Genetic and thermal variation influence adaptation to fluctuating temperature in the seed beetle, *Callosobruchus maculatus*

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Summary

Climate change is associated with both the increase in mean and variability of

thermal conditions. The use of more realistic thermal regimes is therefore the

most appropriate laboratory method to correctly predict population responses to

thermal heterogeneity. However, both the long- and short-term implications of

evolving under such conditions are not well understood. Here, we examined the

effect of fluctuating daily temperatures on several key life history traits in the seed

beetle, *Callosobruchus maculatus*, that was exposed to a short-term thermal

switch into a novel environment. Populations were kept for 19 generations at one

of two temperatures: constant control temperature (T=29°C) or a fluctuating daily

cycle (T_{mean}=33°C, T_{max}=40°C, and T_{min}=26°C) and were subsequently exposed to

a switch to the opposite condition. We found that beetles that had evolved in

stressful environments were smaller in size when switched to a constant 29°C

and had far greater reproductive fitness compared to beetles from both the

constant control and continuously stressful 33°C environments. This suggests

that beetles raised in environments with stressful fluctuating temperatures were

more phenotypically plastic and had greater genetic variability than control

treatment beetles and indicates that populations that experience fluctuations in

temperature may be better able to respond to short-term changes in

environmental conditions.

Introduction

A multitude of studies have shown the negative impact of increasing mean temperature on important life history traits in invertebrate species (Bauerfeind & Fischer, 2014; Rogell *et al.*, 2014; Vasudeva *et al.*, 2014; Berger *et al.*, 2017; Chen *et al.*, 2018; Klepsatel *et al.*, 2019; Ivimey-Cook *et al.*, 2021). In particular, heat stress caused by high temperatures outside of a species' thermal optimum can disrupt reproduction, reduce longevity and survival in insects (Berger *et al.*, 2017; Ivimey-Cook *et al.*, 2021), particularly if outside of a species Thermal Fertility Limit (TFL, reviewed in Walsh *et al.*, 2019).

Increasing mean temperatures, as well as the increasing frequency of Extreme High Temperature events, (EHTs, Ma *et al.*, 2021), are two of the chief outcomes of rising anthropogenic gas emissions that characterise global climate change (Lashof & Ahuja, 1990; Pereira *et al.*, 2012; Pachauri *et al.*, 2014; Ummenhofer & Meehl, 2017). This change in temperature and frequency of EHTs can influence populations both directly, for example, by increasing the rate of genome wide *de novo* mutations (Berger *et al.*, 2017, 2021), or indirectly, for example, by triggering phenological mismatches between species and prey (Visser *et al.*, 1998, 2012; see also Parmesan, 2006 for an extensive review). This increase in environmental stress leads populations to either adapt and track environmental conditions through phenotypic plasticity, to shift their geographic boundaries to match thermal tolerance (either by changing latitude or altitude), or to go extinct (Holt, 1990; Pereira *et al.*, 2012; Hetem *et al.*, 2014; Kellermann *et al.*, 2019; Lehmann *et al.*, 2020; Trisos *et al.*, 2020). Until recently, species in tropical habitats were predicted to be especially vulnerable, as they were thought to have evolved far more narrow and specialized thermal ranges (Janzen, 1967; Deutsch *et al.*, 2008; Walters *et al.*, 2012). However recent work using multiple *Drosophila* species (n = 22) has questioned this idea, with results showing that

73   the breadth of thermal performance and point of thermal optimum did not differ

74   between temperate and tropical species (MacLean *et al.*, 2019).

75   Not only is the Earth's mean temperatures rising, but it is also becoming

more variable (Folguera *et al.*, 2011; Vasseur *et al.*, 2014; Masson-Delmotte *et*

al., 2021). This increase in environmental variability is likely to intensify the

already detrimental impacts of elevated temperatures (Vasseur *et al.*, 2014).

Building on work by Deutsch *et al.* (2008), Vasseur *et al.* (2014) found that

changes to both the mean and variance in environmental temperature produced

long-term changes to population fitness. More specifically, performance data

collected from 38 globally distributed invertebrate species indicated that whilst

increasing mean temperature had a mixture of both positive and negative effects

on performance, which were largely latitude-dependent, increased variation was

associated with more negative effects (Vasseur *et al.*, 2014). In addition, the

authors highlighted the relative contribution of mean and variance in determining

projected performance in the years 2050-2059. They found that a change in

mean temperature explained only 32% of future species performance, whereas

combining both the mean and variance simultaneously explained 93%. This

highlights the importance of understanding how species react not only to changes

in mean temperature, but also to changes in temperature *variation* in order to

form accurate predictions of a population's response to climate change.

93   Until recently, studying the effects of climate warming and the resulting

adaptive responses of organisms was confined to field studies, with little control

over multiple variables, or laboratory studies that maintained populations at

constant temperatures (Fischer *et al.*, 2011; Folguera *et al.*, 2011; Thompson *et*

al., 2013; Bauerfeind & Fischer, 2014). However, we now know that populations

often exhibit marked life history differences when exposed to fluctuating rather

than constant thermal stress in the laboratory (Folguera *et al.*, 2011; Bauerfeind &

Fischer, 2014; Kellermann & van Heerwaarden, 2019; Buckley & Kingsolver,

2021). For example, reaction norms of the mosquito *Anopheles stephensi* under

fluctuating thermal regimes were fundamentally different to those under constant

temperatures (Paajimans *et al.,* 2013). Similarly, in the tropical butterfly *Bicyclus*

anyana, life history traits were strongly influenced by both the mean and the

amplitude of the experimental thermoperiod (Brakefield & Mazzotta, 1995)*.*

Indeed, the use of constant temperatures might significantly underestimate the

impact of global warming on life history evolution (Fischer *et al.* 2011).

Fortunately, there is now a well-accepted requirement that empirical studies

incorporate more realistic thermal regimes into their experimental design

(Niehaus *et al.*, 2012; Paaijmans *et al.*, 2013; Buckley & Kingsolver, 2021). As a

result, the number of laboratory studies involving invertebrates and "natural"

thermal variation is ever increasing (Colinet *et al.*, 2015; Morash *et al.*, 2018; Ma

et al., 2021b; Morgan Fleming *et al.*, 2021; Chang *et al.*, 2022). However, there is

still the need to understand the long-term implications of evolving under natural

conditions that mimic the thermal stress associated with climate warming on the

short-term ability to adapt to novel temperatures, and contrasting these outcomes

with populations evolving under constant stress-free conditions.

118   To this end, we investigated the long-term effects of thermal stress

caused by realistically fluctuating temperatures on the phenotypic plasticity and

adaptation of two laboratory populations of seed beetle, *Callosobruchus*

maculatus. In addition, we examined the short-term effects of exposure to a novel

environment both into and from the fluctuating environment. Two different thermal

regimes were used: in one regime, beetles were kept at a constant control

temperature of 29°C, and in the second regime we exposed beetles to a more

stressful and realistic fluctuating daily cycle with a mean temperature of 33°C

(representative of a May day in southern India, where the laboratory lines were

originally collected). The two beetle populations were then either kept in these

two environments for the entirety of the experiment or were *switched* to the other

environment for two generations without selection prior to assaying several key

life history traits (development time, body mass and various measures of

reproductive fitness). Previous work in the same species of beetle has highlighted

the negative effect of increasing temperature with environmental fluctuation on

fecundity traits (with little to no effect on hatching success, development time and

body mass; Hallsson & Björklund, 2012). Importantly, our definition of fluctuating

environments differs from theirs. Whilst the term employed here represents daily

sinusoidal fluctuations around a constant mean, representative of the natural

environment that a seed beetle could experience, Hallsson and Björklund (2012)

used the term to describe the addition of thermal noise around a linear increase

from 30°C to 36°C. Thus, we predict that beetles will exhibit entirely different life-

history responses when populations are exposed to stressful but repeating

sinusoidal fluctuations without a corresponding linear increase in mean

temperature.

Methods

Study system

C. maculatus is an agricultural pest that originates from Africa and Asia but is

currently found throughout the world. Adult seed beetles are facultatively aphagous –

that is, they do not require food or water to survive and acquire all the resources they

need during the larval stage within the bean. Aphagous adults can live up to two

weeks but adults with access to nutrients can live three weeks or more (Fox, 1993;

Ursprung *et al.*, 2009). Females lay their eggs on the surface of dried legumes, such

as mung beans (*Vigna radiata*) or black-eyed beans (*Vigna unguiculata*). Larvae from

the fertilized eggs burrow into the bean and eclose as adults 23-27 days later.

Females of this species start to mate and lay eggs as soon as they emerge (Beck &

Blumer, 2014).

Laboratory evolution lines and climatic conditions

In our experiment, we used two different strains of *C. maculatus,* South India (SI)

USA and SI Leicester, both derived from a population of beetles collected in

Tirunelveli, India, in 1979 (Mitchell, 1991) and then subsequently raised at the

University of Kentucky, USA, and the University of Leicester, UK (from 1992),

respectively (Fricke & Arnqvist, 2004). We obtained these strains from Uppsala

University in Sweden and maintained them at the American University of Paris for

approximately 25 generations before establishing the replicates for the current

experiment. Beetles were cultured exclusively on mung beans and kept in climate

chambers at a constant 29°C, 50% relative humidity, and a 12:12h light:dark cycle.

They were housed at aphagy in 1L jars with 250g of beans, and approximately 250-

350 newly hatched beetles were transferred to new jars with fresh beans every 24

days on a continual basis.

For 19 generations prior to the experiment, we subdivided SI USA and SI

Leicester populations (Fig. S1A) into four replicates each. Two "Control" replicates of

each were maintained at a constant temperature of 29°C, while two "Stress"

replicates were subject to a daily temperature cycle (Fig. S1B) consisting of 12

separate 2hr periods of constant temperature T_i,

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$$T_i = T_{mean} + \Delta T \sin\left(\frac{i-12}{12}\pi\right),$$

where T_{mean} = 33 °C, ΔT = 7°C, and i = 0,1…. 11. This is a stepwise sinusoidal

temperature cycle with T_{max}=40 and T_{min}=26 that mimics typical late spring condition

in Southern India, where this species evolved. Humidity and light cycles remained the

same for all replicates: 50% relative humidity, and a 12:12 h light:dark cycle.

Prior to the assays of body size, development time, and reproductive fitness (see

next section), we created two replicates of two populations (SI USA and SI Leicester;

see Fig. S1A/B) for:

1. beetles adapted to and assayed at Control conditions (**USA**-C and **LEI**-C);

2. beetles adapted (for one year) to and assayed in Stress conditions (**USA**-S

and **LEI**-S);

3. beetles adapted to Control conditions that were then acclimatized to Stress

conditions for two generations without selection prior to being assayed (**USA**-

C-to-S and **LEI**-C-to-S); and

4. beetles adapted to Stress conditions that were acclimatized to Control

conditions for two generations without selection prior to being assayed (**USA**-

S-to-C, **LEI**-S-to-C).

To separate genetic adaptation from phenotypic plasticity – that is, to control

for the influence of parental effects – we created "acclimatized" treatments by

allowing beetles from one set of conditions to adjust to the new set of conditions for

two generations prior to assays (C-to-S and S-to-C; Fig. S1B). Critically, to remove

the possible effects of natural selection and rule out the possibility that rapid genetic

responses might influence our measurements for the "acclimatized" treatments, we

randomly paired 50 pairs of virgin beetles during each of the two generations. That is,

we removed the effects of assortative mating.

For the Stress-to-Control (USA S-to-C, LEI S-to-C) and the Control-to-Stress

(USA C-to-S, LEI C-to-S) treatments, the following steps were performed. First, we

moved beans with fertilized eggs from jars into 48-well virgin chambers. When

enough males and females had hatched (from day 21-24 after hatch), we paired 60

males and 60 females in 60 60-mm petri dishes with 100 beans in each dish and

placed these dishes in the opposing chamber. We made sure that there were

sufficient number of beans in each dish for females to lay just one egg per bean,

thereby eliminating competition among multiple larvae within a bean. To further

reduce larval competition, we removed adult beetle pairs from the petri dishes after

72 hours.

After 19 days, we then chose the 50 petri dishes with the most fertilized eggs

and put 48 fertilized eggs from each petri dish into individual marked 48-well virgin

chambers. One day after eclosion, we randomly selected and paired 50 females and

50 males and put them into 50mm petri dishes with 80 beans. After 72 hours, the

adult males and females were removed from the petri dishes. After 19 days, beans

with fertilized eggs from each petri dish were transferred into 48-well virgin

chambers. We then marked the date of hatch and sex of all offspring and conducted

assays of development time, body mass, and reproductive fitness.

For the continuous C and S treatments, we skipped the acclimatization steps

and simply moved beans with fertilized eggs into virgin chambers prior to hatch,

selecting one-day old males and females for all subsequent assays.

Body mass assay

Across two replicates, 8 males and 8 females were weighed for each of the 16 lines

(2 populations, 2 sexes, 4 temperature treatments; note for USA-C, 16 males and 16

females were weighed) using an Ohaus Pioneer Plus Analytical Balance (Model

PA214C). All virgin chambers were weighed empty, prior to adding the beetles to be

weighed. We then calculated the difference between the weight of the virgin chamber

before the beetles were placed inside and the weight of the virgin chamber after the

beetles were placed inside. Beetles from the body mass assay were not used for the

other assays.

Development time and fitness assays

Development time and fitness assays were done concurrently. We paired 50 1-day

old male and female beetles and placed them into 60mm petri dishes filled with 85

beans. After 24 hours, each pair was moved together into a new 60mm petri dish

filled with 75 beans, and the first dish was set aside in the same climate chamber.

The next day, this procedure was repeated. The beetles were left in the third and

final set of dishes until they died. The first dishes for each pair were marked "Day 0",

the second dishes were marked "Day 1", and the third and final dishes were marked

"Day 2+". After 19 days for each dish, all the beans with fertilized eggs were placed

into virgin chambers, which were monitored daily for the date of eclosion and the sex

of all offspring. To calculate development time, we counted the number of days

between the date that an egg was laid and the date the adult offspring eclosed. To

calculate LRS, we calculated the number of male and female offspring that emerged

for each pair, from all three sets of dishes (Days 0, 1, and 2+). To calculate individual

fitness (or λind), we took the dominant eigenvalue (using the popbio v. 2.7 package,

(Stubben & Milligan, 2007) from an age-structured Leslie matrix (Leslie, 1945) where

the top row denotes fertility and the sub-diagonal represents survival from age *t* to

t+1. 24 days of development time were added prior to day 0-2+ fertility schedule.

Statistical analyses

All statistical analyses were performed in R v. 4.1.0 (R Core Team, 2016) using

glmmTMB v. 1.0.2.9000 (Brooks *et al.*, 2017; Magnusson *et al.*, 2019) with pairwise

interactions and slopes compared using emmeans v. 1.6.1 (Lenth *et al.*, 2019).

Ggplot2 v. 3.3.4 (Wickham, 2009) was used for all graphical visualization. The overall

effects of each variable were identified using the Type 3 Anova function from car v.

3.0-10 package (Fox *et al.*, 2012).

For development time, body mass, and individual fitness, a Gaussian linear

mixed effects model was fitted (after log-transforming development time to reduce

right-skew) with the fixed effects of Population, Treatment, Sex (for development time

and body mass), and all higher order interactions. In addition to these main effects, a

fixed two-level factor of replicate number was added. Lastly, for the models involving

development time, the random effect of parental ID was added to account for

potential pseudoreplication. If the three-way interaction was non-significant (identified

from the Anova function), it was removed in order to reduce model complexity. A

generalized linear mixed effects model with Poisson distribution and similar fixed

effect structure was fitted for LRS and age-specific reproduction, albeit without the

variable Sex and all subsequent two/three-way interactions. In addition to a covariate

of Day (and all higher-order interactions with Population and Treatment), a random

effect of individual ID was added to the age-specific reproduction model to account

for repeated measures. Both models were checked for overdispersion and zero-

inflation (ZI) using DHARMa v. 0.4.1, (Hartig, 2020) by simulating the residuals of a

Poisson model. If significant, a variety of error distributions with/without zero-inflated

parameters (if ZI was identified) were then fitted and the best model identified by

Akaike's Information Criterion (AIC).

Results

Body mass

Individual body mass was significantly affected by both of the interactions involving

Sex (Sex and Population: $\chi^2(1) = 25.95$, p<0.001; Sex and Treatment: $\chi^2(3) = 19.18$,

p<0.001; Table S1A) but not by the remaining two-way interaction of Population and

Treatment ($\chi^2(3) = 2.51$, p = 0.47) or the three-way interaction ($\chi^2(3) = 6.37$, p =

0.09). Females were generally heavier than males (Fig. 1) in both populations. The

difference was more pronounced in the USA population (Average body mass (g): F-

LEI = 0.087, M-LEI = 0.075, estimate = 0.013, p<0.001; F-USA = 0.089, M-USA =

0.068, estimate = 0.021, p<0.001; Fig. 1, Tables S1A-B). The females of both

populations were similar in weight, but the USA males were smaller (F-LEI = 0.087,

F-USA = 0.089, estimate = -0.002, *p* = 0.35; M-LEI = 0.075, M-USA = 0.068,

estimate = 0.007, p<0.001; Fig. 1, Tables S1A-B). The relative difference between

male and female weight was largely dependent on temperature treatment (Fig. 1).

Overall, beetles raised in the S-to-C regime were smaller for both sexes in

comparison to other treatments (all comparisons significant to p = 0.05; Tables S1A-

B). However, the difference between male and female weights was far less

pronounced in the constant stress (S) treatment (albeit all differences were still

significant to p<0.001; F-S-to-C = 0.083, F-S = 0.089, F-C-to-S = 0.091, F-C = 0.089;

M-S-to-C = 0.064, M-S = 0.079, M-C-to-S = 0.071, M-C = 0.071; Tables S1A-B).

Figure 1. Body mass of individuals from the Leicester (triangle) or USA (circle)

populations in the C (Control), C-to-S (Control-to-Stress), S (Stress), or S-to-C

(Stress-to-Control) temperature treatments. Sex is denoted with either blue (male) or

red (female) points. Points represent mean values with accompanying standard

errors. Half violins show the distribution of raw data.

Development time

Development time was influenced by both two-way interactions involving

Temperature treatment (Treatment and Population: χ^2 (3) = 105.94, *p* <0.001;

Treatment and Sex: $\chi^2 (3) = 11.76$, $p = 0.008$). Similar to body mass, no detectable

three-way interaction was found ($\chi^2 (3) = 1.71$, p = 0.635). The USA and Leicester

populations responded differently to the four temperature treatments, with beetles

from the Leicester population developing faster on average. Populations from USA

took significantly longer to develop in comparison to populations from Leicester in

both the Control and S-to-C Treatments (Average Development Time (Days): LEI-C

= 23.7, USA-C = 24.7, Ratio = 0.960, $p<0.001$; LEI-S-to-C = 23.1, USA-S-to-C =

24.1, Ratio = 0.961, $p<0.001$; Fig. 2) but not in C-to-S (LEI-C-to-S = 23.0, USA-C-to-

S = 23.0, Ratio = 0.999, p = 1.00) or S Treatments (LEI-S = 22.5, USA-S = 22.3,

Ratio = 1.01, p = 0.38; Fig. 2, Tables S2A-B). Despite these differences, both

populations in the S treatment developed faster compared to other temperature

treatments (LEI-S = 22.5, LEI-S-to-C = 23.1, LEI-C-to-S = 23.0, LEI-C = 23.7; USA-S

= 22.3, USA-S-to-C = 24.1, USA-C-to-S = 23.0, USA-C = 24.7). In addition, whilst

males typically developed faster in both populations (shown with lower mean values

for 6 out of 8 population/treatment combinations, Fig. 2), only in the S-to-C treatment

was this difference significant (F-S-to-C = 23.7, M-S-to-C = 23.50, Ratio = 1.008,

$p<0.001$; Fig. 2, Tables S2A-B). However, both males and females in the S treatment

developed faster than other temperature treatments and showed no sex difference in

development time (F-S = 22.4, F-S-to-C = 23.7, F-C-to-S = 23.0, F-C = 24.2; M-S =

22.4, M-S-to-C = 23.5, M-C-to-S = 22.9, M-C = 24.1).

Figure 2. Development time in days of individuals from the Leicester (Red) or USA

(Blue) populations in the C (Control), C-to-S (Control-to-Stress), S (Stress), or S-to-C

(Stress-to-Control) temperature treatments. Sex is denoted with either circle

(Female) or triangle (Male) points. Points represent mean values with accompanying

standard errors. Half violins with associated jittered points show the distribution of

raw data.

Lifetime reproductive success

LRS was significantly influenced by the interaction between Population and

Treatment ($\chi^2(1)$ = 12.61, *p* = 0.005). Across all temperature treatments, LRS was

lower in the USA population than in the Leicester population (Average LRS: LEI =

53.2, USA = 40.2, Ratio = 1.32, *p*<0.001; Fig. 3A, Tables S3A-B). The largest

differences between populations occurred in the C-to-S and C treatments (LEI-C-to-S

= 50.2, USA-C-to-S = 33.6, Ratio = 1.49, *p*<0.001; LEI-C = 52.6, USA-C = 37.2, Ratio

= 1.41, *p*<0.001; Fig. 3A, Tables S3A-B). Despite these differences, LRS was highest

in the S-to-C treatment for both populations (LEI-C = 52.6, LEI-S-to-C = 69.7, Ratio =

0.75, *p*<0.001; USA-C = 37.2, USA-S-to-C = 60.9, Ratio = 0.61, *p*<0.001; Fig. 3A,

Tables S3A-B).

Age-specific reproduction

The interaction between population, treatment and day significantly influenced age-

specific reproduction (χ^2(3) = 203.54, *p*<0.001, Fig. 3C). Whilst continuous C and S

treatments exhibited similar age-specific patterns across both populations (Fig. 3C),

there were large differences between S-to-C and C-to-S treatments. This was

particularly apparent on Days 1 and 3 of reproduction (Fig. 3C). Individuals from both

LEI-S-to-C and LEI-C-to-S treatments exhibited far greater Day 1 reproduction than

all other treatments from both populations (including the analogous S-to-C and C-to-

S treatments). In contrast, USA-S-to-C exhibited increased reproduction *after* Day 1,

with the result that Day 3 of reproduction was comparable with the Day 1

reproduction for LEI S-to-C (Fig. 3C). This variation in reproductive schedule resulted

in large differences in age-specific slopes between the USA S-to-C and LEI S-to-C

treatments (Average change in average offspring produced per day: LEI S-to-C = -

7.14, USA S-to-C = 8.78, estimate = -15.92, p<0.001; Fig. 3C, Tables S4A-B).

Individual fitness

Whilst the individual main effects of Population and Temperature treatment

significantly influenced λind (χ^2(1) = 81.02, *p* <0.001, χ^2(3) = 111.23, *p* <0.001,

respectively; Fig. 3B), the interaction between these two did not (χ^2(3) = 7.64, *p* =

0.054). In a similar manner to LRS, the USA population had reduced λ_{ind} over all

temperature treatments (Average λ_{ind}: LEI = 1.164, USA = 1.146, estimate = 0.018,

p<0.001; Fig. 3B, Tables S5A-B). Across both populations, individuals from the S-to-

C treatment had the highest λ_{ind} (C = 1.154, C-to-S = 1.148, S = 1.146, S-to-C =

1.173, all comparisons p<0.001; Tables S5A-B). This was also consistent when

looking within each population (all comparisons p<0.001).

Figure 3. (A) Lifetime reproductive success (LRS) and **(B)** fitness (Lambda) of individuals from the Leicester (Red) or USA (Blue) populations in the C (Control), C-to-S (Control-to-Stress), S (Stress), or S-to-C (Stress-to-Control) temperature treatments. Points represent mean values with accompanying standard errors. Half violins show the distribution of raw data. **(C)** Age-specific reproduction of individuals from Leicester (dash-dot) or USA (solid) populations in the C (Control, Red), C-to-S (Control-to-Stress, Green), S (Stress, Blue), or S-to-C (Stress-to-Control, Purple) temperature treatments. Points with error bars represent mean values with accompanying standard errors. Jittered points represent raw data.

Discussion

The overall aim of this experiment was to evaluate the long- and short-term impacts

of realistic stressful thermal fluctuations, conditions that are becoming biologically

more and more relevant, on life history parameters of populations experiencing both

constant (remaining within the same treatment group) and switching (changing to a

different treatment group) thermal regimes. Previous hypotheses (Lewontin, 1974;

Nevo, 1978) have suggested that evolution in fluctuating environments should select

for genetically variable individuals that are robust to a wide range of thermal

conditions with wide thermal performance curves (TPCs; Kassen, 2002; Jin & Agustí,

2018). In this experiment, individuals exposed to novel benign conditions (S-to-C)

(although not those exposed to continuously stressful environments, S, see below)

had higher reproductive fitness (higher LRS and λind) than those that were exposed

to novel stressful conditions (C-to-S) or kept continuously in a benign environment

(C). These results are broadly in line with previous research conducted in the

opportunistic bacterial pathogen, *Serratia marcescens* (Ketola *et al.*, 2013)*.*

Heterogenous environments selected for bacterial clones that had faster growth and

higher yield than those grown under constant environments, even when introduced

into the same control temperature of 31°C (Ketola *et al.*, 2013). This increased

growth may be due to far greater selective pressure to remove mutations that could

otherwise accumulate in more constant benign environments (Ketola *et al.*, 2013).

However, results from a digital evolution experiment have suggested that this may

only allow for optimization in short-term rather than long-term evolvability (Canino-

Koning *et al.*, 2019).

Moreover our results suggest that individuals were able to tolerate and

survive at wide thermal breadth, presumably owing to the evolution of phenotypic

plasticity, but they reached maximal performance and experienced increased LRS

only when conditions were optimal (Gilchrist, 1995; Ketola *et al.*, 2013). This could in

part be due to differential gene expression as a result of exposure to a novel thermal

environment (also known as cryptic genetic variability, McGuigan & Sgro, 2009;

Paaby & Rockman, 2014). Similarly, this release of cryptic genetic variation could

explain why individuals that were predicted to perform poorly when switching from a

benign control to stressful fluctuating environment (C-to-S) suffered no fitness cost.

However, the relative merits of this form of variation have been queried and require

additional empirical testing (McGuigan & Sgro, 2009; Edwards & Yang, 2021;

Johansson *et al.*, 2021). We note that not detecting costs of phenotypic plasticity

does not mean that they do not exist. There might not be a sustainable cost to fitness

if individuals are able to accurately predict future environmental conditions and avoid

the expression of suboptimal genes (Auld *et al.*, 2010; Hoffmann & Bridle, 2022).

Quantifying these costs would require an experimental design with additional thermal

regimes beyond the scope of this current experiment.

When comparing body mass across treatments, individuals from the S-to-C

group were significantly smaller (across both populations and sexes), despite having

similar development times to those of the constant control group. Smaller body size

could therefore be a cost of adaptation (Kassen, 2002; Ketola *et al.*, 2013) to the

fluctuating conditions that is only detected in the benign environment and results in

reduced body size (albeit with no negative effects on fitness). However, whether this

reduction in mass is a disadvantage is difficult to determine. Large size provides a

fitness advantage due to sexual selection (Andersson & Iwasa, 1996) and offers

protection from desiccation (Le Lagadec *et al.*, 1998; Chown & Gaston, 2010)

whereas small size decreases larval competition (Messina, 2004) and reduces heat

stress (Chown & Gaston, 2010). Interestingly, similar to Hallsson & Björklund

(2012a), we found that sexual dimorphism in adult body size decreased in the

continuously stressful environment (S), although this could be considered population-

specific as individuals from USA failed to show such a decrease.

Lastly, there were consistent population-level differences across all

environmental treatments. Beetles from the USA population produced fewer

offspring, took longer to develop (although this difference disappeared under

stressful conditions), and had greater sexual dimorphism in body size compared to

individuals from the Leicester population. Such genotypic variation between

populations of the same species (particularly in *Callosobruchus maculatus*) has been

found to impact larval competition (Messina, 1991), various morphometric measures

(Rankin & Arnqvist, 2008), egg-to-adult survival and offspring production (Rankin &

Arnqvist, 2008), and adult longevity and mortality (Fox *et al.*, 2004a; b). However, in

this experiment, one particular observation stood out. Whilst a switch from a stressful

environment to a benign regime (S-to-C) was associated with an increase in LRS and

λind in both USA and Leicester populations, there was a noticeable difference in the

age-specific reproductive schedules between the USA and Leicester populations.

Leicester beetles produced more offspring on the first day and fewer on days two and

three, whilst in the USA population the opposite was observed. Why such a

difference in reproductive schedule exists deserves deeper investigation. If genetic

variance differed between populations, this may explain why Leicester individuals

were able to respond more quickly, with greater Day 1 reproduction. This could also

in part explain why development time was similar across all experimental

temperature regimes for the Leicester population. Together this clearly highlights the

benefits of comparing and contrasting results from multiple strains, as the response

of species to environmental change can often be highly population-specific.

As we have shown, successfully mimicking natural conditions within the

laboratory is key to understanding how species will react to climate change. As

temperatures increase and become more variable, the incorporation of more realistic

conditions into laboratory studies such as these will allow us not only to predict more

accurately how wild species will respond to climate change, specifically thermal

stress, but also to produce accurate species- and population-specific thermal

reaction norms (Paaijmans *et al.*, 2013; Buckley & Kingsolver, 2021). Therefore, this

study further reinforces the importance of considering natural temperature conditions

in order to better understand population- and species-specific responses to climate

change both in response to short- and long-term environmental changes. Beyond

this, there is also further need to extend thermal reaction norms to include additional

environmental variables that may also vary in response to climate change (Buckley &

Kingsolver, 2021).

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