Variation in plasticity in response to combined thermal-nutritional stress is genetically

independent between sexes and across traits

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Abstract:

Phenotypic plasticity helps animals to buffer the effects of increasing thermal and

nutritional stress created by climate change. Studies have shown that plastic responses to

single and combined stressors can vary among genetically diverged populations. However,

less is known about how plasticity in response to combined stress varies among individuals

within a population or whether such variation changes across life-history traits. This is

important because individual variation within populations shapes population level

responses to environmental change. Here, we used isogenic lines of *Drosophila*

melanogaster to assess plasticity of egg-adult viability and sex-specific body size for

combinations of two temperatures (25°C or 28°C) and three diets (standard diet, low caloric

diet, or low protein:carbohydrate ratio diet). Our results reveal substantial within-

population genetic variation in plasticity for egg-to-adult viability and wing size in response

to combined thermal-nutritional stress. This genetic variation in plasticity was a result of

cross-environment genetic correlations that were generally < 1 rather than changes in the

expression of genetic variation across environments. Cross-sex genetic correlations for body

size were weaker when the sexes were reared in different conditions, suggesting wing size

has the potential to evolve independently across sexes. Further, our results suggest that

plasticity in egg-adult viability is genetically independent from plasticity in body size. By

quantifying plasticity in response to combined stress between sexes and across traits, our

study aims to develop a more nuanced understanding of the potential for populations to

adapt to ongoing climate change.

Introduction

Rises in temperatures and increased frequency of extreme weather events caused by global

change are placing many organisms at a higher risk of extinction (Diffenbaugh and Field

2013; Wiens 2016; Midgley and Hannah 2019). In addition to exposing organisms to more

stressful thermal environments, climate change is also creating shifts in precipitation, which

in combination with the increasing CO_2 concentration, are affecting the distribution,

abundance (Van Der Putten *et al.* 2010; Pecl *et al.* 2017), and nutritional composition of

plants (Kreuzwieser and Gessler 2010; Lukac *et al.* 2010; Jin *et al.* 2019). This will expose

herbivorous and frugivorous animals to greater nutritional stress. In particular, ectothermic

herbivores and frugivores will be at a greater risk as they rely on ambient temperatures to

maintain their metabolism (Hawlena and Schmitz 2010; Walters *et al.* 2012). As one of the

largest groups of primary consumers, small changes in the population dynamics of these

ectotherms could affect the whole food chain and disturb ecosystem function (Rosenblatt

and Schmitz 2016). Understanding how ectothermic frugivores respond to combined

thermal and nutritional stress will be crucial in predicting how species and ecosystems will

respond to ongoing climate change.

When an environment becomes stressful, organisms can initially mitigate stress via

phenotypic plasticity (Huey *et al.* 2002) – the ability of a single genotype to express different

phenotypes in different environments. Life-history traits can respond plastically to

environmental variation, acting act as a short-term buffer to help organisms survive and

reproduce in the face of environmental change (Via *et al.* 1995; Schilthuizen and Kellermann

2014; Urban *et al.* 2014; Seebacher *et al.* 2015; Sgrò *et al.* 2016; Abram *et al.* 2017). For

instance, in insects, body size (French *et al.* 1998; Bochdanovits and De Jong 2003),

development time (Schou *et al.* 2017), and reproductive success (Janowitz and Fischer 2011;

Wang *et al.* 2013) have been shown to decrease with increasing temperature. Pre-adult

viability (Min *et al.* 2007; Jang and Lee 2018), development time (Economos and Lints 1984),

body size (Min *et al.* 2007; Jang and Lee 2018), and reproductive success (Bader and

Williams 2012) also shift plastically in response to reductions in food quality and quantity.

Although both temperature and nutrition can individually cause plastic shifts in key life-

history traits (Hoffmann *et al.* 2003, 2013; Zhang *et al.* 2015), wild animals are exposed to

multiple stressors simultaneously (Stillwell *et al.* 2007; Rosenblatt and Schmitz 2016), which

makes it important to understand plastic shifts in response to combinations of

environmental stressors predicted to occur under climate change.

More recently, research has focussed on understanding plastic responses to combinations

of stressors (Polak *et al.* 2004; Bubliy *et al.* 2012; Kutz *et al.* 2019; Chakraborty *et al.* 2020).

Studies examining plastic responses to combined thermal-nutritional stress in insects reveal

wide-ranging effects on life-history traits including viability, developmental time, body size,

and lifespan (Tun-Lin *et al.* 2000; Couret *et al.* 2014; Clissold and Simpson 2015; Rho and Lee

2017; Kutz *et al.* 2019). For example, in adult mealworm beetles (*Tenebrio molitor*), higher

temperatures significantly reduced survival on sub-optimal diets, whereas diet did not

impact survival at a lower temperature (Rho and Lee 2017). Similarly, in *Drosophila*

melanogaster, the negative impacts of sub-optimal diets on viability were exacerbated at

higher temperatures (Kutz *et al.* 2019). These studies suggest that temperature and

nutrition may interact to pose greater levels of stress than they do individually.

Plastic responses to environmental stress can vary among populations and between

individuals within populations, quantified as genotype by environment interactions (G × E)

(Via and Lande 1985; Dreyer *et al.* 2016; Frankino *et al.* 2019; Chakraborty *et al.* 2022).

Several studies have looked at among-population variation in plasticity along latitudinal

gradients (Schmidt *et al.* 2005; Sgrò *et al.* 2010; Sisodia and Singh 2010; Chakraborty *et al.*

2020), while fewer studies have quantified genetic variation in plasticity within a population

or between individual genotypes (Mossman *et al.* 2016; Wang *et al.* 2017; Lafuente *et al.*

2018; Frankino *et al.* 2019; Chakraborty *et al.* 2022). Understanding the distribution of

plastic responses between individuals of a population is vital for determining whether

populations will persist with climate change, given that within-population variation in

plasticity shapes variation in plasticity at the population level and the response of the

population to selection (Ghalambor *et al.* 2007; Frankino *et al.* 2019).

A powerful approach for measuring within-population variation in plasticity is to create

isogenic lines – inbred lines that are initiated from a natural population with each line

representing a fixed genotype (Ørsted *et al.* 2018; Franěk *et al.* 2020) – and then expose

them to different environments. Variation among isogenic lines within environments

represent genetic variation of the sampled population. By measuring differences in their

response to multiple environments and calculating slopes of reaction norms for all

genotypes, we can quantify variation in plasticity among genotypes (Scheiner 1993; Via and

Conner 1995). Variation in plasticity among genotypes (or significant G × E) can be caused

by significant variation in genes regulating the expressed phenotype (quantified by changes

in genetic variance across environments), or a significant genetic correlation between two

trait characters that is less than one (Via and Conner 1995), or both. Understanding within-

population variation, and decoupling its cause, is essential for predicting a population's

adaptability to long-term environmental stress (Ghalambor *et al.* 2007).

In addition to plasticity varying among genotypes within a population, plasticity can also

potentially vary between sexes. However, evidence for sex-specific plasticity is mixed.

Studies of a range of life-history and stress resistance traits have failed to find evidence for

sex-specific plasticity. In contrast, males and females differ in their plastic responses to

developmental conditions for body size (Pétavy *et al.* 2001; Teder and Tammaru 2005;

Stillwell and Fox 2007) and cold resistance (Pottier *et al.* 2021; Hangartner *et al.* 2022).

Although size differences between sexes (sexual size dimorphism) is common across insect

taxa (Teder and Tammaru 2005; Blanckenhorn *et al.* 2006; Stillwell *et al.* 2010a), no studies

have looked at sex-specific plasticity in size response to combined thermal-nutritional

stress. Sex-specific variation may further complicate the prediction of a population's

response and its dynamics under climate change (Hangartner *et al.* 2022), making it crucial

to measure sex-specific plasticity in life-history traits in response to combined stress.

In this study, we used a set of newly derived isogenic lines of *D. melanogaster* initiated from

a population collected along the east coast of Australia. These lines allow us to extend upon

previous studies that have examined variation in plasticity between populations (Sgrò *et al.*

2010; Cockerell *et al.* 2014; van Heerwaarden *et al.* 2016; Chakraborty *et al.* 2020).

Specifically, we used these lines to quantify sex-specific variation in plasticity in response to

combined thermal and nutritional stress. We subjected developing larvae to six

combinations of thermal and nutritional conditions that included two temperatures: 25°C

and 28°C, and three diets: standard, low caloric, and low protein to carbohydrate (P:C) diets.

These conditions were chosen to best simulate climate change, which is expected to cause a

3°C increase in average temperature (Australian Government 2014), and to reduce protein

and vary carbohydrate contents in plants (DaMatta *et al.* 2010; Gowik and Westhoff 2011;

IPCC 2018). We assessed plasticity of egg-to-adult viability and adult wing centroid size,

which have previously shown sensitivity to combined thermal and nutritional stress (Kutz *et*

al. 2019; Chakraborty *et al.* 2020). Given that *D. melanogaster* shows sexual size

dimorphism, and that the sexes may vary in their plasticity (Stillwell *et al.* 2010b; Shingleton

et al. 2017; Pottier *et al.* 2021; Hangartner *et al.* 2022), we assessed size plasticity separately

for males and females. By quantifying the genetic and sex-specific variation in plasticity

within a population in response to combinations of environmental stressors, our study

sheds new insight into how animal populations may respond to ongoing climate change.

Methods

Fly stocks - isogenic lines

We used isogenic lines that were established by Chakraborty *et al.* (2022). Briefly, two

hundred field-inseminated female *D. melanogaster* were collected in Duranbah, New South

Wales, Australia (28.3° S, 153.5° E) in 2018. From each of these females, two independent

iso-female lines were established and bred into four hundred lines. Full-sibling mating was

performed in each of these four hundred lines for twenty generations following MacKay *et*

al. (2012), resulting in 72 isogenic lines. Four copies of each isogenic line were reared at

25°C on standard diets (1:3 P:C ratio and 320 kcal/ L) under 12:12 light:dark cycle for twelve

generations prior to the experiment, as described below. The standard diet was prepared by

mixing water with potato flakes (18.18 g/ L), yeast (36.36 g/ L), agar (6.36 g/ L), and dextrose

(27.27 g/ L), with addition of nipagin and propionic acid to prevent bacterial and fungal

growth (Holleley *et al.* 2008).

Developmental treatment conditions and choice of traits

We used six thermal-nutritional conditions to simulate the possible shifts in temperature

(IPCC 2018) and nutrition (DaMatta *et al.* 2010; Gowik and Westhoff 2011; IPCC 2018) under

climate change. They included combinations of two temperatures: 25°C and 28°C, and three

diets: standard diet (1:3 P:C ratio and 320 kcal/L), low caloric diet (1:3 P:C and 80kcal/L), and

low P:C diet (1:12 P:C and 320kcal/L). 25°C represents the average summer temperature in

south-east Australia, whilst 28°C represents the 3°C temperature increase projected in

twenty years under climate change (Australian Government 2014). The low caloric diet and

the low P:C diets simulate a reduction of protein and variation of carbohydrates in plants

composition projected under climate change (DaMatta *et al.* 2010). These conditions have

been previously shown to successfully induce plastic responses in our traits of interest, egg-

to-adult viability and wing size (Kutz *et al.* 2019; Chakraborty *et al.* 2020).

Egg-to-adult viability and wing size were chosen because they are fitness-related

developmental traits known to be sensitive to nutrition and diet individually and in

combination (Kutz et al. 2019; Chakraborty et al. 2020). Egg-to-adult viability is a direct

indication of an individual's ability to survive to the reproductive adult stage (Kristensen et

al. 2015), and larger adult body size often correlates with greater fitness in ectotherms,

including Drosophila (Kingsolver and Huey 2008). Assessing variation in plasticity within a

population using these fitness-related developmental traits will allow us to better

understand how well species survive under stressful environments at the population level.

Experimental set up - Egg lays to obtain experimental flies

Adults from isogenic lines were transferred to laying plates containing apple juice, agar,

nipagin, and a surface layer of autoclaved yeast to encourage oviposition. Laying plates

were maintained at 25°C for 18 hours to allow egg laying.

Egg-to-adult viability assay

Eggs were collected from laying plates and transferred to 7.2 ml vials containing their

respective diets. Three replicate vials were included for each treatment and line

combination, with a density of twenty eggs per vial (Agnew et al. 2002). Vials containing

fresh eggs were kept at their respective treatment temperature at a 12:12 hour light: dark

cycle until adult eclosion. Egg-to-adult viability was calculated as the number of eclosed

adults relative to the initial number of eggs deposited into each vial (20 eggs).

Adult body size measurement

Wing size was used as a proxy for body size (Partridge et al. 1994). After eclosing, adults

were sexed and preserved in a 70% ethanol-30% glycerol solution for wing dissection. Left

wings of each sex were removed with fine forceps, transferred to glass slides, and

suspended in 70% ethanol-30% glycerol solution for imaging. To measure the wing centroid

size, landmarks were positioned at eight vein intersections as indicated in Fig. 1, and the X-

and Y- coordinates of landmarks were determined using the software package tpsDIG (Rohlf

2015). Using the software CoorDGen8 (Sheets 2014), wing area was calculated as square

root of the sum of the squared distances between each landmark.

Statistical analysis

Testing for overall genotype-by-environment (G × E) interactions

R was used to perform all data analysis and visualization (version 3.4.3) (R Core Team,

2017). To test for significant G × E, we used the *lme4* package (Bates *et al.* 2015), data of

egg-to-adult viability and wing size were fitted using linear mixed effects models. As both

traits had normal error distributions, they were fitted with a Gaussian error distribution. For

both traits, temperature and diet were treated as fixed effects, and line and block as

random effects. Both intercepts and slopes were allowed to vary in all models, since

differences in the slope of the reaction norm of each isogenic line would reflect significant G

× E. Wing size was analysed separately for each sex.

Models were fitted separately for each trait. Random effects of block, line, and

temperature-by-diet-by-line were added sequentially (see equations 1-3) and the

significance of each variable was tested using log-likelihood ratio tests from the *lrtest*

package (Zeileis and Hothorn, 2002).

Specifically, the first model (equation 1) included diet and temperature as the fixed effects,

and block as a random effect. This estimates the overall population response to

combinations of temperature and diet, while accounting for the differences in egg-to-adult

viability/wing size among blocks.

$$y \sim 1 + \text{Temperature} * \text{Diet} + (1|\text{Block}) \qquad \text{Eqn. 1}$$

In the second model (equation 2), line was added as an additional random effect to test for

differences in egg-to-adult viability/wing size across the isogenic lines.

$$y \sim 1 + \text{Temperature} * \text{Diet} + (1|\text{Block}) + (1|\text{Line}) \qquad \text{Eqn. 2}$$

In the third model (equation 3), the diet-by-temperature interaction was added to the

random line term to test for overall G × E, allowing for random intercepts and random

slopes.

$$y \sim 1 + \text{Temperature} * \text{Diet} + (1|\text{Block}) + (1 + \text{Diet: Temperature}|\text{Line}) \quad \text{Eqn. 3}$$

Quantifying genetic (co)variance

To determine whether significant G × E was due to changes in genetic variance across

environments and/or genetic correlations that are less than one, genetic (co)variance

matrices for egg-to-adult viability and wing size were estimated across treatments, and

across sexes (the latter only for wing size) (Via and Lande 1985). We treated each

combination of diet (low calorie and low P:C), temperature (25°C and 28°C), and sex (only

for wing size) as separate traits, resulting in six traits for viability, and twelve traits for wing

size across both sexes following Falconer (1952) and Via and Lande (1985). Our analyses

were performed on the raw data.

Specifically, we used the *MCMCglmm* package (Hadfield, 2010) to implement linear mixed

effects models, fitted using Markov Chain Monte Carlo (MCMC), to estimate genetic

(co)variances and genetic correlations. For each model, substantial burn-in (100,000

iterations) and thinning intervals (500 iterations) were included to ensure model

convergence. Effective sample sizes were checked to ensure more than 85% of samples

were saved. Uninformative parameter-expanded priors were used for variance components.

We checked their sensitivities by changing scale parameters to ensure no changes in the

posterior distribution. Each model was fitted with a Gaussian error distribution. A thousand

iterations were kept from each model, which provided the posterior distribution for each

parameter estimated.

Quantifying genetic (co)variance in egg-to-adult viability

To estimate genetic (co)variance in egg-to-adult viability within and across environments,

we used this equation

$$y_{jklm} = T_j + l_{k(j)} + b_{l(jk)} + e_{m(jkl)} \,,$$ Eqn. 4

where we included viability as the response variable y_{jklm} and treatment T_j as the only

fixed effect. Random effects included k^{th} isogenic line $l_{k(j)}$ and l^{th} block $b_{l(j)}$ within the

treatments, to remove any variance due to differences between experimental blocks. The

term $e_{m(jkl)}$ represents residual variance. For the isogenic line component, random

intercepts of each treatment and random slopes between treatments were estimated. This

respectively calculates the genetic variance in egg-to-adult viability in each treatment and

genetic covariance between treatments, resulting in a 6×6 genetic (co)variance matrix.

Genetic correlations between treatments were calculated from the covariance matrix

(Walter *et al.* 2020).

Quantifying genetic (co)variance in wing size

To estimate genetic (co)variance in wing size within and across environments, we used this

equation

$$y_{ijklm} = T_i + S_j + l_{k(ij)} + b_{l(ijk)} + e_{m(ijkl)}$$ Eqn. 5

where we included wing size as the response variable y_{ijklm}, and treatment T_i and sex S_j as

fixed effects. Random effects included k^{th} isogenic line $l_{k(ij)}$ and l^{th} block $b_{l(ijk)}$ within the

treatments, to remove any variance due to differences between experimental blocks. The

term $e_{m(ijkl)}$ represents residual variance. The random intercepts of each treatment and

sex, as well as the random slopes between treatments and sex, were estimated. These

values represent genetic variances of wing size among isogenic lines in each sex and

treatment, and genetic covariances between sex and treatment respectively, which were

then arranged into a 12×12 (co)variance matrix. Genetic correlations of wing size within

and between the sexes and treatments were further calculated from the (co)variance matrix

(Walter *et al.* 2020).

Genetic correlations between egg-to-adult viability and wing size

To estimate genetic correlations between egg-to-adult viability and wing size across

treatments, we applied equation 4 but included both egg-to-adult viability and wing size as

a bivariate response variable (note that wing size was averaged over both sexes and

estimated without sex as a fixed effect). As egg-to-adult viability and wing size are measured

on different scales, we standardised each trait by dividing trait values by their grand mean

(Houle 1992). Treatment (the six thermal-nutritional conditions) was initially included as a

fixed effect, however, this returned inflated (co)variance estimates. To obtain more

conservative estimates of genetic (co)variance, equation 4 was applied separately within

each treatment, and only included isogenic line and block as random effects. Random slopes

and intercepts were estimated, representing the genetic variance in viability and wing size,

and the genetic covariance between viability and wing size respectively. This produced six 2

× 2 genetic (co)variance matrices. Genetic correlations between traits for each treatment

were then calculated from each (co)variance matrix.

Results

We aimed to characterise genetic variation (G × E) in plasticity for both egg-to-adult viability

and sex-specific wing size in response to combined stressors within a population. We

subjected *D. melanogaster* isogenic lines to six different thermal-nutritional conditions

(25°C—standard diet, 25°C—low caloric diet, 25°C—low P:C diet, 28°C—standard diet,

28°C—low caloric diet, and 28°C—low P:C diet) and tested for significant genetic variation in

plasticity in egg-to-adult viability and wing size. We then calculated genetic (co)variances

and genetic correlations between traits within and across environments to understand the

causes of the significant G × E observed for each trait.

Genotype-by-environment interactions in egg-to-adult viability

Temperature and diet had significant individual effects on egg-to-adult viability (Fig. 2A and

Table S1). On average, viability was higher at 25°C compared to 28°C, and higher on

standard diets compared to low caloric and low P:C diets (Fig. 2A). The best fit model

included the random effect of temperature-by-diet-by-line interactions (Table 1), indicating

significant genetic variation in plasticity for viability (G × E) in response to combinations of

temperature and diet, captured by non-parallel individual reaction norms among lines (Fig.

2A).

Genetic (co)variances in egg-to-adult viability

We estimated genetic (co)variance matrices to determine whether significant G × E for

viability was caused by differences in the distribution of genetic variance across

environments and/or cross-environment genetic correlations that are less than one (Via and

Lande 1985). We found that the estimates of genetic variance did not differ across

treatments (Fig. 2B and Fig. S1), evidenced by the overlapping 95% highest posterior density

(HPD) intervals across treatments (Fig 2B). This indicates that significant G × E in viability

was not due to differences in genetic variance across environments.

Genetic correlations between treatment pairs were all positive and significantly greater

than zero, but mostly less than one (Fig. 2C and Fig. S2). This suggests that significant G × E

for viability results from differences in how isogenic lines respond to environments

(Falconer 1952; Via and Lande 1985).

Genotype-by-environment interactions in wing size

Initially, we analysed wing size separately for males and females. Temperature and diet

were found to significantly affect both male and female wing size (Table S2 and Table S3).

Wing sizes in both sexes were larger at 25°C compared to 28°C, and when larvae were

reared on standard diets compared to low caloric and low P:C diets (Fig. 3A and Fig. 3B). As

evidence for genetic variance in plasticity for wing size in males and females, we found the

best fit models included the random effect of temperature-by-diet-by-line interaction (Table

2). Such significant G × E in male and female wing size within the population is visualised as

non-parallel reaction norms (Fig. 3A and Fig. 3B).

Genetic (co)variances in wing size

We found significant genetic variance in wing size for all treatments within each sex;

however, the distribution of genetic variance did not differ across treatments (Fig. 3C and

Fig. S3). Thus, significant G × E in wing size in both males and females was not caused by the

differences in the distribution of genetic variance across the environments.

Genetic correlations in wing size across the six thermal-nutritional treatments within each

sex were all positive, significantly greater than zero, and mostly less than 1 (Fig. 3D, Fig. S4

and Fig. S5). This suggests that, similar to what we found for viability, significant G × E in

wing size of both males and females was caused by differences in the alleles contributing to

the response across environments (Falconer 1952; Via and Lande 1985).

Cross-sex genetic correlations for wing size

To determine whether wing size has a similar genetic bases in both sexes, we estimated the

cross-sex genetic correlation for wing size within and between all thermal-nutritional

treatments and sexes. This helps us to understand the potential for size to evolve

independently in each sex and in each environment (Falconer 1952; Via and Lande 1985).

Cross-sex correlations within treatments (indicated in red in Fig. 4, Fig S.6) were significantly

greater than zero, and large, but less than one, indicating that even though sexes share

some genetic basis for these traits, there is also some degree of genetic independence.

Furthermore, cross-sex genetic correlations were smaller when males and females

developed in different treatments. Specifically, the correlation between males from 28°C

standard diet condition and females from 25°C low P:C diet condition (indicated in blue in

Fig. 4) was significantly lower than correlations within 25°C standard diet and 28°C standard

diet conditions. This suggests that males and females share less of a genetic basis for wing

size when reared in different environments, which could allow sexes to evolve more

independently as conditions become more variable.

Genetic correlations between egg-to-adult viability and wing size

Finally, we estimated genetic correlations between egg-to-adult viability and wing size

(sexes combined) across all thermal-nutritional treatments to determine whether these

traits shared similar genetic basis, and whether they can evolve independently in different

environments (Falconer 1952; Via and Lande 1985). Correlations between viability and wing

size were not significantly different from zero in all treatments (Fig. 5 and Fig. S7), indicating

that they are genetically independent.

Discussion

Climate change is simultaneously imposing thermal and nutritional stress on animals (Van

Der Putten *et al.* 2010; Pecl *et al.* 2017), and is expected to negatively affect biodiversity in

the long term (Walters *et al.* 2012; Rosenblatt and Schmitz 2016; IPCC 2018). Phenotypic

plasticity will be an important means by which animals will mitigate the increasing stress

under climate change (Urban *et al.* 2014; Seebacher *et al.* 2015; Sgrò *et al.* 2016). Single-

population studies have shown that there are shifts in plastic responses of life-history traits

to changes in temperature (French *et al.* 1998; Hoffmann *et al.* 2003; Schou *et al.* 2017) and

nutrition individually (Min *et al.* 2007; Bader and Williams 2012; Jang and Lee 2018).

Temperature has also been shown to modify plastic responses of life history traits to

nutritional stress (Lee and Roh 2010; Kutz *et al.* 2019; Chakraborty *et al.* 2020). While these

studies improve our understanding of how animals may respond to combined stress

resulting from climate change, they have not accounted for genetic variation in plasticity

within a population.

Individuals within a population can also show substantial variation in plasticity (Mossman *et*

al. 2016; Wang *et al.* 2017; Lafuente *et al.* 2018; Frankino *et al.* 2019). In particular,

understanding within-population variation matters because it may shape the capacity for

populations to adapt and persist in the face of ongoing environmental change (Lande 2009;

Chevin *et al.* 2010; Dreyer *et al.* 2016; Frankino *et al.* 2019).

Consistent with previous studies performed at the population level (Petersen *et al.* 2000;

Stillwell *et al.* 2007; Lee and Roh 2010; Kutz *et al.* 2019; Chakraborty *et al.* 2020), we found

that low quality diets exacerbated the negative effects of elevated temperatures on two life

history traits, egg-adult viability and adult body size. Specifically, both viability and wing size

were reduced on low quality diets; this effect was greater at 28°C compared to 25°C. This

suggests that exposure to combined thermal-nutritional stress, projected under climate

change, may negatively impact population persistence (DaMatta *et al.* 2010; Gowik and

Westhoff 2011; IPCC 2018; Kutz *et al.* 2019). Vitally, we found that individual genotypes

within a population can also vary in the extent and direction of plasticity for both traits.

Previous studies investigating a range of taxa have reported extensive within-population

variation in plastic responses to temperature and nutrition individually, for a range of life-

history traits and stress resistance traits (Mossman *et al.* 2016; Wang *et al.* 2017; Lafuente

et al. 2018; Frankino *et al.* 2019), including viability (Duun Rohde *et al.* 2016) and body size

(Barker and Krebs 1995; Imasheva *et al.* 1999; Lafuente *et al.* 2018). We have found that

populations also harbour significant genetic variation in plasticity for both viability and body

size in response to combinations of temperature and diet.

The extent to which genotypes within a population vary in their reaction norm will

determine how the population will respond to selection imposed by environmental change

(Chevin *et al.* 2010; Dreyer *et al.* 2016; Frankino *et al.* 2019). As a result, populations with

similar mean reaction norms may vary markedly in the distribution of their genotype-

specific reaction norms, and this would cause them to respond differently to selection

(Dreyer *et al.* 2016; Frankino *et al.* 2019). Predictions of long-term evolutionary responses to

environmental changes using population-level reaction norms, could be inaccurate, unless

the genotype-specific reaction norms are also considered (Reed *et al.* 2010; Dreyer *et al.*

2016; Frankino *et al.* 2019).

We found significant genetic variance for viability across all combinations of diet and

temperature. However, the expression of genetic variance did not vary across

environments. Bubliy *et al.* (2001), and Bubliy and Loeschcke (2002) both used half-sib

analyses to investigate genetic variance in plasticity for viability to changes in temperature.

Consistent with the present study, Bubliy and Loeschcke (2002) found no significant

difference in the expression of genetic variance for viability between 13°C and 25°C. In

contrast, Bubliy *et al.* (2001) observed a significant increase in genetic variance for viability

at 32°C compared to 25°C. Perhaps if we had increased the rearing temperature above 28°C,

we might have observed differences in expression of genetic variance. Instead, we found

that significant G × E interactions for viability was a result of genetic correlations across

environments that were above zero and often less than one. This indicates that viability

across some thermal-nutritional conditions is controlled by different alleles or differently by

the same alleles (Via and Lande 1985), meaning that viability has some capacity to evolve

independently across different thermal-nutritional environments (Via and Lande 1987).

Although body size plasticity has been extensively shown to vary within a population in

response to temperature (Barker and Krebs 1995; Lafuente *et al.* 2018) and nutrition

(Imasheva *et al.* 1999), the source of G × E differed across studies. De Moed *et al.* (1997)

found that the significant G × E for body size was due to differences in the expression of

genetic variance across environments. In contrast, we found that the significant G × E for

body size for both sexes was due to genetic correlations across treatments that were

significantly different from zero but often less than one. Similarly, Barker and Krebs (1995)

and Imasheva *et al.* (1999) have also reported the same source of G × E for body size

plasticity to changes in temperature and dietary yeast concentration respectively. These

differences across studies are likely to arise due to differences in the source populations and

experimental conditions used.

As expected from previous studies, we found that wing size exhibited sexual dimorphism

(females were larger than males), and there were strong and positive cross-sex genetic

correlations within treatments (Cowley *et al.* 1986; Cowley and Atchley 1990; Reeve and

Fairbairn 1996; Lasne *et al.* 2018). Strong and positive cross-sex genetic correlations indicate

that the genetic basis of plasticity in wing size is largely shared in males and females, though

because these correlations are less than one there is some potential for independent

evolution of size plasticity between the sexes (Lande 1980; Via and Lande 1987). Cross-sex

genetic correlations were reduced when males and females developed in different

environments. Thus, there is a greater possibility of independent evolution in wing size

plasticity when the sexes experience markedly different nutritional-thermal environments.

Delcourt *et al.* (2009) and Berger *et al.* (2014) have also reported changes in magnitude of

cross-sex genetic correlation of fitness when rearing males and females in different

environments. This matters because, in the wild, individual *Drosophila* are often found in

different microhabitats – different temperatures due to daily thermal fluctuations (Noer *et*

al. 2020) and different nutrients due to different niches, resources (Diepenbrock and

Burrack 2017), and nutritional requirements (Lee *et al.* 2013; Camus *et al.* 2018; Duxbury

and Chapman 2021). Estimating cross-sex genetic correlation between males and females

that developed in different environments may help improve the accuracy when estimating

the individual evolvability between sexes.

Finally, genetic correlations between viability and wing size across all six thermal-nutritional

treatments were not different from zero. This means that these two traits do not share a

similar genetic basis, and are able to evolve independently (Via and Lande 1985). Our

findings differ from earlier studies. For instance, Teuschl *et al.* (2007) artificially selected

dung flies with different body sizes – small, control, and large – and assessed their pre-adult

viability in combinations of high temperature and limited food. Interestingly, larger males

had higher pre-adult mortality, suggesting body size and viability might be negatively

genetically correlated. Dingle (1992) also observed a similar phenomenon in milkweed bugs

under food shortage, such that higher pre-adult survival was traded off with smaller body

size, which again indicates a negative genetic correlation between these two traits (Via and

Lande 1985). The fact that we found no correlation between viability and wing size suggests

that the genetic correlation between viability and body size may be species- and condition-

specific.

In summary, we explicitly assessed within-population variation in plasticity of egg-to-adult

viability and sex-specific wing size in *D. melanogaster*, in response to combined thermal-

nutritional conditions. We demonstrated that, even though combined thermal-nutritional

stress reduced viability and wing size (i.e., reduced performance) on average, individual

genotypes still varied in their plastic responses, such that some genotypes had increased

viability/wing size under increasingly stressful conditions. Additionally, our results suggest

that the independent evolution of wing size between the sexes may be possible when the

sexes experience different environmental conditions, and that viability and wing size are

also genetically independent. Our research sheds light on the importance of measuring the

extent of plasticity of fitness-related life-history traits in response to combined stressors, as

well as measuring cross-sex genetic correlation between treatments. This will be crucial for

making accurate predictions of how species may respond to climate change.

Results – Tables and graphs

Table 1. Linear models testing for genotype (Line) by environment interactions in egg-to-
adult viability in response to combined developmental temperature and diet conditions.

Model number	Egg-to-adult viability (y) model	Likelihood ratio test	P-value
1.1	y ~ 1 + Temperature * Diet + (1|Block)	-	-
1.2	y ~ 1 + Temperature * Diet + (1|Block) + (1|Line)	1.2 to 1.1	<0.001
1.3	y ~ 1 + Temperature * Diet + (1|Block) + (1|Line) + (Temperature:Diet|Line)	1.3 to 1.2	<0.001

526
527   **Table 2**. Linear models testing for genotype (Line) by environment interactions in wing size
528   of both sexes in response to combined developmental temperature and diet conditions.

Model number	Male wing size (y) model	Likelihood ratio test	P-value
2.1	y ~ -1 + Temperature * Diet + (1|Block)	-	-
2.2	y ~ -1 + Temperature * Diet + (1|Block) + (1|Line)	2.2 to 2.1	<0.001
2.3	y ~ -1 + Temperature * Diet + (1|Block) + (Temperature:Diet|Line)	2.3 to 2.2	<0.001
	Female wing size (y) model		
3.1	y ~ -1 + Temperature * Diet + (1|Block)	-	-
3.2	y ~ -1 + Temperature * Diet + (1|Block) + (1|Line)	3.2 to 3.1	<0.001
3.3	y ~ -1 + Temperature * Diet + (1|Block) + (Temperature:Diet|Line)	3.3 to 3.2	<0.001

530
531 **Fig. 1.** Landmakrs used for calculating wing centroid size, indicted by red dots.

532
533 **Fig. 2.** Mean egg-to-adult viability of each isogenic lines (**A**), estimates of its genetic variance
534 in response to six combined thermal-nutritional treatments, (**B**) and the genetic correlation
535 within and across environments for viability (**C**). Black line presents the population mean in

536 panel A. Error bars shows 95% upper and lower highest posterior density (HPD) intervals in
537 panels B and C.

538
539 **Fig. 3.** Mean wing size of (**A**) males and (**B**) females of isogenic lines, estimates of their (**C**)
540 genetic variance, and (**D**) the genetic correlation within and across six combined thermal-
541 nutritional treatments. Black line presents the population mean in panels A and B. Error bars
542 shows 95% upper and lower HPD intervals in panels C and D.

543
Fig. 4. Cross-sex genetic correlation for wing size between six combined thermal-nutritional
treatments. Error bars shows 95% upper and lower HPD intervals. Red error bars indicate
cross-sex genetic correlation within treatments. The blue error bar shows a significantly
smaller cross-sex genetic correlation between females from 25°C low P:C diet and males
from 28°C standard diet, compared to cross-sex genetic correlations within 25°C standard
diet and 28°C standard diet.
550

Fig. 5. Genetic correlation between egg-to-adult viability and wing size within each of six combined thermal-nutritional treatments. Wing size of both sexes was combined for estimating the genetic correlation between egg-to-adult viability and wing size. Error bars shows 95% upper and lower HPD intervals.

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