.0297	0.020072	1.389179	0.1711
Somatochlora arctica	24	190.1	61.9	-2.928	-41.123	3.064	1.3711	1.8187	0.0025	0.009623	1.033340	0.0437

Species	#											
Somatochlora flavomaculata	25	190.5	57.9	0.810	184.057	5219.785	0.6361	0.7264	0.0012	0.005339	0.996544	0.0064
Somatochlora metallica	26	201.7	58.5	0.325	-3.016	1.194	0.1539	0.6943	0.0002	0.008832	1.051026	0.4046
Sympetrum danae	27	235.4	58.7	0.577	5.620	0.368	0.8295	0.6413	0.0025	0.003751	0.852406	0.1093
Sympetrum flaveolum	28	209.9	57.9	1.027	-58.311	5.308	0.1120	1.1227	0.0000	0.000851	1.001921	0.0198
Sympetrum sanguineum	29	221.6	57.4	1.452	-21.563	1.009	1.0001	0.7844	0.0075	0.009955	1.046382	0.0365
Sympetrum striolatum	30	238.3	56.9	1.856	-5.498	15.219	0.6316	1.2205	0.0013	0.010595	1.114881	1.0232
Sympetrum vulgatum	31	230.6	57.8	1.142	1.295	1.082	1.0242	0.7465	0.0061	0.008825	0.209107	29.8587
Calopteryx splendens	32	179.4	57.1	1.653	-0.220	1.310	0.6685	0.8075	0.0033	0.009491	4.034132	9.7274
Calopteryx virgo	33	184.0	58.7	0.208	-16.654	1.325	0.8775	0.5640	0.0046	0.005008	1.052692	0.0346
Coenagrion armatum	34	150.7	58.5	0.187	-8.651	3.439	1.9120	2.3426	0.0156	0.059467	0.778982	0.2984
Coenagrion hastulatum	35	166.3	58.6	0.311	-11.758	0.463	0.7438	0.6654	0.0036	0.008095	1.063258	0.0566
Coenagrion johanssoni	36	186.5	60.7	-1.658	1.245	0.377	1.9119	1.0268	0.0547	0.051148	0.535081	0.5853
Coenagrion lunulatum	37	155.3	57.4	1.281	100.991	3427.786	0.1397	0.7116	0.0001	0.004499	0.998617	0.0086
Coenagrion puella	38	173.8	57.2	1.514	-3.466	1.194	0.2790	0.5345	0.0021	0.012848	0.919508	0.2366
Coenagrion pulchellum	39	170.1	57.4	1.390	-4.426	0.650	0.3369	0.4939	0.0011	0.006491	1.076123	0.1158
Enallagma cyathigerum	40	191.2	56.9	1.677	1.596	0.502	-0.0496	0.4573	0.0000	0.004072	0.968954	0.2893
Erythromma najas	41	176.8	57.7	1.216	5.112	0.595	1.7870	0.7510	0.0155	0.010195	0.650404	0.1576
Erythromma viridulum	42	208.1	55.7	2.723	-1.092	0.531	-0.1602	1.5354	0.0003	0.041118	0.853396	35.0739
Ischnura pumilio	43	171.4	56.4	2.697	6.200	2.925	-0.6999	2.6840	0.0020	0.033518	1.112892	2.2247
Lestes dryas	44	189.8	57.1	1.833	40.366	2.767	2.3172	1.9056	0.0011	0.002662	1.057406	0.0462
Lestes sponsa	45	213.0	57.5	1.223	-10.889	0.572	0.9240	0.6146	0.0038	0.006110	1.084856	0.0554
Lestes virens	46	231.0	56.6	2.259	184.289	25.457	-0.0969	1.6426	0.0000	0.003050	1.000526	0.0093
Platycnemis pennipes	47	185.6	57.8	1.058	-0.759	7.638	0.4768	0.7596	0.0019	0.010137	1.628500	1.5016
Pyrrhosoma nymphula	48	165.3	57.6	1.342	-31.494	5.328	0.6777	-0.5652	0.0049	0.006708	0.978481	0.0195
Sympecma fusca	49	144.7	57.9	1.232	-172.664	96.182	1.1082	2.7190	0.0007	0.005742	0.993582	0.0150

Directional selection gradient on phenology

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1131   **Figure S1. Variation in standardized directional selection gradients.** Histogram shows

1132   BLUP estimates of annual directional selection on phenology, from a model with copulation

1133   success as response and globally-standardized (sd = 1) day as a fixed effect. Blue dashed line

1134   indicates the overall (main effect) estimate of directional selection across all 18 study years. Data

1135   come from a mixed effects model with random variation in slope and intercept among years.

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A

B

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Figure S2. Comparison of parameter estimates from bivariate mixed effects reaction norm

model and direct estimates of B and b. In panel A, Long-dashed blue and black lines are

(respectively) the estimates of the population mean reaction norm, b, and the temperature-

dependence of the optimum phenology, B, estimated from a bivariate mixed model with fixed

and random effects of space and time (see text) using observational data from the Swedish

Artportalen and NOAA GFS ANL. Other graph features are as in Figure 3C; although sampling

effects result in slight differences in the grey lines showing error in B. Short-dashed blue line is

the reaction norm b estimated in a laboratory experiment, solid black line is the estimate of B

from individual fitness data from wild-caught damselflies. Panel B shows the posterior

distributions of the observational estimates of B (black) and b (blue), along with the direct point

estimates of these parameters. The direct estimate of B (b) differs significantly from the indirect

measure of B (b).

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Figure S3 Comparison of model fits between identical bivariate mixed models fit to

temperature and phenology data using either the mean of the first 120 days of the year or the

mean April temperature. The difference in Deviance shows that on average across the 49 species

studied that the mean 120 days fit on average 14322 (95% CI: -19713.136 – -8932.425, P <

0.0001) DIC units better than mean April temperature. Note that these are identical datasets

(equal N) and identical models, differing only in the values of mean temperature and so

comparing the likelihoods in this way provides one approach to assessing fit.

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