Cross-tolerance evolution driven by selection on heat tolerance in

Drosophila subobscura

Luis E. Castañeda

Programa de Genética Humana, Instituto de Ciencias Biomédicas (ICBM), Facultad de

Medicina, Universidad de Chile, Santiago, Chile

Corresponding author: Luis E. Castañeda (luis.castaneda@uchile.cl)

ABSTRACT

Evolution of heat tolerance is a crucial mechanism for the adaptive response to global

warming, but it depends on the genetic variance harbored by populations and the

thermal stress intensity in nature. Selection experiments on heat tolerance have been key

to understand the heat tolerance evolution but the effect of variable heat stress intensity

on the correlated responses of resistance traits has not been explored. Here, the effects

of heat intensity selection (fast and slow ramping temperatures) for increasing

knockdown temperature in *Drosophila subobscura* were evaluated on the knockdown

time at different stressful temperatures (35, 36, 37, and 38 ºC), the thermal-death-time

curves (TDT curves), the desiccation and starvation resistance. Correlated evolution was

found for these four resistance traits in *D. subobscura*, which demonstrates that the

evolutionary response to tolerate higher temperatures also confers the capacity to

tolerate other stress such as desiccation and starvation. However, these correlated

responses depended on the intensity of thermal selection and sex, which could limit our

capacities to transfer these findings to natural scenarios. Nevertheless, this study

reaffirms the value of experimental evolutionary approach to explore and to understand

the adaptive responses of natural populations to global warming.

Keywords: correlated evolution, global warming, heat stress intensity, stress resistance

evolution, thermal tolerance landscape.

INTRODUCTION

Increasing environmental temperatures represent an important challenge for ectotherms

(i.e., organisms whose body temperature depends on the environmental temperature)

because their morphology, physiology, behavior, and performance depend on the

thermal environment [1–3]. Additionally, the rise in environmental temperatures

increases the extinction risk of many species that live close to their upper thermal limits

[4–6]. However, ectotherms can avoid the negative effects of heat via behavioral

thermoregulation, evolutionary change, and/or phenotypic plasticity of the upper

thermal limits [7].

Evolutionary adaptation depends on the genetic variation exhibited by upper

thermal limits, but some studies have suggested that these traits have a limited

evolutionary potential to respond to increasing environmental temperatures [8–10].

Nevertheless, theoretical and empirical evidence shows that heritability estimates of

heat tolerance tend to be lower when heat tolerance is measured in long assays (e.g.,

slow ramping assays or static assays using sublethal temperatures) than in short assays

(e.g., fast ramping assays or static assays using extremely high temperatures) [8,10–14]-

. Therefore, heat stress intensity can influence our predictions regarding the

evolutionary potential of heat tolerance; however, how do populations respond to

variable selection driven by heat stress? Selection in laboratory conditions has a long

tradition and provides information about the adaptive evolution of specific selective

agents [15–18]. In particular, the experimental evolution of heat tolerance has been

explored in multiple species, including fishes, corals, and insects [19–22]. Experimental

evolution of heat tolerance has also been studied in several *Drosophila* species,

including D. melanogaster [23,24] and *D. subobscura* [25–27], and *D. buzzatti* [28,29].

Most of these studies reported the evolution of heat tolerance using fast ramping

protocols, ranging from 0.4 ºC/min in Folk et al. [24] to 1 °C/min in Gilchrist and Huey

[23], or high-temperature static assays (40 °C), as in Bubliy and Loeschcke (28).

Recently, Mesas et al. [26] reported that selected lines of *D. subobscura* evolved higher

heat tolerance, regardless of the warming rate used during the selection experiments

(slow ramping rate: 0.08 °C/min and fast ramping rate: 0.4 °C/min).

Interestingly, several of these selection experiments on heat tolerance in

Drosophila have found correlated responses in other traits such as starvation resistance,

desiccation resistance, and heat shock proteins [29–31]. However, it is expected that the

intensity of thermal stress has important effects on the correlated responses of other

traits to heat tolerance selection [32]. For instance, fast-ramping selected lines have

evolved thermal performance curves with higher optimal temperatures and narrower

thermal breadths than slow-ramping selected lines [26]. Additionally, Mesas and

Castañeda [27] reported that the evolution of heat tolerance was associated with reduced

activity of the enzymes involved in the glucose-6-phosphate branch point and increased

performance of life-history traits in slow-ramping selected lines. However, they did not

observe any changes in the metabolic rate of the selected lines, as predicted by Santos et

al. [33]. In summary, there is evidence that heat stress intensity determines the

magnitude of the evolutionary responses of performance, metabolic, and life-history

traits to heat tolerance selection; however, the correlated evolution of resistance traits

has not yet been tested. This information provides important clues regarding how the

intensity of thermal stress could determine the evolution of cross-tolerance to stressful

environmental conditions. Natural populations are exposed to multiple environmental

stressors, and it is known that increased tolerance to one stressor can boost tolerance to

another [34]. The cross-tolerance induced by thermal stress has been widely explored in

several arthropod species and increasing traits such as desiccation, insecticide, pathogen

resistances [35–37]. However, the cross-tolerance response at the evolutionary level can

be constrained or facilitated by genetic correlations among resistance traits [38].

Here, effects of heat intensity selection for increasing knockdown temperature

was explored on the cross-tolerance evolution of four different resistance traits in *D.*

subobscura: knockdown time at different stressful temperatures, thermal-death-time

curves (TDT), desiccation resistance, and starvation resistance. TDT curves represent an

integrative approach for assessing how the probability of survival depends on the

intensity and duration of heat stress [39]. This approach allows to estimate the critical

thermal maxima (CT_{max}) and thermal sensitivity using the heat tolerance measurement

obtained from different exposure temperatures. It is expected that fast-ramping selected

lines would exhibit higher knockdown time at highly stressful temperatures and higher

CT_{max} because fast-ramping protocols reduce the confounding effects on heat tolerance

associated with the assay length. In contrast, slow-ramping selection lines should

exhibit higher desiccation and starvation resistance, because individuals with higher

starvation and desiccation resistance exhibit higher thermal tolerance during long assays

(11,32).

Materials and Methods

Sampling and maintenance

D. subobscura females were collected in the spring of 2014 at the Botanical Garden of

Universidad Austral de Chile (Valdivia, Chile; 39º 48' S, 73º 14' W) using plastic

traps containing banana/yeast baits. A total of 200 females were collected and

individually placed in plastic vials with David's killed-yeast *Drosophila* medium to

establish isofemale lines. In the next generation, 100 isofemale lines were randomly

selected, and 10 females and 10 males per line were placed in an acrylic cage to set up

one large outbred population. In the next generation, the cages were split into three

replicate cages (R1, R2, and R3). After three generations, each replicate cage was

divided into four population cages. Thus, our experimental design had four different

artificial selection protocols in triplicate: fast-ramping selection, fast-ramping control,

slow-ramping selection, and slow-ramping control lines (see Mesas & Castañeda

[27]). During the selection experiments, population cages were maintained at 18 °C

(12:12 light-dark cycle) in a discrete generation, controlled larval density regime [40].

Each population cage had a population size of 1000-1500 breeding adults.

Heat tolerance selection

For each replicated line, 120 four-day-old virgin females were randomly mated with

two males for two days, and then females were individually placed in a capped 5-mL

glass vial and males were discarded. Vials attached to a plastic rack were immersed in

a water tank with an initial temperature of 28 °C, controlled by a heating unit (Model

ED, Julabo Labortechnik, Seelbach, Germany). After an equilibration time of 10 min,

the temperature was increased to a rate of 0.08 ºC min^{-1} for the slow-ramping selection

protocol or 0.4 ºC min^{-1} for the fast-ramping selection protocol. The assays were

terminated when all flies collapsed. Each assay was video recorded using a high-

resolution camera (D5100, Nikon, Tokyo, Japan) and then visualized to score the

knockdown temperature for each fly, which was defined as the temperature at which

each fly ceased to move. Flies were ranked according to their knockdown temperature,

and four virgin females from the offspring of the 40 most tolerant females (upper 30%

of each assay) were selected to found the next generation. For the fast-control and

slow-control lines, the knockdown temperature was measured as mentioned above, but

the offspring were randomly chosen to found the next generation, regardless of the

knockdown temperature of their mother.

This artificial selection experiment was performed for 16 generations after which

flies from each selection treatment were dumped in separate acrylic cages and

maintained without selection at 18 °C (12:12 light-dark cycle). The present

experiments were performed in generation 23.

Knockdown time in static assays

Eggs were collected from each population cage and transferred to vials at a density of

40 eggs/vial. At 4 days of age, ten females and ten males from each population cage

were assayed to measure their heat knockdown time at four different static

temperatures: 35, 36, 37, and 38 °C. This experimental setup allowed the measurement

of 960 flies in 16 assays (10 flies × 2 sexes × 4 static temperatures × 4 selection

treatments × 3 replicated lines). Static assays were similarly performed as knockdown

temperature assays, but static temperatures were used instead of using ramping

temperatures. A total of 240 flies were measured for each static temperature, except for

the assay at 35 °C (178 flies) because two flies died before the beginning of the assay,

and a video file of one assay was corrupted (60 flies). At 37 °C assay, four flies died

before the beginning of the assay, and the collapse time could not be measured for six

flies. Finally, for the assay at 38 ºC assay, three flies died before at the beginning of the

assay and the collapse time could not be measured for five flies.

Desiccation and starvation resistance

Eggs from each replicate cage were collected and maintained in vials at a density of 40

eggs/vial. Only fast control lines were measured as control lines. This decision was

based on logistic reasons (i.e., the high number of vials) and statistical support because

fast-control and slow-control lines did not differ in their knockdown times and CT_{max}

values (see *the Results* section).

For desiccation resistance assays, five flies were placed in a vial containing five

desiccant droplets (Drierite), which were sealed with parafilm (flies had no access to

food or water during the assay). For starvation resistance assays, five flies were placed

in a vial containing agar only (flies had access to water but not food). For both

desiccation and starvation resistance assays, the number of live flies was recorded every

3 h until all the flies were dead. The experiments were performed at 18 °C.

Statistical analysis

Normality and homoscedasticity were tested for all variables, and the knockdown times

were log_{10}-transformed to meet the parametric assumptions. All analyses were

performed using R software [41].

Heat tolerance

Analysis to evaluate the evolutionary response of the knockdown temperature to

ramping selection was separately performed for the fast and slow ramping selection

because it is widely known that knockdown temperature is higher in fast ramping than

slow ramping assays [8,26]. Mixed linear models (full model) with ramping selection

(fixed effect), sex (fixed effect), and replicated lines nested within thermal selection

(random effect) were performed on knockdown temperature and knockdown time using

the library *lme4* package for R [42].Fixed effects were tested through a type-III

ANOVA using the library *lmerTest* package for R [43], whereas the random effect was

tested using a likelihood-ratio test comparing the model with versus without the

replicated lines. When the selection effect was significant, posteriori comparisons were

performed using Tukey tests implemented in the *emmeans* package for R [44].

Knockdown times were also employed to plot the survival curves based on the

Kaplan-Meier formula using the function *survfit* implemented in the *survival* package

for R [45].

Thermal death time curves (TDT)

Average knockdown times were calculated for each sex, replicated lines, and selection

treatment combination (Table S1). These values were regressed against the assayed

temperatures according to eqn. 1 (Fig. 1; Rezende et al. [39]):

$$log_{10}t = \frac{CT_{max}-T}{z} \qquad \text{eqn. 1}$$

, where T is the assayed static temperature (ºC), CT_{max} is the upper thermal limit (ºC), t

is knockdown time (min), and z is the thermal sensitivity. These curves allowed the

estimation of CT_{max} as the extrapolated temperature that would result in a knockdown

time of $log_{10}t = 0$ (i.e., knockdown time at 1 min) and the estimation of the thermal

sensitivity ($z = -1/slope$), where the lower z-values, the higher thermal sensitivity.

Using eqn. 1, 18 TDT curves (2 sexes × 3 replicated lines × 3 selection

protocols) were fitted, from which CT_{max} and z values were estimated as explained

above. A linear model with ramping selection treatment, sex, and their interaction was

performed to evaluate their effects on CT_{max} and z values.

Desiccation and starvation resistance

To determine the lethal time at 50% of flies of each vial were dead (LT_{50}), a generalized

linear model following a binomial distribution was performed with the proportion of

alive flies as a dependent variable and time as a predictor variable. The generalized

linear model was run using the function g*lm* of the *lme4* package for R [42]. Then, the

LT_{50} of each vial was estimated using the function *dose.p* of the package *MASS* for R

[46].

To estimate the median LT_{50} and the 95% confidence intervals for each selection

treatment and sex, each LT_{50} was transformed into a survival object using the functions

Surv and *survfit* of the package *survival* for R . This procedure also allowed to create the

survival curves. Finally, to test the effect of selection treatment and sex on desiccation

and starvation resistances, a Cox proportional regression model was fitted with LT_{50} as

a dependent variable, and selection protocol and sex as predictor variables. The Cox

model was run using the function *coxph* of the *survival* package.

RESULTS

Knockdown temperature evolution

Knockdown temperature evolved in response to artificial selection for increasing heat

tolerance, regardless of ramping assay protocol: knockdown temperature was

significantly higher in fast-ramping selected lines compared to fast-ramping control

lines (mean$_{fast-ramping}$ ± SD = 37.71 ± 0.68 ºC and mean$_{fast-control}$ ± SD = 37.23 ± 0.79 ºC;

$F_{1,4}$ = 32.0, P = 0.005); and knockdown temperature in slow-ramping selected lines

was significantly higher than in slow-ramping control lines (mean$_{slow-ramping}$ ± SD =

35.48 ± 0.66 ºC and mean$_{slow-control}$ ± SD = 34.97 ± 0.72 ºC; $F_{1,4}$ = 41.7, P = 0.003).

These findings have been previously reported by Mesas et al. [25] and reported here to

contextualize the following results.

Knockdown time evolution

As expected, knockdown time significantly decreased towards higher assayed

temperatures ($F_{1,876}$ = 647.8, P < 0.0001): static assay at 35º C = 33.77 ± 11.63 min;

static assay at 36º C = 16.98 ± 6.87 min; static assay at 37º C = 8.84 ± 3.56 min; and

static assay at 38º C = 6.78 ± 2.68 min.

Knockdown times significantly differed between selection treatments when flies

were assayed at 36 and 37 ºC (Table 1; Fig. 1). At these temperatures, slow-selected and

fast-selected lines exhibited higher heat tolerance than slow- and fast-control lines

(Table S1, S2; Fig. 1C, E). Also, fast-selected lines showed a higher heat tolerance than

slow-selected lines in flies assayed at 37 ºC but not at 36 º C (Table S1, S2; Fig. 1C, E),

whereas fast and slow control lines did not differ between them (Table S2; Fig 1). On

the other hand, replicate lines had not a significant effect on knockdown time, indicating

that replicate lines showed a consistent response within each selection and control

treatment (χ^2_1 = 0 and P =1 for all static assays). Regarding sex, females showed a

higher thermal tolerance than males but only when flies were assayed at 35 and 38 ºC

(Table 1; Fig. 1B, H). Finally, non-significant interactions between selection and sex

were found for any assayed temperatures (Table 1).

TDT curves evolution

Linear regressions between $\log_{10}(LT_{50})$ and assayed temperatures allowed to estimate 24

TDT curves (4 selection treatments × 3 replicated lines × 2 sexes) with high coefficients

of determination (average $R^2 = 0.946$, range: $0.820 - 0.989$; Table S3), corroborating

that heat knockdown time is linearly associated to stressful sublethal temperatures.

From these TDT curves, the average CT_{max} was 41.21ºC (SD = 0.46ºC) and the average

z was 4.18ºC (SD = 0.34ºC). CT_{max} were significantly different between selection

treatments ($F_{3,20} = 4.46$, $P = 0.015$; Fig. 2A). *A posteriori* analysis showed that only fast-

ramping selected and slow-control lines significantly differed in their CT_{max} values (t_{20}

= 3.195, $P = 0.02$), whereas fast-control and slow-control showed similar CT_{max} values

($t_{20} = -0.911$, $P = 0.80$). Thus, if control lines are pooled, CT_{max} still differs between

selection treatments ($F_{2,18} = 6.69$, $P = 0.007$), with fast-ramping ($CT_{max} = 41.55 \pm 0.36$

ºC) and slow-ramping selected lines ($CT_{max} = 41.43 \pm 0.35$ ºC) showing higher CT_{max}

than control lines ($CT_{max} = 40.94 \pm 0.41$ ºC) ($t_{18} = 3.27$, $P = 0.01$ and $t_{18} = 2.64$, $P =$

0.04, respectively). CT_{max} between selected lines was not different between them ($t_{18} =$

0.54, $P = 0.85$). On the other hand, sex and the interaction between selection treatments

and sex had no significant effects on CT_{max} ($F_{1,18} = 0.004$, $P = 0.95$ and $F_{3,18} = 2.11$, $P =$

0.15, respectively). Regarding z (i.e., thermal sensitivity), it did not exhibit significant

effects of selection treatments ($F_{3,16} = 0.91$, $P = 0.46$; Fig. 2), sex ($F_{1,16} = 1.30$, $P =$

0.27), nor the interaction between selection treatments and sex ($F_{3,16} = 2.23$, $P = 0.12$).

Summarizing, the evolution of a higher CT_{max} is not related to an evolutionary change

of the thermal sensitivity (Fig. 2B). Indeed, the relationship between CT_{max} and z did

not change with the evolution of increasing heat tolerance ($r_{control-lines} = 0.979$ and

$r_{selected-lines} = 0.929$; Z-test = 0.76, $P = 0.45$).

Desiccation resistance evolution

Survival analysis showed a significant interaction between selection treatments and sex

on desiccation resistance (LTR$_5$ = 83.55, $P < 2 \times 10^{-16}$). Males showed a higher

desiccation risk than female flies (Hazard ratio = 7.11, $P < 2 \times 10^{-7}$; Fig. 3). Females

showed a significant difference between selected and control lines (LTR: χ^2_2 = 6.72, P

= 0.03; Fig. 3A). Specifically, females of the slow-ramping selection lines showed a

higher desiccation resistance than females of the control lines (Hazard ratio = 0.42, P =

0.009), whereas females of the fast-ramping selection and control lines showed similar

desiccation risk (Hazard ratio = 0.56, P = 0.072). On the other hand, males showed no

differences in desiccation resistance between selected and control lines (LTR: χ^2_2 =

1.88, P = 0.4; Fig. 3B). Results of the desiccation survival analysis testing the effect of

selection protocol, sex, and its interaction are reported in the Table S4.

Starvation resistance evolution

Survival analysis showed a significant interaction between selection treatments and sex

on desiccation resistance (LTR$_5$ = 94.89, P-value $< 2 \times 10^{-16}$). Males showed a higher

starvation risk than female flies (Hazard ratio = 22.75, $P < 1 \times 10^{-16}$; Fig. 4). For female

flies (Fig. 4A), fast-ramping selection and slow-ramping selection lines showed a higher

starvation risk than control lines (Hazard ratio = 2.37, P-value = 0.009 and Hazard ratio

= 2.20, P-value = 0.014, respectively). Whereas male flies showed an oppositive pattern

(Fig. 4B): slow-ramping selection lines showed a lower starvation risk than control lines

(Hazard ratio = 0.50, P-value = 0.03), but non-significant differences were found

between fast-ramping selection and control lines (Hazard ratio = 0.64, P-value = 0.16).

Results of the starvation survival analysis testing the effect of selection protocol, sex,

and its interaction are reported in the Table S5.

Discussion

Studying the evolutionary responses of thermal limits is key to understanding the

adaptive responses and evolutionary constraints to global warming. Then, cross-

tolerance studies can provide valuable information about the evolutionary response to

multiple environmental stressors. Cross-tolerance evolution has been reported among

different resistance traits [29,35,47,48], but the magnitude of the evolutionary response

could be explained by the trait under direct selection or the stress intensity [38]. Here,

an artificial selection experiment was performed on knockdown temperature to explore

whether the intensity of thermal selection influences the cross-tolerance evolution of

resistance traits in *D. subobscura*. Briefly, a direct response heat knockdown

temperature to selection was found (see also 25,26), which resulted into a correlated

responses on heat knockdown time (static assays), the thermal tolerance landscape

(TDT curves), desiccation resistance, and starvation resistance. These findings

demonstrate that the evolutionary response to tolerate higher temperatures also confers

the capacity to tolerate other stress such as desiccation and starvation. Interestingly,

these correlated responses depend on the intensity of thermal selection and sex (Table

2).

Different approaches used to measure the upper thermal limit of ectotherms

generate different genetic and phenotypic estimates. In general, fast ramping assays

estimate higher upper thermal limits and higher heritabilities than slow ramping assays

[8,12]. As heritability is commonly used as a predictor of the evolutionary response of a

trait to natural or artificial selection, it is expected that the evolutionary response of heat

tolerance depends on the ramping rate used during selection. However, previous work

did not support this prediction for *D. subobscura*, finding that the evolution of the

knockdown temperature was independent of the ramping rate [26], but the correlated

responses of the thermal performance curves or the energy metabolism depended on the

intensity of the thermal selection [26,27]. Here, the evolution of knockdown

temperature induced a correlated response on heat knockdown time when it was assayed

at intermediate temperatures (36 and 37 ºC), but not at less or more extreme assayed

temperatures (35 and 38ºC). These findings can be explained because stress tolerance at

35ºC should depend on the physiological status of the organism during the thermal

assay (e.g., availability of energy resources) rather than only heat tolerance, whereas

heat tolerance at 38ºC could be constrained to physical properties of ectotherms (e.g.,

protein denaturation, membrane permeability). A previous study compared *D.*

subobscura populations distributed along a latitudinal gradient and found a clinal

pattern for heat tolerance only for flies assayed in static assays (specifically at 38ºC),

but this clinal pattern was not detected using ramping assays [40]. The difference

between both studies could be explained by the number of generations under thermal

selection, which could result in a difference in the evolutionary response of heat

tolerance. According to Begon [49], *D. subobscura* has between 4 to 6 generations per

year. Thus, it is feasible to estimate almost 125 generations since the *D. subobscura*

population studied by Castañeda et al. [40] was introduced in Chile, whereas the present

artificial selection experiment lasted 16 generations. Anyway, beyond these results from

specific thermal assays, these findings support the idea that (1) the use of a single static

temperature would miss genetic or phenotypic effects on heat tolerance, and (2)

unifying several knockdown time estimates into a single approach (TDT curves) should

be necessary to elucidate genetic and phenotypic patterns of heat tolerance in

ectotherms [39,50].

TDT curves evolved in response to the selection of heat tolerance in *D.*

subobscura. TDT curves revealed that fast- and slow-ramping selected lines evolved

higher CT_{max} than control lines ($\Delta CT_{max} = 0.49$ ºC). This differential CT_{max} value is

slightly lower than population differences (0.9ºC) observed between the lowest- and

highest-latitude populations (~8 latitudinal degrees) of *D. subobscura* studied by

Castañeda et al. (2015), and even lower than the CT_{max} variation reported among

Drosophila species [51,52]. On the other hand, despite CT_{max} and z (i.e., thermal

sensitivity) are phenotypically correlated (see 40,53), the evolutionary increase in CT_{max}

was not associated with a correlated response on thermal sensitivity (z). This result

suggests that both thermal parameters are not genetically constrained, but further

evidence from quantitative genetic studies is needed to evaluate the genetic correlation

between CT_{max} and z. A caveat for this finding could be related to the fact that thermal

selection on heat tolerance was performed by 16 generations followed by 7 generations

of relaxed selection (i.e., no selection). However, previous evidence indicates that

differences in heat tolerance between control and selected lines were consistent between

generations 16 and 25 [26]. Passananti et al. [54] also reported that phenotypic values

did not change after 35 generations of relaxed selection in desiccation-selected

populations of *D. melanogaster*.

According to our expectation, flies selected for higher heat tolerance using slow

ramping rate protocols should exhibit greater desiccation and starvation resistance than

flies selected using fast-ramping selection protocols (see Santos et al. [33]). However,

both desiccation resistance as well as starvation resistance evolved in a context-

dependent manner. For instance, females evolved higher desiccation resistance in the

slow-ramping selected lines, whereas males showed no correlated response. On the

other hand, males evolved for a higher starvation resistance in the slow-ramping

selected lines, whereas females evolved for a lower starvation resistance regardless of

the thermal intensity selection. Differential evolutionary responses between sexes could

be explained because heat thermal selection was only performed on females, which

could have exacerbated the evolutionary responses of female flies. However, previous

studies performing artificial selection on exaggerated male traits found fitness

consequences in females [55]. Then, dimorphic correlated responses between females

and males can be explained by sexually antagonistic selection on genetically correlated

traits [56,57]. Kwan et al. [58] reported that desiccation-selected females evolved for a

higher desiccation resistance than males (see also 59), which is explained because males

lose weight, water, and metabolites at a faster rate than female flies. Indeed, sexual

dimorphism in stress resistance traits has been mainly explained by differences in

cuticular composition, resource storage, and energy conservation between sexes [60,61].

However, here the energy content was not measured in the different control and selected

lines, which could have provided additional information about the evolutionary

response in metabolite storage. However, body mass and metabolic rate were similar

between control and selected lines [27], suggesting that neither difference in resource

storage nor energy conservation explain sex-dependent correlated response for stress

resistance traits. However, direct evaluation of the underlying mechanisms related to

desiccation and starvation resistance should be explored to provide a better idea of the

physiological basis of the evolution of stress resistance traits.

In conclusion, heat tolerance evolution induced evolutionary responses in other

stress resistance traits, which could be explained by pleiotropic effects or linkage

disequilibrium among evaluated traits. However, further evidence is needed (e.g.,

quantitative genetic or genome-wide analysis studies) to elucidate the genetic basis of

the cross-tolerance evolution in *D. subobscura*. In addition, this study provides evidence

of rapid evolutionary responses in fruit flies mediated by thermal selection, even the

evolutionary outcomes depend on the intensity of the thermal stress as has been reported

by Mesas & Castañeda [27]. Interestingly, insect species can evolve in response to

selection for higher thermal resistance, which should mean an adaptive advantage in the

global warming context. However, it is necessary to know if these evolutionary

responses will be fast enough to adjust to the accelerated rate of climate change.

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Table 1. Mixed linear effect model for the knockdown time of *Drosophila subobscura*

assayed in four static temperature assays. For simplicity, results for the random effect

(replicate lines) are not shown because they were not statistically significant (see

Materials and Methods). Significant P-values (< 0.05) are indicated in boldface type.

Knockdown time	Selection	Sex	Selection × Sex
Static assay at 35ºC	$F_{3,170} = 0.62$ *P*-value = 0.60	$F_{1,170} = 8.64$ ***P*-value = 0.004**	$F_{3,170} = 0.64$ *P*-value = 0.59
Static assay at 36ºC	$F_{3,232} = 9.86$ ***P*-value = 3.8×10⁻⁶**	$F_{1,232} = 2.65$ *P*-value = 0.10	$F_{3,232} = 0.74$ *P*-value = 0.53
Static assay at 37ºC	$F_{3,222} = 18.39$ ***P*-value = 1.1×10⁻¹⁰**	$F_{1,222} = 0.001$ *P*-value = 0.97	$F_{3,222} = 2.05$ *P*-value = 0.11
Static assay at 38ºC	$F_{3,224} = 1.93$ *P*-value = 0.13	$F_{1,224} = 4.63$ ***P*-value = 0.032**	$F_{3,224} = 2.44$ *P*-value = 0.07

609   **Table 2**. Summary of the correlated responses of different stress resistance traits to

610   selection on heat tolerance in *D. subobscura*. Note: ↑ symbol indicates an increased

611   resistance, and ↓ symbol indicates a decreased resistance.

Trait	Female response to heat tolerance selection	Male response to heat tolerance selection
Knockdown time at 35 ºC	No correlated response	No correlated response
Knockdown time at 36 ºC	↑ fast-ramping selection ↑ slow-ramping selection	↑ fast-ramping selection ↑ slow-ramping selection
Knockdown time at 37 ºC	↑ fast-ramping selection ↑ slow-ramping selection	↑ fast-ramping selection ↑ slow-ramping selection
Knockdown time at 38 ºC	No correlated response	No correlated response
CT_{max}	↑ fast-ramping selection ↑ slow-ramping selection	↑ fast-ramping selection ↑ slow-ramping selection
Thermal sensitivity (z)	No correlated response	No correlated response
Desiccation resistance	↑ slow-ramping selection	No correlated response
Starvation resistance	↓ fast-ramping selection ↓ slow-ramping selection	↑ slow-ramping selection

Figure 1. Thermal-induced mortality in *Drosophila subobscura* flies assayed at four

static temperatures. Left panels show the heat knockdown time of slow-ramping control

(solid black line), fast-ramping control (dashed black line), slow-ramping selection (red

line), and fast-ramping selection lines (blue lines). Right panels show the heat

knockdown time of female (purple line) and male flies (green line). The dotted lines

indicate the median knockdown time for each selection protocol (left panels) and sex

(right panels).

Figure 2. (A) Thermal death curves for control (solid and dash black lines) and selected

(red and blue lines) lines for increasing heat tolerance in *Drosophila subobscura*.

Symbols represent the average knockdown time at the different assayed temperatures.

(B) Relationship between CT_{max} and z for slow-ramping control (solid black line), fast-

ramping control (dashed black line), slow-ramping selection (red line), and fast-ramping

selection lines (blue lines). Each symbol represents the average value for each replicated

population and the polygons represent the space that occupies each selection protocol in

the thermal tolerance landscape.

Figure 3. Desiccation survival curves of (A) females and (B) males of control (black

line), slow-ramping selection (red line), and fast-ramping selection lines (blue lines) of

Drosophila subobscura. Dashed lines indicate the median mortality time for each

selection protocol (pooled replicated cages).

Figure 4. Starvation survival curves of (A) females and (B) males of control (black

line), slow-ramping selection (red line), and fast-ramping selection lines (blue lines) of

Drosophila subobscura. Dashed lines indicate the median mortality time for each

selection protocol (pooled replicated cages).

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