Microbiome-mediated resilience and cross-generational consequences in male *Drosophila*

exposed to combined environmental stressors

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Abstract

Environmental stressors like heat extremes and pesticide exposure can significantly threaten

insect reproduction, yet the interplay of these stressors and the potential mitigating role of the

gut microbiome remain poorly understood, particularly across generations. This study

investigated the interactive effects of acute heat stress and sublethal imidacloprid exposure on

male *Drosophila melanogaster* reproductive success and the subsequent fitness of their

offspring. We manipulated the gut microbiome of male flies (germ-free or colonized with one

or five bacterial species) and subjected them to individual or combined stress. Our findings

reveal that combined stress synergistically impairs male fitness traits, an effect partially

buffered by higher microbiome diversity. We further demonstrate cross-generational

consequences, with paternal stress exposure also impacting offspring fitness. Our results

highlight the crucial role of the gut microbiome in mediating resilience to environmental stress

and underscore the importance of considering multi-stressor and intergenerational effects in

ecological risk assessments.

Introduction

The increasing prevalence of human-induced stressors poses a significant challenge to global

biodiversity (Navarro-Ortega *et al.* 2015; Piggott *et al.* 2015b, a; Przeslawski *et al.* 2015;

Segner *et al.* 2014), with climate change and pesticide being key drivers of biodiversity loss

and their interaction presenting unique ecological risks (Beketov *et al.* 2013; Heino *et al.* 2009;

Stehle & Schulz 2015). Rising temperatures are projected to intensify pesticide use due to

intensified pest outbreaks (Deutsch *et al.* 2018), while simultaneously altering the response of

ectotherms to chemical exposure (Fournier-Level *et al.* 2016; Hooper *et al.* 2013; Noyes *et al.*

2009). For ectotherms, which lack internal temperature regulation (Deutsch *et al.* 2008;

Paaijmans *et al.* 2013), warming elevates metabolic rates and feeding activity (potentially

increasing pesticide uptake), leading to energetic trade-offs between detoxification and

essential functions like growth or reproduction (Jutfelt *et al.* 2021; Pörtner *et al.* 2017).

While the individual effects of temperature and pesticides are relatively well-documented

(Dougherty *et al.* 2024; Wan *et al.* 2025), their combined impacts remain poorly resolved but

have shown variable outcomes. Studies report additive (Arambourou & Stoks 2015),

antagonistic (Meng *et al.* 2022), or synergistic (Wang et al., 2019) interactions, with synergism

being most concerning for non-target species as their combined harm exceeds the sum of

individual effects (Folt *et al.* 1999; Siviter *et al.* 2021; Verheyen & Stoks 2019, 2023). Such

synergisms may arise from physiological trade-offs, such as heat stress diverting resources

from detoxification (Dai *et al.* 2023) combined with a pesticide-induced antioxidant depletion,

crucial for thermal resilience (Silva *et al.* 2025). This dual depletion could disproportionately

harm gonads and gametes that are particularly prone to oxidative stress due to their high cell

proliferation, metabolic rate and generation of reactive oxygen species (Simmons *et al.* 2018).

By eroding reproductive resilience, synergisms threaten to accelerate biodiversity loss in ways

that single stressors would not (Shahid *et al.* 2024).

Beyond direct physiological impacts, host-associated microbial communities

(microbiomes) are increasingly recognized as mediators for environmental stress tolerance

(Feldhaar 2011; Osborne *et al.* 2023; Sepulveda & Moeller 2020; Shokal *et al.* 2016).

Commensal microbes can enhance host thermal performance (Renoz *et al.* 2019; Sepulveda &

Moeller 2020), either as obligate or facultative symbionts (Dunbar *et al.* 2007; Gruntenko *et*

al. 2017; Montllor *et al.* 2002; Russell & Moran 2006; Zhang *et al.* 2008), and a healthy

microbiome can bolster insect resistance to insecticides through direct pesticide metabolism or

by inducing the expression of host detoxification genes (Cheng *et al.* 2017; Jones *et al.* 2015;

Kikuchi *et al.* 2012; Pang *et al.* 2018). Despite progress in studying individual stressors, how

microbiomes modulate *combined* effects remains largely unknown, but microbiome disruption

by one stressor could amplify susceptibility to another, potentially explaining observed

synergisms (Karimzadeh *et al.* 2020; Mao *et al.* 2019; Zhang *et al.* 2008; Zhang, Cai, *et al.*

2021).

Another critical knowledge gap concerns stress effects on male reproduction. While

much research focuses on acute toxicity or sterility thresholds (De França *et al.* 2017; Desneux

et al. 2007; Walsh *et al.* 2014; Zwoinska *et al.* 2020), sublethal exposures can have significant

fitness consequences. Sublethal effects on female reproductive function are relatively well-

characterized, the studies on males are lagging behind but have already revealed that male

fertility can be more vulnerable than female fecundity, at least to heat stress (Iossa 2019; Sales

et al. 2018; Zwoinska *et al.* 2020). Heat and pesticides can impair spermatogenesis, sperm

DNA integrity, and overall ejaculate quality (Aulsebrook *et al.* 2020; Dougherty *et al.* 2024;

Walsh *et al.* 2019), key determinants fertlization success, particularly under competitive

conditions in promiscuous species (Fitzpatrick & Lüpold 2014; Parker & Pizzari 2010; Pizzari

& Parker 2009; Simmons & Fitzpatrick 2012).

Sperm damage can also extend the environmental stress effects across generations

through epigenetic modifications or sperm-borne small RNAs (Bonduriansky *et al.* 2012;

Morgan & Watkins 2019), affecting population stability and evolution (Aulsebrook *et al.* 2020;

Crean & Immler 2021). While parental exposure to combined thermal and chemical stress has

been shown to reduce offspring performance in some species (DeCourten & Brander 2017;

Fathy 2024), other studies find no clear effects (Massot *et al.* 2021; Meng *et al.* 2022) or even

reduced offspring vulnerability (Tran *et al.* 2018), indicating interspecific variation due to

stressor intensity (including the thermal sensitivity of pesticides themselves), species-specific

acclimation, or compensatory maternal provisioning. Understanding these cross-generational

impacts is crucial for predicting long-term ecological consequences and evolutionary

adaptation potential.

To address these knowledge gaps, we investigated the interactive effects of acute heat

stress and sublethal pesticide exposure on the reproductive fitness of male *D. melanogaster*,

focusing on microbiome mediation and cross-generational consequences. We combined

sublethal acute heat stress (4 hours at 36°C), previously shown to negatively affect testicular

function and the fertilizing capacity of sperm (Meena *et al.* 2024a, b), with exposure to

imidacloprid, a widely used systemic insecticide targeting nicotinic acetylcholine receptors

(nAChRs) in the central nervous system (Ihara *et al.* 2017). Sublethal imidacloprid exposure is

known to affect various aspects of insect physiology and fitness (De França *et al.* 2017; He *et*

al. 2011; Kang *et al.* 2018; Li *et al.* 2018; Xiao *et al.* 2016; Zhang *et al.* 2021b; Zhou *et al.*

2017). To isolate the role of the microbiome, we compared germ-free (axenic) males with

males associated with defined bacterial communities: mono-association of *Acetobacter*

tropicalis or *Lactobacillus brevis*, or a five-species consortium of *Acetobacter* and

Lactobacillus species that are common in *Drosophila* (Broderick & Lemaitre 2012; Gould *et*

al. 2018; Newell & Douglas 2014; Ridley *et al.* 2013). This gnotobiotic approach permitted

precise assessment of microbial contributions to stress tolerance. Furthermore, we assessed the

cross-generational consequences of paternal stress exposure on offspring fitness, testing if the

father's microbiome status influenced these effects while minimizing bacterial transmission to

offspring to focus on direct paternal effects (Marshall *et al.* 2010; Moore *et al.* 2019; Mousseau

et al. 2009).

Based on the evidence outlined above, we tested the following five predictions: (1)

Combined sublethal heat and imidacloprid exposure will synergistically reduce male

reproductive fitness. (2) Gut microbes will partially mitigate the negative impacts of individual

and combined stressors on male reproductive fitness compared to germ-free males. (3)

Different bacterial compositions will vary in their protective capacity, with the complex

community offering greater resilience than either mono-association. (4) Paternal exposure to

individual and combined stressors will negatively impact offspring fitness (cross-generational

effects), with potential synergistic amplification. (5) The paternal microbiome composition will

influence the magnitude of these cross-generational effects.

Material and Methods

Detailed methods are available in the supplementary information. The following is a concise

description of the experimental procedures.

Experimental populations

We used an outbred *D. melanogaster* (LH_m wild-type) population maintained at 25°C, 60%

humidity, and a 12h:12h light:dark cycle. To generate axenic (germ-free) focal flies, eggs

collected within 6h of oviposition were dechorionated using bleach and ethanol washes, then

transferred to sterile glass vials containing autoclaved standard fly food supplemented with

ampicillin, kanamycin, erythromycin, and tetracycline. Axenic status of flies was confirmed

by plating homogenates on LB and MRS agar and by PCR for bacterial DNA using universal

16S rRNA primers.

Bacterial cultures and gnotobiotic associations

Axenic males were associated with defined gut microbiota isolated from wild-type flies

(Obadia *et al.* 2017): mono-associations of *Acetobacter tropicalis* (*At*) or *Lactobacillus brevis*

(*Lb*), or a five-species community (*A. tropicalis*, *A. orientalis*, *A. pasteurianus*, *L. plantarum*,

L. brevis). Bacterial strains were cultured overnight at 30°C in appropriate media (MRS +

mannitol and MRS broth), centrifuged, and resuspended in sterile phosphate-buffered saline

(PBS) to a concentration of 10^8 cells/mL (Koyle *et al.* 2016; Newell & Douglas 2014).

Sterile food vials were inoculated with 50μL of bacterial suspension (approx. 5×10^6 CFUs,

with equal representation in the five-species consortium) (Gould *et al.* 2018; Newell & Douglas

2014). Ten 1-day-old axenic males were added to each vial and transferred to fresh inoculated

vials every 48h for 4d to ensure stable colonization. Successful colonization was confirmed by

plating homogenates and checking for characteristic colony morphologies.

Stress treatments

After 4d of colonization, males were transferred to sterile vials and subjected to a fully factorial

design of pesticide and heat stress. Half of the males in each microbial group were exposed for

18h to food containing 1ppm imidacloprid, a concentration low enough to avoid immediate

lethality while inducing sublethal effects on behavior, reproduction, and physiology

(Charpentier *et al.* 2014; Frantzios *et al.* 2008; Martelli *et al.* 2020). Subsequently, half of the

males from each microbiome and pesticide treatment were exposed to acute heat stress at 36°C

for 4 hours in vials containing 1% agar to prevent dehydration, while the remaining males were

kept at 24.5°C as thermal controls. All males were then allowed to recover overnight in

standard food vials under standard conditions.

Hatching success and fertility

The day after stress treatments, individual experimental males were mated with virgin standard

females reared under axenic conditions. Following mating, females laid eggs for 24h, and 30h

later, oviposition vials were frozen. Hatching success (proportion of hatched eggs) and male-

mediated fecundity (total number of larvae) were then quantified. This assay was performed in

two blocks with 25 males per treatment combination (i.e., total 800 males).

Sperm competitiveness

Sperm competitiveness was assessed using a similar experimental design. Standard females were pre-mated with competitor males ubiquitously expressing green fluorescent protein (GFP) (Lüpold *et al.* 2012, 2020) 2d before mating with the experimental males. Matings events were recorded, and before isolating remated females to determine offspring paternity (focal vs. competitor) by GFP fluorescence to calculate P_2 (proportion of offspring sired by the focal male). Non-remating females were excluded. The design included 30 trials per treatment combination in each of two blocks (i.e., total 960 trials).

Bacterial abundance in males

To assess the impact of stress on bacterial load, colony forming units (CFUs) were compared in ten random males per treatment. Surface-sterilized males were homogenized, serially diluted, and plated on MRS media. For groups with both *Acetobacter* and *Lactobacillus*, MRS agar was supplemented with ampicillin or incubated in a CO_2 atmosphere for selective counting. Colony morphologies were used to identify bacterial species, and total species-specific CFUs per fly were calculated (Koyle *et al.* 2016).

Cross-generational effects

To assess cross-generational effects of paternal stress, hatching success and fecundity were quantified in F_1 offspring. From each block, up to 20 freshly hatched larvae from each of 10 randomly selected males per paternal treatment combination were transferred to vials containing sterile food and reared under standard conditions. Two to three days upon eclosion, three virgin F_1 males and females from each lineage were individually mated with axenically reared standard flies of the opposite sex. Hatching success and fecundity were then measured

in these F_1 offspring as for their fathers (above). This experiment involved two independent

blocks of 480 offspring per sex from 160 F_0 males (i.e. total 1,920 mating trials).

Statistical analysis

Data were analyzed in R version 4.4.0 (R Core Ream, 2024), using linear and generalized linear

mixed-effects models (LMMs and GLMMs). Models included microbiome composition,

thermal and pesticide treatments (and their interactions) as fixed effects, and experimental

block as a random effect. Hatching success was analyzed with a quasibinomial GLMM, male-

mediated female fecundity with a zero-inflated truncated Poisson model (glmmTMB; Brooks

et al. 2017), and sperm competitiveness (P_2) with a Tweedie GLMM (glmmTMB). Pairwise

comparisons were performed using the emmeans package (Searle *et al.* 1980).

Bacterial abundance was analyzed using a linear mixed-effects model. Microbiome

community composition in the five-species consortium was analyzed using Hellinger, Bray-

Curtis distances (*vegdist* in vegan; Oksanen *et al.* 2023), and PERMANOVA (*adonis2* in

vegan), with non-metric multidimensional scaling (NMDS) (*metaMDS*) for visualization.

Additionally, relative abundances were compared at the genus level using a binomial GLMM.

Finally, offspring fitness data were analyzed using GLMMs with F_0 treatments and their

interactions as fixed effects, and block and sire ID as random effects. Model performance was

checked using the DHARMa package (Florian 2016).

Results

Hatching success

To assess the combined effects of heat stress, pesticide exposure, and microbiome composition

on male reproductive function, we first investigated fertilization success, estimated as the

proportion of eggs hatched out of all eggs laid by females. A GLM revealed a significant three-

way interaction between microbiome, temperature, and pesticide ($N = 650$, $\chi^2 = 16.07$, $df = 3$,

$p = 0.0011$; Fig. 1A, Supplementary Table S1), highlighting that the combined effects of these

stressors depended on the microbial composition of the focal males. Overall, males associated

with all five bacterial strains exhibited the highest hatching success, followed by *At-* and *Lb-*

associated males, with axenic males being most severely affected. These general patterns were

also confirmed by the significant two-way interactions of temperature × microbiome ($\chi^2 = $

12.13, $df = 3$, $p = 0.007$) and temperature × pesticide ($\chi^2 = 43.32$, $df = 1$, $p < 0.0001$), as well

as by all main effects (all $\chi^2 \geq 520.76$, $df \geq 3$, $p \leq 0.001$; Supplementary Table S1).

Male-mediated fecundity

Next, we investigated male-mediated fecundity, quantified as the total number of larvae

produced per female. In contrast to hatching success, the three-way interaction was not

significant ($\chi^2 = 0.319$, df = 3, $p = 0.956$; Supplementary Table S2) for this metric and was

removed from the final model. The simplified model revealed significant two-way interactions

between microbiome and temperature ($N = 650$, $\chi^2 = 7.85$, df = 3, $p = 0.049$) and between

temperature and pesticide ($\chi^2 = 5.41$, df = 1, $p = 0.020$; Supplementary Table S2). All main

effects were again significant (all $\chi^2 \geq 5.41$, p ≤ 0.001). The relative differences in fecundity

between males with different microbiome statuses largely mirrored the patterns observed for

hatching success (Fig. 1B).

Sperm competitiveness

Given reports of adverse effects of increased temperatures and pesticide exposure on sperm

quality and function (Chirault *et al.* 2015; Meena *et al.* 2024a; Moreira *et al.* 2022; Roy *et al.*

2017; Sales *et al.* 2018, 2024), we evaluated the combined effects of our treatments on the

proportion of progeny sired by focal males relative to their standard competitors (i.e., P_2).

Although the three-way interaction was not significant ($N = 331$, $\chi^2 = 1.003$, df = 3, $p = 0.800$),

all two-way interactions were (Supplementary Table S3): temperature $\times$ microbiome ($\chi^2 = $

22.92, df = 3, $p < 0.001$), microbiome $\times$ pesticide ($\chi^2 = 11.89$, df = 3, $p < 0.001$), and

temperature $\times$ pesticide ($\chi^2 = 27.33$, df = 1, $p < 0.001$). Similarly, all main effects on P_2 were

significant (all $\chi^2 \geq 472.33$, $p \leq 0.001$). These results indicate strong interdependent effects of

the treatments on sperm competitiveness, with the relative performance across different

microbiome groups again showing similar patterns to those observed for hatching success and

fecundity (Fig. 1C).

Bacterial abundance in males in response to heat stress and pesticide exposure

We also analyzed the effect of heat stress, pesticide exposure and their interactions on the

growth and viability of commensal bacteria inside their host under the different stress

treatments by quantifying their colony forming units in homogenates of focal males

immediately after mating. For total CFU counts, we found a significant three-way interaction

($\chi^2 = 5.06$, df = 2, $p = 0.008$; Supplementary Table S4), suggesting that the bacterial strains

differed in their accumulation patterns in adult flies depending on the combined effects of stress

treatments. Additionally, we documented significant two-way interactions and main effects of

all three factors (all $\chi^2 \geq 42.31$, $p \leq 0.001$), except for the two-way interaction between the two

stressors ($\chi^2 = 2.36$, df = 2, $p = 0.127$). Among these and relative to the control microbiome,

higher temperature had a stronger negative effect on the total number of CFUs than pesticide

exposure (Fig. 2; Supplementary Table S4).

A PERMANOVA controlling for block effects ($F_{1,35} = 0.20$, $p = 0.874$, Supplementary

Table S5) revealed that temperature was also the dominant driver of variation in the relative

abundances of the five bacterial species constituting the consortium, explaining 26.3% of the

variation in community composition ($F_{1,35} = 13.88$, $p = 0.0001$; Supplementary Table S5). In

contrast, the main effect of pesticide was not statistically significant (2.2% of variation, $F_{1,35} =$

1.16, $p = 0.314$), and the temperature × pesticide interaction showed a marginal effect (4.8%

of variation, $F_{1,35} = 2.55$, $p = 0.068$). NMDS based on Bray-Curtis dissimilarities provided a

visual representation of community shifts across treatments. The NMDS ordination (Fig. 3A)

indicated that the first axis (NMDS1) predominantly tracked the temperature gradient, while

the second axis (NMDS2) aligned more, but only weakly, with pesticide exposure. Overlaying

species vectors revealed notable differences in species associations (all $R^2 \geq 0.54$, $p \leq 0.0001$),

in that both *Lactobacillus* species showed positive (≥ 0.68), and all *Acetobacter* exhibited

negative ($\leq$ -0.38), loadings on NMDS1 (Supplementary Table S6), suggesting an increase in

the relative abundance of *Acetobacter* in the high-temperature regimes. By contrast, loadings

on NMDS2 were negative for *A. tropicalis* (-0.92) and *L. brevis* (-0.44) but positive for all

remaining species (≥ 0.56). This axis tended to be biased toward negative values in the absence

of imidacloprid, but more ambiguous in its presence.

Finally, in a binomial GLMM focusing only on the relative abundances of acetic acid

versus lactic acid bacteria, where the three *Acetobacter* species should theoretically constitute

60% of the total CFUs among the five species, temperature and pesticide presence interacted

significantly ($N = 40$, $z = 2.15$, $p = 0.032$). Specifically, the relative representation of

Acetobacter was increased to around 66% under heat stress ($z = 2.84$, $p = 0.013$), whereas

pesticide exposure reduced its representation ($z = $ -2.32, $p = 0.021$), although only at the benign

temperature (Fig. 3B).

Cross-generational effects on offspring fitness

Finally, we investigated how paternal stress exposure affects the next generation by measuring

the hatching success and fecundity of F_1 offspring produced by F_0 males from each treatment

group.

We found a significant interactive effect between paternal temperature and pesticide

treatments on the hatching success of both male ($N = 726$, $\chi^2 = 19.39$, df = 1, $p < 0.001$;

Supplementary Table S7) and female offspring ($N = 750$, $\chi^2 = 10.084$, df = 1, $p < 0.001$;

Supplementary Table S8), indicating that the effects of paternal stress exposure were

transmitted to the next generation. However, the paternal microbiome did not significantly

influence offspring hatching success ($\chi^2 \leq 4.76$, df = 3, $p \geq 0.19$). The interactive effect of

paternal temperature and pesticide exposure was not significant for the fecundity induced by

sons ($\chi^2 = 0.36$, df = 1, $p = 0.55$; Supplementary Table S9), but the same interaction showed

significant effect on fecundity of F_1 daughters ($N = 750$, $\chi^2 = 3.990$, df = 1, $p = 0.006$;

Supplementary Table S10). There was also a non-significant trend for a main effect of paternal

microbiome composition on offspring fecundity in daughters ($\chi^2 = 7.26$, df = 3, $p = 0.06$;

Supplementary Table S10).

Discussion

We investigated the role of the gut microbiome in modulating male reproductive success in *D.*

melanogaster under individual and combined exposure to acute heat stress and the pesticide

imidacloprid. Our results confirm and extend previous work demonstrating the detrimental

effects of sublethal temperatures (Canal Domenech & Fricke 2022; David *et al.* 2005; Fasolo

& Krebs 2004; Gandara & Drummond-Barbosa 2022, 2023; Meena *et al.* 2024a; Pilakouta &

Baillet 2022; Sales *et al.* 2024; Walsh *et al.* 2019) or imidacloprid (Charpentier *et al.* 2014;

Xiao *et al.* 2016; Zhang *et al.* 2021b; Zhou *et al.* 2017) on reproductive functions. Importantly,

our study revealed both the combined effects of these stressors and the critical role of the

microbiome in mediating the response of stressed males, highlighting the importance of the gut

microbiome in mitigating fitness losses. *Acetobacter* generally provided stronger protection

than *Lactobacillus*, especially in males with a complex microbial community. Furthermore, we

demonstrated that paternal stress exposure imposes fitness costs on the next generation,

although these cross-generational effects were not significantly mediated by the paternal

microbiome under our experimental conditions designed to minimize direct microbial

transmission.

Interactive effects of combined stressors on male reproduction

Our study revealed that initial exposure to imidacloprid followed by heat shock reduced male

reproductive functions to a greater extent than either stressor alone, consistent with previous

studies indicating complex, often order-dependent interactions between thermal stress and

pesticide toxicity (Ahmed *et al.* 2023; Deng *et al.* 2016; Meng *et al.* 2022; Ricupero *et al.* 2020;

Wang *et al.* 2021). While heat stress has been shown to increase the tolerance to subsequent

insecticide exposure in diverse insect pests (Cao *et al.* 2019; Ge *et al.* 2013; Gu *et al.* 2010),

the reverse order of stress exposure can have opposing effects (Delnat *et al.* 2019; Wang *et al.*

2021), emphasizing the importance of stress sequence in cross-protection.

Pre-exposure to insecticides can also decrease heat stress tolerance, suggesting that

warmer temperatures may exacerbate insecticide toxicity depending on the exposure sequence.

Increased imidacloprid toxicity at higher temperatures has been documented in mayflies

(Macaulay *et al.* 2020), earthworms and collembolans (Bandeira *et al.* 2020), and the terrestrial

ectotherm *Hypogastrura viatica* (Silva *et al.* 2023). Our study supports these findings, showing

decreased male reproductive success when pesticide exposure preceded heat stress. These

multi-stressor studies highlight the complex temperature-toxicity interplay, which can be

positive or negative depending on the insecticide mode of action, exposure route, and insect

species. Therefore, the sequence of exposure must be carefully considered when evaluating

combined stressor effects on insect performance.

The mechanisms underlying these sequence-dependent interactions likely involve

intricate physiological adjustments. Exposure to one stressor might compromise pathways

needed to cope with the subsequent stressor (lack of cross-tolerance) or trigger shared signaling

pathways that amplify susceptibility (negative cross-talk). Resource allocation trade-offs are

also probable (Sokolova 2013), where coping with pesticide toxicity may deplete energy

reserves or specific molecules (e.g., antioxidants, chaperones) needed for an effective heat

stress response. Generally, stressful environments can alter resource allocation among essential

processes like growth, reproduction or immune defense to optimize fitness outcomes

(Kooijman 2000). As such, elevated temperature may increase somatic maintenance costs

(Verberk *et al.* 2016), potentially reducing resources for defense and repair (Hallman & Brooks

2015).

While the precise mechanisms underlying increased toxicity at high temperatures remain

unclear, they may overlap with those explaining the increased toxicity of organophosphate

pesticides at higher mean temperatures (Noyes *et al.* 2009; Noyes & Lema 2015). Increased

temperatures can enhance the activity of detoxification enzymes like cytochrome P450s (Wang

et al. 2021), accelerating pesticide breakdown (Ahmad 2007). Increased uptake of chemicals

at higher temperatures (Holmstrup *et al.* 2010) has been shown to increase membrane

permeability (Noyes & Lema 2015) or inhibit growth (Gardner *et al.* 2011), possibly due to

higher basal metabolism (Hooper *et al.* 2013). Stressful conditions can promote the

accumulation of reactive oxygen species (ROS) due to reduced respiration and increased water

loss, thereby negatively affecting development and reproduction (Dampc *et al.* 2021). Low

doses of imidacloprid, for example, can cause ROS formation and metabolic impairment in *D.*

melanogaster (Martelli *et al.* 2020). Both pesticide tolerance (Bagchi *et al.* 1996) and heat

stress (Neven 2000) are also associated with overexpression of heat-shock proteins. In

honeybees, Hsp70 and Hsp90 are upregulated in response to both thermal stress and

imidacloprid (Manzi *et al.* 2020). Such chaperone activation could also protect *D.*

melanogaster males against combined stressors. If so, the observed fitness loss under both

stressors might at least in part be attributable to the costs associated with enhanced Hsp

expression (Hoekstra *et al.* 2013; Li *et al.* 2015), which may become overwhelming under

combined stress.

Microbiome as a modulator of stress resilience

A key finding of our study was the significant role of the gut microbiome in mitigating the

detrimental reproductive consequences of heat and pesticide stress. Axenic males consistently

performed worse than colonized males across all measured fitness components, highlighting

the baseline importance of the microbiome for reproduction and its crucial role under stress.

The reduced fitness of axenic males under combined stress suggests an impaired ability to

metabolize and excrete imidacloprid, potentially leading to higher internal toxin loads and

increased vulnerability to subsequent heat stress.

Interestingly, the degree of protection depended on microbial composition. While both

Lactobacillus brevis and *Acetobacter tropicalis* mono-associations offered benefits over the

axenic state, the five-species community consistently provided the greatest resilience,

underscoring the potential importance of microbial diversity and inter-species interactions for

robust host function (Coyte *et al.* 2015; Freilich *et al.* 2011; Levy & Borenstein 2013;

Magnúsdóttir *et al.* 2017; Noecker *et al.* 2019; Zelezniak *et al.* 2015). Mono-associations might

lack the metabolic versatility or synergistic cross-feeding capabilities present in more complex

consortia, limiting their ability to buffer the host against multiple stressors.

Our results partially contrast with Daisley *et al.* (2017), who reported that *Lactobacillus*

plantarum (Lp39) supplementation rescued *D. melanogaster* from harmful imidacloprid

effects, accompanied by increased *Acetobacter* and *Lactobacillus* abundance. We did not

observe such a strong rescue with *L. brevis*, nor an increased abundance of either bacterial

genus. This discrepancy could stem from strain-specific functions, similar to opposing effects

on chlorpyrifos (CP) toxicity between *L. plantarum* ISO and *Lactobacillus ATCC* in *D.*

melanogaster (Daisley *et al.* 2017), or differences in experimental protocols (e.g., our acute

18h imidacloprid exposure versus Daisley *et al.*'s (2017) continued exposure).

We also observed shifts in the relative abundance of *Acetobacter* and *Lactobacillus*

within the host, aligning with studies showing heat-induced microbiome disruptions (Jaramillo

& Castañeda 2021; Kokou *et al.* 2018; Moghadam *et al.* 2018). *Lactobacillus* appeared more

abundant and less affected by treatments in mono-associations, whereas *Acetobacter* seemed

to be overrepresented in the five-species consortium relative to the expected proportion of 60%.

Generally, we found a higher proportional representation of *Acetobacter* following acute heat

stress, consistent with prior work (Moghadam *et al.* 2018). Beyond Moghadam *et al.*'s (2018)

thermal treatments throughout development, however, our findings demonstrate that such

compositional shifts can occur within hours.

The mechanisms by which the microbiome enhances stress tolerance likely involve

multiple pathways. Beyond direct detoxification (Cheng *et al.* 2017; Jones *et al.* 2015; Kikuchi

et al. 2012; Pang *et al.* 2018), gut microbes significantly impact host nutrition and metabolism

(Douglas 2009; Ridley *et al.* 2012), which are intrinsically linked to thermal tolerance in

ectotherms (Henry *et al.* 2020; Moeller *et al.* 2020; Moghadam *et al.* 2018; Semsar-Kazerouni

et al. 2020). In *D. melanogaster*, the gut microbiota influences nutrient allocation and the

thermo-protectant trehalose (Overgaard *et al.* 2007; Ridley *et al.* 2012; Schwasinger-Schmidt

et al. 2012). It can also modulate host immune responses and potentially Hsp expression in the

gut epithelium (Arnal & Lalles 2016; Liu *et al.* 2014). Given the critical role of Hsps in

mitigating thermal stress in *D. melanogaster* (Calabria *et al.* 2012; Sørensen *et al.* 2003), and

their rapid induction after heat exposure (Hoekstra *et al.* 2013), the microbiota may enhance

heat tolerance by promoting higher Hsp levels. Disrupting the microbiome can alter these

processes, as seen with heat-induced reductions in *Buchnera aphidicola* in pea aphids lowering

heat resistance (Dunbar *et al.* 2007), and temperature-driven microbiome shifts increasing

imidacloprid susceptibility in *Nilaparvata lugens* (Zhang *et al.* 2021a).

Cross-generational impacts of parental stress

We found clear evidence for cross-generational fitness costs of paternal stress exposure, with

reduced hatching success and fecundity in offspring of stressed fathers. Cross-generational

effects can either increase or decrease offspring vulnerability to stressors (Brausch & Salice

2011; Kim *et al.* 2014; Pölkki *et al.* 2012; Reátegui-Zirena *et al.* 2017; Schultz *et al.* 2016).

Our results corroborate studies reporting detrimental cross- or transgenerational effects of

paternal heat stress (Ferrer *et al.* 2013; Guillaume *et al.* 2016; Shama *et al.* 2014; Walsh *et al.*

2014) or toxicant exposure (Bhandari *et al.* 2015; Kimberly & Salice 2015; Schultz *et al.* 2016;

Yu & Liao 2016), possibly through epigenetic processes (Schultz *et al.* 2016). The observed

synergism between paternal heat and pesticide exposure in offspring fitness underscores the

potential for long-lasting consequences of multi-stressor events.

Offspring from stressed fathers exhibited reduced fecundity and hatching success,

indicating that paternal exposure does not buffer against these environmental stressors. Our

findings support the view that cross-generational effects of stress are often non-adaptive or

costly for offspring (Uller *et al.* 2013), highlighting the potential for cumulative fitness declines

across generations in populations facing recurrent multi-stressor events.

Intriguingly, the paternal microbiome did not significantly mediate these cross-

generational effects in our study. This could be attributable to our experimental design, which

deliberately minimized vertical transmission of microbes by using axenic mothers and

transferring these and their offspring to sterile food vials immediately after mating or hatching,

respectively. This allowed us to isolate direct paternal effects (potentially epigenetic or related

to gamete quality) based on the sire's microbial status. However, we cannot rule out a role for

the paternal microbiome if transmission occurs naturally (e.g., during copulation) (Guilhot *et*

al. 2025), potentially triggering differential maternal effects or microbial deposition on eggs

(direct paternal transmission of microbes to their offspring seems rather unlikely as males have

little control over female oviposition). Future studies explicitly allowing or manipulating

vertical transmission would be needed to explore this.

Conclusions and broader implications

In conclusion, our study demonstrates that acute heat stress and sublethal pesticide exposure

interact, often synergistically, to negatively impact male reproductive fitness in *D.*

melanogaster, with consequences extending to offspring viability and fecundity. Crucially, we

show that the gut microbiome is a key determinant of resilience, offering significant protection

against these stressors, with benefits enhanced by microbial complexity. However, the

microbiome itself is vulnerable to disruption by these same stressors.

Our findings underscore the critical need to consider multi-stressor interactions and the

role of host-associated microbes when assessing the ecological risks posed by climate change

and agrochemical use. The observed negative cross-generational effects further highlight the

potential vulnerability of insect populations, particularly those with depleted or altered

microbiomes. Future research should explore these interactions across diverse species,

environments, and stressor combinations to improve ecological forecasting and develop

strategies for mitigating biodiversity loss in the Anthropocene.

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Figure 1 Effects of varying thermal and pesticide conditions and microbiome types on (A)

hatching success, (B) male-mediated female fecundity, and (C) competitive fertilization

success. Each circle represents the mean of all replicates in that treatment combination with

error bars corresponding to 95% confidence intervals.

Figure 2 Bacterial abundance/colony forming units of different microbial treatments in
response to varying thermal and pesticide conditions. Each circle represents the mean of all
replicates in that treatment combination with error bars corresponding to 95% confidence
intervals.

Figure 3 Bacterial abundances in the five-species consortium in response to thermal and

pesticide treatments. A: Non-metric multidimensional scaling (NMDS) ordination (Bray-

Curtis distance, $k = 4$, stress = 0.046) of microbial community composition across temperature

and pesticide treatments. Shaded convex hulls denote 95% confidence areas for each

temperature × pesticide group, and arrows the direction and strength of species (Hellinger-

transformed) most strongly correlated with the ordination space, as identified by *envfit* (species

abbreviations: Ao = *Acetobacter orientalis*, Ap = *A. pasteuriensis*, At = *A. tropicalis*, Lb =

Lactobacillus brevis, Lp = *L. plantarum*). B: Proportion of acetic acid bacteria in the five-

species consortium in response to heat and pesticide stress. Each circle represents the mean of

all replicates in that treatment combination with error bars corresponding to 95% confidence

intervals.

Sons: **Daughters:**

942   **Figure 4** Fitness consequences of paternal thermal and pesticide treatments on fitness measures

943   in male (A, B) and female (C, D) offspring. Panels A and C depict the proportion of eggs

944   hatched out of total number of eggs fertilized, panels B and D the fecundity either of the sons'

945   mates (B) or of the daughters (D). Each circle represents the mean of all the replicates in that

946   treatment combination with error bars corresponding to 95% confidence intervals.